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<p>(21) International Application Number: PCT/US98/04493</p> <p>(22) International Filing Date: 6 March 1998 (06.03.98)</p> <p>(30) Priority Data:</p> <table border="0"> <tr><td>60/040,162</td><td>7 March 1997 (07.03.97)</td><td>US</td></tr> <tr><td>60/040,333</td><td>7 March 1997 (07.03.97)</td><td>US</td></tr> <tr><td>60/038,621</td><td>7 March 1997 (07.03.97)</td><td>US</td></tr> <tr><td>60/040,161</td><td>7 March 1997 (07.03.97)</td><td>US</td></tr> <tr><td>60/040,626</td><td>7 March 1997 (07.03.97)</td><td>US</td></tr> <tr><td>60/040,334</td><td>7 March 1997 (07.03.97)</td><td>US</td></tr> <tr><td>60/040,336</td><td>7 March 1997 (07.03.97)</td><td>US</td></tr> <tr><td>60/040,163</td><td>7 March 1997 (07.03.97)</td><td>US</td></tr> <tr><td>60/043,580</td><td>11 April 1997 (11.04.97)</td><td>US</td></tr> <tr><td>60/043,568</td><td>11 April 1997 (11.04.97)</td><td>US</td></tr> </table> <p><i>(Continued on the following page)</i></p> <p>(71) Applicant (for all designated States except US): HUMAN GENOME SCIENCES, INC. [US/US]; 9410 Key West Avenue, Rockville, MD 20850 (US).</p> <p>(72) Inventors; and</p> <p>(75) Inventors/Applicants (for US only): RUBEN, Steven, M. [US/US]; 18528 Heritage Hills Drive, Olney, MD 20832 (US). ROSEN, Craig, A. [US/US]; 22400 Rolling Hills Road, Laytonsville, MD 20882 (US). FISCHER, Carrie, L. [US/US]; 5810 Hall Street, Burke, VA 22015 (US). SOPPET, Daniel, R. [US/US]; 15050 Stillfield, Place, Centreville, VA 22020 (US). CARTER, Kenneth, C. [US/US]; 11601 Brandy Hall Lane, North Potomac, MD 20878 (US). BEDNARIK, Daniel, P. [US/US]; 8822 Blue Sea Drive, Columbia, MD 21046 (US). ENDRESS, Gregory, A. [US/US]; 9729 Clagett Farm Drive, Potomac, MD 20854 (US). YU, Guo-Liang [CN/US]; 13524 Straw Bale Lane, Darnestown, MD 20878 (US). NI, Jian [CN/US]; 5502 Manorfield Road, Rockville, MD 20853 (US). FENG, Ping [CN/US]; 4 Relda Court, Gaithersburg, MD 20878 (US). YOUNG, Paul, E. [US/US]; 122 Beckwith Street, Gaithersburg, MD 20878 (US). GREENE, John, M. [US/US]; 872 Diamond Drive, Gaithersburg, MD 20878 (US). FERRIE, Ann, M. [US/US]; 13203 L Astoria Hill Court, Germantown,</p>		60/040,162	7 March 1997 (07.03.97)	US	60/040,333	7 March 1997 (07.03.97)	US	60/038,621	7 March 1997 (07.03.97)	US	60/040,161	7 March 1997 (07.03.97)	US	60/040,626	7 March 1997 (07.03.97)	US	60/040,334	7 March 1997 (07.03.97)	US	60/040,336	7 March 1997 (07.03.97)	US	60/040,163	7 March 1997 (07.03.97)	US	60/043,580	11 April 1997 (11.04.97)	US	60/043,568	11 April 1997 (11.04.97)	US	<p>MD 20874 (US). DUAN, Roxanne [US/US]; 4541 Fairfield Drive, Bethesda, MD 20814 (US). HU, Jing-Shan [CN/US]; 1247 Lakeside Drive #3034, Sunnyvale, CA 94086 (US). FLORENCE, Kimberly, A. [US/US]; 12805 Atlantic Avenue, Rockville, MD 20851 (US). OLSEN, Henrik, S. [DK/US]; 182 Kendrick Place #24, Gaithersburg, MD 20878 (US). EBNER, Reinhard [DE/US]; 9906 Shelburne Terrace #316, Gaithersburg, MD 20878 (US). BREWER, Laurie, A. [US/US]; 14920 Mount Nebo Road, Poolesville, MD 20837 (US). MOORE, Paul, A. [GB/US]; Apartment #104, 1908 Holly Ridge Drive, McLean, VA 22102 (US). SHI, Yanggu [CN/US]; 437 West Side Drive, Gaithersburg, MD 20878 (US). LAFLEUR, David, W. [US/US]; 1615 Q Street, N.W. #807, Washington, DC 20009 (US). LI, Yi [CN/US]; 1247 Lakeside Drive #3034, Sunnyvale, CA 94086 (US). ZENG, Zhizhen [CN/US]; 13950 Saddlevue Drive, Gaithersburg, MD 20878 (US). KYAW, Hla [BU/US]; 520 Sugarbush Circle, Frederick, MD 21703 (US).</p> <p>(74) Agents: BROOKES, Anders, A. et al.; Human Genome Sciences, Inc., 9410 Key West Avenue, Rockville, MD 10850 (US).</p> <p>(81) Designated States: AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE, DK, EE, ES, FI, GB, GE, GH, GM, GW, HU, ID, IL, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, UA, UG, US, UZ, VN, YU, ZW, ARIPO patent (GH, GM, KE, LS, MW, SD, SZ, UG, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, CH, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, ML, MR, NE, SN, TD, TG).</p> <p>Published <i>Without international search report and to be republished upon receipt of that report.</i></p>
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<p>(54) Title: 186 HUMAN SECRETED PROTEINS</p> <p>(57) Abstract</p> <p>The present invention relates to 186 novel human secreted proteins and isolated nucleic acids containing the coding regions of the genes encoding such proteins. Also provided are vectors, host cells, antibodies, and recombinant methods for producing human secreted proteins. The invention further relates to diagnostic and therapeutic methods useful for diagnosing and treating disorders related to these novel human secreted proteins.</p>																																

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186 Human Secreted Proteins

Field of the Invention

This invention relates to newly identified polynucleotides and the polypeptides encoded by these polynucleotides, uses of such polynucleotides and polypeptides, and
5 their production.

Background of the Invention

Unlike bacterium, which exist as a single compartment surrounded by a membrane, human cells and other eucaryotes are subdivided by membranes into many functionally distinct compartments. Each membrane-bounded compartment, or
10 organelle, contains different proteins essential for the function of the organelle. The cell uses "sorting signals," which are amino acid motifs located within the protein, to target proteins to particular cellular organelles.

One type of sorting signal, called a signal sequence, a signal peptide, or a leader sequence, directs a class of proteins to an organelle called the endoplasmic reticulum
15 (ER). The ER separates the membrane-bounded proteins from all other types of proteins. Once localized to the ER, both groups of proteins can be further directed to another organelle called the Golgi apparatus. Here, the Golgi distributes the proteins to vesicles, including secretory vesicles, the cell membrane, lysosomes, and the other organelles.

Proteins targeted to the ER by a signal sequence can be released into the
20 extracellular space as a secreted protein. For example, vesicles containing secreted proteins can fuse with the cell membrane and release their contents into the extracellular space - a process called exocytosis. Exocytosis can occur constitutively or after receipt of a triggering signal. In the latter case, the proteins are stored in secretory vesicles (or
25 secretory granules) until exocytosis is triggered. Similarly, proteins residing on the cell membrane can also be secreted into the extracellular space by proteolytic cleavage of a "linker" holding the protein to the membrane.

Despite the great progress made in recent years, only a small number of genes encoding human secreted proteins have been identified. These secreted proteins include
30 the commercially valuable human insulin, interferon, Factor VIII, human growth hormone, tissue plasminogen activator, and erythropoietin. Thus, in light of the pervasive role of secreted proteins in human physiology, a need exists for identifying and characterizing novel human secreted proteins and the genes that encode them. This knowledge will allow one to detect, to treat, and to prevent medical disorders by using
35 secreted proteins or the genes that encode them.

Summary of the Invention

The present invention relates to novel polynucleotides and the encoded polypeptides. Moreover, the present invention relates to vectors, host cells, antibodies, and recombinant methods for producing the polypeptides and polynucleotides. Also provided are diagnostic methods for detecting disorders related to the polypeptides, and therapeutic methods for treating such disorders. The invention further relates to screening methods for identifying binding partners of the polypeptides.

Detailed Description

Definitions

The following definitions are provided to facilitate understanding of certain terms used throughout this specification.

In the present invention, "isolated" refers to material removed from its original environment (e.g., the natural environment if it is naturally occurring), and thus is altered "by the hand of man" from its natural state. For example, an isolated polynucleotide could be part of a vector or a composition of matter, or could be contained within a cell, and still be "isolated" because that vector, composition of matter, or particular cell is not the original environment of the polynucleotide.

In the present invention, a "secreted" protein refers to those proteins capable of being directed to the ER, secretory vesicles, or the extracellular space as a result of a signal sequence, as well as those proteins released into the extracellular space without necessarily containing a signal sequence. If the secreted protein is released into the extracellular space, the secreted protein can undergo extracellular processing to produce a "mature" protein. Release into the extracellular space can occur by many mechanisms, including exocytosis and proteolytic cleavage.

As used herein, a "polynucleotide" refers to a molecule having a nucleic acid sequence contained in SEQ ID NO:X or the cDNA contained within the clone deposited with the ATCC. For example, the polynucleotide can contain the nucleotide sequence of the full length cDNA sequence, including the 5' and 3' untranslated sequences, the coding region, with or without the signal sequence, the secreted protein coding region, as well as fragments, epitopes, domains, and variants of the nucleic acid sequence. Moreover, as used herein, a "polypeptide" refers to a molecule having the translated amino acid sequence generated from the polynucleotide as broadly defined.

In the present invention, the full length sequence identified as SEQ ID NO:X was often generated by overlapping sequences contained in multiple clones (contig

analysis). A representative clone containing all or most of the sequence for SEQ ID NO:X was deposited with the American Type Culture Collection ("ATCC"). As shown in Table 1, each clone is identified by a cDNA Clone ID (Identifier) and the ATCC Deposit Number. The ATCC is located at 12301 Park Lawn Drive, Rockville, Maryland 20852, USA. The ATCC deposit was made pursuant to the terms of the Budapest Treaty on the international recognition of the deposit of microorganisms for purposes of patent procedure.

A "polynucleotide" of the present invention also includes those polynucleotides capable of hybridizing, under stringent hybridization conditions, to sequences contained in SEQ ID NO:X, the complement thereof, or the cDNA contained within the clone deposited with the ATCC. "Stringent hybridization conditions" refers to an overnight incubation at 42° C in a solution comprising 50% formamide, 5x SSC (750 mM NaCl, 75 mM sodium citrate), 50 mM sodium phosphate (pH 7.6), 5x Denhardt's solution, 10% dextran sulfate, and 20 µg/ml denatured, sheared salmon sperm DNA, followed by washing the filters in 0.1x SSC at about 65°C.

Also contemplated are nucleic acid molecules that hybridize to the polynucleotides of the present invention at lower stringency hybridization conditions. Changes in the stringency of hybridization and signal detection are primarily accomplished through the manipulation of formamide concentration (lower percentages of formamide result in lowered stringency); salt conditions, or temperature. For example, lower stringency conditions include an overnight incubation at 37°C in a solution comprising 6X SSPE (20X SSPE = 3M NaCl; 0.2M NaH₂PO₄; 0.02M EDTA, pH 7.4), 0.5% SDS, 30% formamide, 100 µg/ml salmon sperm blocking DNA; followed by washes at 50°C with 1XSSPE, 0.1% SDS. In addition, to achieve even lower stringency, washes performed following stringent hybridization can be done at higher salt concentrations (e.g. 5X SSC).

Note that variations in the above conditions may be accomplished through the inclusion and/or substitution of alternate blocking reagents used to suppress background in hybridization experiments. Typical blocking reagents include Denhardt's reagent, BLOTTO, heparin, denatured salmon sperm DNA, and commercially available proprietary formulations. The inclusion of specific blocking reagents may require modification of the hybridization conditions described above, due to problems with compatibility.

Of course, a polynucleotide which hybridizes only to polyA+ sequences (such as any 3' terminal polyA+ tract of a cDNA shown in the sequence listing), or to a

complementary stretch of T (or U) residues, would not be included in the definition of "polynucleotide," since such a polynucleotide would hybridize to any nucleic acid molecule containing a poly (A) stretch or the complement thereof (e.g., practically any double-stranded cDNA clone).

5 The polynucleotide of the present invention can be composed of any polyribonucleotide or polydeoxribonucleotide, which may be unmodified RNA or DNA or modified RNA or DNA. For example, polynucleotides can be composed of single- and double-stranded DNA, DNA that is a mixture of single- and double-stranded regions, single- and double-stranded RNA, and RNA that is mixture of single- and
10 double-stranded regions, hybrid molecules comprising DNA and RNA that may be single-stranded or, more typically, double-stranded or a mixture of single- and double-stranded regions. In addition, the polynucleotide can be composed of triple-stranded regions comprising RNA or DNA or both RNA and DNA. A polynucleotide may also contain one or more modified bases or DNA or RNA backbones modified for stability
15 or for other reasons. "Modified" bases include, for example, tritylated bases and unusual bases such as inosine. A variety of modifications can be made to DNA and RNA; thus, "polynucleotide" embraces chemically, enzymatically, or metabolically modified forms.

 The polypeptide of the present invention can be composed of amino acids joined
20 to each other by peptide bonds or modified peptide bonds, i.e., peptide isosteres, and may contain amino acids other than the 20 gene-encoded amino acids. The polypeptides may be modified by either natural processes, such as posttranslational processing, or by chemical modification techniques which are well known in the art. Such modifications are well described in basic texts and in more detailed monographs,
25 as well as in a voluminous research literature. Modifications can occur anywhere in a polypeptide, including the peptide backbone, the amino acid side-chains and the amino or carboxyl termini. It will be appreciated that the same type of modification may be present in the same or varying degrees at several sites in a given polypeptide. Also, a given polypeptide may contain many types of modifications. Polypeptides may be
30 branched, for example, as a result of ubiquitination, and they may be cyclic, with or without branching. Cyclic, branched, and branched cyclic polypeptides may result from posttranslation natural processes or may be made by synthetic methods. Modifications include acetylation, acylation, ADP-ribosylation, amidation, covalent attachment of flavin, covalent attachment of a heme moiety, covalent attachment of a
35 nucleotide or nucleotide derivative, covalent attachment of a lipid or lipid derivative, covalent attachment of phosphatidylinositol, cross-linking, cyclization, disulfide bond formation, demethylation, formation of covalent cross-links, formation of cysteine,

formation of pyroglutamate, formylation, gamma-carboxylation, glycosylation, GPI anchor formation, hydroxylation, iodination, methylation, myristoylation, oxidation, pegylation, proteolytic processing, phosphorylation, prenylation, racemization, selenoylation, sulfation, transfer-RNA mediated addition of amino acids to proteins such as arginylation, and ubiquitination. (See, for instance, PROTEINS - STRUCTURE AND MOLECULAR PROPERTIES, 2nd Ed., T. E. Creighton, W. H. Freeman and Company, New York (1993); POSTTRANSLATIONAL COVALENT MODIFICATION OF PROTEINS, B. C. Johnson, Ed., Academic Press, New York, pgs. 1-12 (1983); Seifter et al., Meth Enzymol 182:626-646 (1990); Rattan et al., Ann NY Acad Sci 663:48-62 (1992).)

"SEQ ID NO:X" refers to a polynucleotide sequence while "SEQ ID NO:Y" refers to a polypeptide sequence, both sequences identified by an integer specified in Table 1.

"A polypeptide having biological activity" refers to polypeptides exhibiting activity similar, but not necessarily identical to, an activity of a polypeptide of the present invention, including mature forms, as measured in a particular biological assay, with or without dose dependency. In the case where dose dependency does exist, it need not be identical to that of the polypeptide, but rather substantially similar to the dose-dependence in a given activity as compared to the polypeptide of the present invention (i.e., the candidate polypeptide will exhibit greater activity or not more than about 25-fold less and, preferably, not more than about tenfold less activity, and most preferably, not more than about three-fold less activity relative to the polypeptide of the present invention.)

Polynucleotides and Polypeptides of the Invention

FEATURES OF PROTEIN ENCODED BY GENE NO: 1

This gene is expressed primarily in testes tumor and to a lesser extent in fetal brain.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions which include, but are not limited to, cancer particularly of the testes, and defects of the central nervous system such as seizure and neurodegenerative disorders. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly cancer of the testes and central nervous system,

expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., testes and other reproductive tissue, brain and other tissue of the nervous system, and blood cells, and spleen, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal
5 fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for treatment/diagnosis of testicular cancer and
10 treatment of central nervous system disorders since this gene is primarily expressed in the testes tumor and developing brain.

FEATURES OF PROTEIN ENCODED BY GENE NO: 2

This gene is expressed primarily in cancer tissues, such as breast cancer and
15 Wilm's tumor, and to a lesser extent in fetal tissues.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions which include, but are not limited to, and/or tumors, particularly, those found in the breast, and developmental
20 abnormalities or disorders. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the glandular tissues, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., mammary
25 tissue, and fetal tissue and, cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a
30 sequence shown in SEQ ID NO. 314 as residues: Pro-11 to Thr-18, Leu-43 to Pro-50, Gly-64 to Leu-72, and Leu-81 to Lys-86.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for treatment/diagnosis of cancers and/or tumors, particularly, those found in the breast since expression is mainly in cancer/tumor
35 tissues. May serve as therapeutic proteins for proliferation/differentiation of fetal tissues.

FEATURES OF PROTEIN ENCODED BY GENE NO: 3

This gene is expressed primarily in CD34 depleted buffy coat and to a lesser extent in spleen, chronic lymphocytic leukemia.

5 Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: blood disorders or leukemias, diseases of the immune system. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for
10 differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., blood cells, and spleen, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or
15 cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

 The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for treatment/diagnosis of blood disorders or
20 leukemias, diseases of the immune system since expression is in tissues related to immune function.

FEATURES OF PROTEIN ENCODED BY GENE NO: 4

This gene is expressed primarily in CD34 depleted buffy coat.

25 Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: blood disorders or lymphocytic diseases. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification
30 of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., blood cells, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual
35 having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for treatment/diagnosis of blood disorders since expression is in tissues related to immune function.

5 FEATURES OF PROTEIN ENCODED BY GENE NO: 5

This gene is expressed primarily in CD34 depleted buffy coat.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: blood or immune
10 diseases. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., blood cells, and cancerous
15 and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 317 as residues:
20 Pro-13 to Lys-21.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for treatment/diagnosis of blood disorders since expression is in tissues related to immune function.

25 FEATURES OF PROTEIN ENCODED BY GENE NO: 6

This gene is expressed primarily in CD34 depleted buffy coat.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: blood or immune
30 diseases. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., and blood cells, and
35 cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level

in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 318 as residues: Lys-31 to Lys-39.

- 5 The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for treatment/diagnosis of blood diseases since it is expressed in tissues related to immune function.

FEATURES OF PROTEIN ENCODED BY GENE NO: 7

- 10 This gene is expressed primarily in CD34 depleted buffy coat and to a lesser extent in pineal gland.

- Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: diseases of the immune system and brain associated diseases. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., blood cells, and pineal gland, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

- 25 The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for treatment/diagnosis of blood disorders, immune diseases or brain associated diseases (specifically of the pineal gland) since expression is in tissues related to immune function.

FEATURES OF PROTEIN ENCODED BY GENE NO: 8

- 30 The translation product of this gene shares sequence homology with an organic cation transporter which is thought to be important in organic cation uptake in the kidney and liver. (See Accession No. 2343059.) Preferred polypeptide fragments comprise the amino acid sequence ITIAIQMICLVNXELYPTFVRNXGVMVCSSLCDIGGIITP FIVFRLREVWQALPLILFAVLGLLAAGVTLLLPETKGVLPETMKDAENLGRKAKPKENTTYLK VQTSEPSGT (SEQ ID NO: 615) or TMKDAENLGRKAKPKENT (SEQ ID NO: 616) as well as N-terminal and C-terminal deletions of these fragments. Also preferred are polynucleotide fragments encoding these polypeptide fragments.

This gene is expressed primarily in liver.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: hepatic and renal
5 diseases where drug elimination/cation exchange (organic cation uptake) in the liver and kidney are problematic. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the hepatic or renal system, expression of this gene at significantly higher
10 or lower levels may be routinely detected in certain tissues and cell types (e.g., kidney and liver, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the
15 disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 320 as residues: Asn-64 to Asn-74, and Gln-81 to Gly-87.

The tissue distribution and homology to organic cation transporter indicate that polynucleotides and polypeptides corresponding to this gene are useful as a polyspecific transporter that is important for drug elimination in the liver (and possibly kidney) since
20 expression is found in the liver.

FEATURES OF PROTEIN ENCODED BY GENE NO: 9

This gene is expressed primarily in eosinophil induced with IL-5 and to a lesser extent in fetal liver and spleen. This gene also maps to chromosome 15, and therefore
25 can be used in linkage analysis as a marker for chromosome 15.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: diseases of the immune system, particularly allergies or asthma. Similarly, polypeptides and antibodies directed
30 to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., blood cells, liver, and spleen, and cancerous and wounded tissues) or
35 bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the

standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for treating/diagnosis of diseases involving eosinophil reactions since expression seems to be concentrated in eosinophils and other tissues involved in immunity such as the liver and spleen.

FEATURES OF PROTEIN ENCODED BY GENE NO: 10

This gene is expressed primarily in tissues of hematopoietic lineage and to a lesser extent in Hodgkins lymphoma. Any frame shifts in this sequence can easily be clarified using known molecular biology techniques.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions which include, but are not limited to, and immune deficiency or dysfunction. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., hematopoietic cells, lymphoid and reticuloendothelial tissues, and cancerous tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for treatment/ diagnosis for lymphomas or immune dysfunction or as a therapeutic protein useful in immune modulation based on expression in anergic T-cells and lymphomas.

FEATURES OF PROTEIN ENCODED BY GENE NO: 11

This gene is expressed primarily in neutrophils and to a lesser extent in activated lymphoid cells.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the cell type present in a biological sample and for diagnosis of diseases and conditions: inflammation. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders

of the above tissues or cells, particularly of the immune system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., blood cells and lymphoid tissue, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another
 5 tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 323 as residues: Glu-40 to Lys-46.

The tissue distribution indicates that polynucleotides and polypeptides
 10 corresponding to this gene are useful for modulation of an immune reaction or as a growth factor for the differentiation or proliferation of neutrophils for the treatment of neutropenia.

FEATURES OF PROTEIN ENCODED BY GENE NO: 12

15 This gene is expressed primarily in brain and to a lesser extent in activated T-cells. It is likely that the open reading frame containing the predicted signal peptide continues in the 5' direction. Preferred polypeptide fragments comprise the amino acid sequence PRVRNSPEDLGLSLTGDSCKL (SEQ ID NO:617).

Therefore, polynucleotides and polypeptides of the invention are useful as
 20 reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: neurodegenerative disorders including ischemic shock, alzheimers and cognitive disorders. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a
 25 number of disorders of the above tissues or cells, particularly of the central nervous system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., blood cells, and brain, and other tissue of the nervous system and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from
 30 an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 324 as residues: Ser-5 to Glu-14, Ile-21 to Pro-35, Ser-65 to Asp-81, Cys-89 to Val-96, Lys-136 to Ser-145, Ile-152 to Met-169, and Arg-189 to Lys-196.

35 The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for diagnostic/treatment for cancers of the given tissue or in the treatment of neurological disorders of the CNS.

FEATURES OF PROTEIN ENCODED BY GENE NO: 13

This gene was also recently cloned by other groups, naming this calcium-activated potassium channel gene, hKCa4. (See Accession No. AF033021, see also, Accession
5 No. 2584866.) This gene is mapped to human chromosome 19q13.2. A second signal sequence likely exists upstream from the predicted signal sequence as described in Table 1. Preferred polypeptide fragments comprise: QADDLQATVAALCVLRGGGPWAG SWLSPKTPGAMGGDLVLGLGALRRRKRL (SEQ NO: 618); or EQEKSLAGWALVLAXXGIGL MVLHAEMLWFGGCSAVNATGHLSDTLWLIPITFLTIGYGDVVPGTMWGKIVCLCTGVMGVCC
10 TALLVAVVARKLEFNKAEKHVHNFMMDIQYTKEMKESAAARVLQEAWMFYKHTRRKESHAAR XHQRXLLAAINAFRQVRLKHKRLREQVNSMVDISKMHMILYDLQQLSSSHRALEKQIDTLAG KLDALTELLSTALGPRQLPEPSQQSK (SEQ ID NO: 619), as well as N-terminal and C-terminal deletions. Also preferred are polynucleotide fragments encoding these polypeptide fragments.

15 This gene is expressed primarily in breast lymph node and T-cells, and to a lesser extent in placenta.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: hematologic and
20 immune disorders. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., lymphoid
25 tissue, blood cells and placenta, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a
30 sequence shown in SEQ ID NO. 325 as residues: Arg-13 to Lys-23.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for the treatment/diagnosis of hematologic and diseases involving immune modulation based on distribution in the lymph node and T-cells.

35

FEATURES OF PROTEIN ENCODED BY GENE NO: 14

This gene was recently cloned by another group, calling it PAPS synthase. (See Accession No. e1204135.) Preferred polypeptide fragments comprise the amino acid sequence YQAHHVSRNKRQVVGTRGGFRGCTVWLTGLSGAGK (SEQ ID NO: 620).

5 Also preferred are the polynucleotide fragments encoding this polypeptide fragment.

It has been discovered that this gene is expressed primarily in benign prostate hyperplasia, Human Umbilical Vein Endothelial Cells and to a lesser extent in smooth muscle and Human endometrial stromal cells-treated with estradiol.

Therefore, polynucleotides and polypeptides of the invention are useful as
10 reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: inflammation, ischemia, and restenosis, based on endothelial cell and smooth muscle cell expression, and prostate diseases such as benign prostate hyperplasia or prostate cancer. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing
15 immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the prostate or vessels of the circulatory system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., prostate, endothelial cells, smooth muscle, and endometrium, and cancerous and wounded tissues) or bodily
20 fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a
25 sequence shown in SEQ ID NO. 326 as residues: Arg-21 to Asp-26, Lys-35 to Lys-44, Glu-49 to Asn-58.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for treating/diagnosing diseases or conditions where the endothelial cell lining of the veins and arteries of underlying smooth muscle are involved.

30

FEATURES OF PROTEIN ENCODED BY GENE NO: 15

This gene is expressed primarily in human 6 week embryo and to a lesser extent in placenta.

Therefore, polynucleotides and polypeptides of the invention are useful as
35 reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: developmental anomalies or fetal deficiencies. Similarly, polypeptides and antibodies directed to these

polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly developmental in nature, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., embryonic
5 tissue, and placenta, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID
10 NO. 327 as residues Lys-50 to Glu-57.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for detection of developmental abnormalities.

FEATURES OF PROTEIN ENCODED BY GENE NO: 16

15 This gene is expressed primarily in kidney and amygdala and to a lesser extent in fetal tissues. This gene is mapped to chromosome 14, and therefore is useful in linkage analysis as a marker for chromosome 14.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) present in a biological sample and
20 for diagnosis of diseases and conditions: kidney diseases, neurological disorders and developmental abnormalities. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s). For a number of disorders of the above tissues, particularly of the renal system or developing fetal tissues, expression of this gene at significantly higher or
25 lower levels may be routinely detected in certain tissues and cell types (e.g., kidney, amygdala, and fetal tissues, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an
30 individual not having the disorder.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for treatment or diagnosis of conditions affecting the brain, kidneys and fetal development.

35 FEATURES OF PROTEIN ENCODED BY GENE NO: 17

This gene is expressed primarily in ovarian cancer.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: solid tumors similar to ovarian cancer. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the reproductive system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., ovarian and other reproductive tissue, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 329 as residues Ser-51 to Val-56.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for the treatment of solid tumors of the reproductive system such as ovarian cancer.

FEATURES OF PROTEIN ENCODED BY GENE NO: 18

This gene is expressed primarily in brain medulloblastoma. Preferred polypeptide fragments comprise the amino acid sequence: IRHEQHPNFSLEMHSGSSLLFLPQL ILLPVCAHLHEELNC (SEQ ID NO: 643) and SFFISEEKGHLLLQAERHPWVAGALVGVSG GLTLTTCSGPTEKPATKNYFLKRLQEMHIRAN (SEQ ID NO: 644), as well as N-terminal and C-terminal deletions. Also preferred are polynucleotide fragments encoding these polypeptide fragments.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: tumors particularly of the CNS or. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the Central nervous system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., brain and other tissue of the nervous system, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene

expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for treating medulloblastoma or similar tumors.

5

FEATURES OF PROTEIN ENCODED BY GENE NO: 19

This gene is expressed primarily in adipocytes.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: obesity. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the adipose tissues expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., adipocytes and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for treating obesity by regulating the function and number of adipocytes

FEATURES OF PROTEIN ENCODED BY GENE NO: 20

This gene is expressed primarily in B cell lymphoma.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions which include, but are not limited to, of the immune system with an emphasis on B cell lymphoma. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the tumors of the immune system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., blood cells, and lymphoid tissue, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e.,

the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for diagnosis and treatment of B cell derived tumors based on its expression in b cell lymphomas

FEATURES OF PROTEIN ENCODED BY GENE NO: 21

This gene is expressed primarily in immune cells and to a lesser extent in fetal tissues

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: inflammatory diseases. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., cells of the immune system, and fetal tissues, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO:333 as residues Asp-10 to Pro-19, Ser-74 to Tyr-79, Glu-95 to Lys-110.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for treatment of diseases involving alterations in T cell activity.

FEATURES OF PROTEIN ENCODED BY GENE NO: 22

It has been discovered that this gene is expressed primarily in ovarian tumor.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: tumors particularly of the ovary. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of tumors of the reproductive organs. expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., ovarian

and other reproductive tissue and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 334 as residues: Leu-22 to Gln-27.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for diagnosis and treatment of ovarian tumors as it has only been identified in ovarian tumors.

FEATURES OF PROTEIN ENCODED BY GENE NO: 23

It has been discovered that this gene is expressed primarily in fetal tissues and to a lesser extent in osteoclastoma cell line

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: osteoporosis or arthritis. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the skeletal expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., bone cells, and fetal tissue, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for treatment of conditions of abnormal bone remodeling due to enhanced activity of osteoclasts. This may be useful as a specific marker for malignancies derived from osteoclasts or their precursors.

FEATURES OF PROTEIN ENCODED BY GENE NO: 24

The translation product of this gene shares sequence homology with a periplasmic ribonuclease which is thought to be important in degrading extracellular polynucleotides

It has been discovered that this gene is expressed primarily in serum treated smooth muscle cells

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: vascular disease such as restenosis. Similarly, polypeptides and antibodies directed to these polypeptides are
5 useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the vasculature expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., smooth muscle, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or
10 spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. Preferred epitopes include those comprising a sequence shown in SEQ ID NO: 336 as residues: Gln-30 to Lys-36, and Pro-41 to Arg-48.

15 The tissue distribution and homology to ribonucleases indicate that polynucleotides and polypeptides corresponding to this gene are useful for treatment of pathological conditions of smooth muscle associated with bacterial or viral infiltration

FEATURES OF PROTEIN ENCODED BY GENE NO: 25

20 This gene is expressed primarily in Early Stage Human Brain.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: human brain development and related diseases. Similarly, polypeptides and antibodies directed to
25 these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the human brain development and related diseases, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., brain and other tissue of the nervous system, and
30 cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

35 The tissue distribution and homology to this gene indicate that polynucleotides and polypeptides corresponding to this gene are useful for diagnosis and treatment of diseases affecting human brain development and related diseases.

FEATURES OF PROTEIN ENCODED BY GENE NO: 26

It has been discovered that this gene is expressed primarily in human brain tissue.

- 5 Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: human brain diseases and other diseases related to brain diseases, which may be caused by brain diseases. Similarly, polypeptides and antibodies directed to these polypeptides are useful in
- 10 providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the human brain diseases, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., brain and other tissue of the nervous system, and cancerous and wounded tissues) or bodily fluids (e.g., serum,
- 15 plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

- The tissue distribution and homology to the gene indicate that polynucleotides
- 20 and polypeptides corresponding to this gene are useful for diagnosis and treatment of human brain diseases and other diseases related.

FEATURES OF PROTEIN ENCODED BY GENE NO: 27

It has been discovered that this gene is expressed primarily in Anergic T-cells.

- 25 Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: immune diseases, inflammatory diseases and diseases related to T lymph cells. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological
- 30 probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune diseases, inflammatory diseases and diseases related to T lymph cells, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., blood cells, and cancerous and wounded tissues) or bodily fluids (e.g.,
- 35 serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene

expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution and homology to the gene indicate that polynucleotides and polypeptides corresponding to this gene are useful for immune diseases,
5 inflammatory diseases and diseases related to T lymph cells.

FEATURES OF PROTEIN ENCODED BY GENE NO: 28

The translation product of this gene shares sequence homology with *Shigella flexneri* positive transcriptional regulator CriR (criR) gene which is thought to be
10 important in regulation of gene expression.

This gene is expressed primarily in human synovial sarcoma and normal human brain tissues.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a
15 biological sample and for diagnosis of diseases and conditions: human brain diseases particularly sarcomas of the synovium. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the human brain and synovium and other related human
20 brain diseases, expression of this gene at significantly higher or lower levels may be routinely detected in certain (e.g., synovial tissue, and brain and other tissue of the nervous system, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e.,
25 the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for diagnosis and treatment of human synovial sarcoma and other related human brain diseases.

30

FEATURES OF PROTEIN ENCODED BY GENE NO: 29

This gene is expressed in bone marrow, infant brain, fetal liver and spleen, prostate and to a lesser extent in pineal gland, adipose tissue, kidney, adrenal gland, umbilical vein endothelial cells, and T cells.

35 Therefore, polynucleotides and polypeptides of the invention are useful as reagents for identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: diseases related to bone marrow or

hematoplastic tissues, prostate, kidney, adrenal gland, and cardiovascular tissue or organs. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the diseases related to hematoplastic tissues, immune system, prostate, kidney, adrenal gland, and cardiovascular tissue or organs, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., bone marrow, hematopoietic cells, pineal gland, adipose tissue, kidney, adrenal gland, endothelial cells, and blood cells, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution and homology to the gene indicate that polynucleotides and polypeptides corresponding to this gene are useful for diagnosis and treatment of diseases related to hematoplastic tissues, immune system, prostate, kidney, adrenal gland, and cardiovascular tissue or organs.

FEATURES OF PROTEIN ENCODED BY GENE NO: 30

This gene is expressed primarily in meningea and to a lesser extent in breast and adult brain.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: Diseases of the meningea and related brain diseases. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the meningea and related brain diseases, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., meningeal, mammary tissue, and brain and other tissue of the nervous system, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for diagnosis and treatment of diseases of the meningea and related brain diseases.

5 **FEATURES OF PROTEIN ENCODED BY GENE NO: 31**

This gene is expressed in meningea, fetal spleen, osteoblast and to a lesser extent in activated T-cells, endometrial stromal cells, fetal lung, HL-60, thymus, testis and endothelial cells.

Therefore, polynucleotides and polypeptides of the invention are useful as
10 reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: meningeal disease, osteoporosis, immune diseases, and hematoplastic diseases. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for identification of the tissue(s) or cell type(s). For a number of disorders of the
15 above tissues or cells, particularly of the meningeal diseases, osteoporosis, immune diseases, and hematoplastic diseases, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., blood cells, endometrium, lung, thymus, testis, and endothelial cells, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal
20 fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution and homology to gene indicate that polynucleotides and polypeptides corresponding to this gene are useful for diagnosis and treatment of
25 meningeal, osteoporosis, immune diseases, hematoplastic diseases, testis diseases and lung diseases.

FEATURES OF PROTEIN ENCODED BY GENE NO: 32

This gene is expressed primarily in human thymus and to a much lesser extent
30 in infant brain, T-cells, smooth muscle, endothelial cells, bone marrow, human ovarian tumor and keratinocytes testes, osteoclastoma, breast, and tonsils.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: Diseases involving the
35 thymus, particularly thymic cancer and diseases involving T-cell maturation. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a

number of disorders of the above tissues or cells, particularly of the thymus, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., thymus, brain, and other tissue of the nervous system, blood cells, bone marrow, ovaries, and testes, and other reproductive tissue, mammary
5 tissue, tonsils, melanocytes and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

- 10 The tissue distribution and homology to gene indicate that polynucleotides and polypeptides corresponding to this gene are useful for diagnosis and treatment of diseases of the thymus particularly thymic cancer and diseases involving T-cell maturation.

15 **FEATURES OF PROTEIN ENCODED BY GENE NO: 33**

This gene is expressed primarily in human tonsils, and placenta, and to a lesser extent in adipocytes, melanocyte, and infant brain.

- Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a
20 biological sample and for diagnosis of diseases and conditions: inflammatory diseases, immune diseases, and obesity. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the inflammatory diseases, immune diseases, and obesity, expression of
25 this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., tonsils, placenta, adipocytes, melanocytes, and brain and other tissue of the nervous system, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard
30 gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution and homology to this gene indicate that polynucleotides and polypeptides corresponding to this gene are useful for diagnosis and treatment of diseases such as inflammation, immune diseases, and obesity.

FEATURES OF PROTEIN ENCODED BY GENE NO: 34

This gene is expressed in activated T cells, and to a lesser extent in pituitary, testis, and breast lymph node.

Therefore, polynucleotides and polypeptides of the invention are useful as
5 reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: diseases relating to T cells. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the
10 disorders of the immune system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., pituitary, testes and other reproductive tissue, mammary tissue, and lymphoid tissue, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a
15 disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for treatment of immune disorders.

20 FEATURES OF PROTEIN ENCODED BY GENE NO: 35

This gene is expressed primarily in infant brain.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: neurological disorders.
25 Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the diseases relating to neurological disorders, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g.,
30 brain, and other tissue of the nervous system, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

35 The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for diagnosis and treatment of neurological disorders.

FEATURES OF PROTEIN ENCODED BY GENE NO: 36

This gene is expressed primarily in infant brain.

Therefore, polynucleotides and polypeptides of the invention are useful as
5 reagents for differential identification of the tissue(s) or cell type(s) present in a
biological sample and for diagnosis of diseases and conditions: neurological disorders.
Similarly, polypeptides and antibodies directed to these polypeptides are useful in
providing immunological probes for differential identification of the tissue(s) or cell
10 type(s). For a number of disorders of the above tissues or cells, particularly of the
diseases relating to neurological disorders, expression of this gene at significantly
higher or lower levels may be routinely detected in certain tissues and cell types (e.g.,
brain and other tissue of the nervous system, and cancerous and wounded tissues) or
bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another
15 tissue or cell sample taken from an individual having such a disorder, relative to the
standard gene expression level, i.e., the expression level in healthy tissue or bodily
fluid from an individual not having the disorder.

The tissue distribution indicates that polynucleotides and polypeptides
corresponding to this gene are useful for diagnosis and treatment of neurological
20 disorders.

FEATURES OF PROTEIN ENCODED BY GENE NO: 37

This gene is expressed primarily in human ovary.

Therefore, polynucleotides and polypeptides of the invention are useful as
reagents for differential identification of the tissue(s) or cell type(s) present in a
25 biological sample and for diagnosis of diseases and conditions: ovarian cancer.
Similarly, polypeptides and antibodies directed to these polypeptides are useful in
providing immunological probes for differential identification of the tissue(s) or cell
type(s). For a number of disorders of the above tissues or cells, particularly of the
ovarian disorders such as those involving germ cells, ovarian follicles, stromal cells,
30 expression of this gene at significantly higher or lower levels may be routinely detected
in certain tissues and cell types (e.g., ovary and other reproductive tissue, and
cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial
fluid or spinal fluid) or another tissue or cell sample taken from an individual having
such a disorder, relative to the standard gene expression level, i.e., the expression level
35 in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that polynucleotides and polypeptides
corresponding to this gene are useful for diagnosis and treatment of ovarioopathy.

FEATURES OF PROTEIN ENCODED BY GENE NO: 38

This gene is expressed primarily in lymph node breast cancer.

Therefore, polynucleotides and polypeptides of the invention are useful as
5 reagents for differential identification of the tissue(s) or cell type(s) present in a
biological sample and for diagnosis of diseases and conditions: breast cancer. Similarly,
polypeptides and antibodies directed to these polypeptides are useful in providing
immunological probes for differential identification of the tissue(s) or cell type(s). For a
number of disorders of the above tissues or cells, particularly of the breast cancer,
10 expression of this gene at significantly higher or lower levels may be routinely detected
in certain tissues and cell types (e.g., mammary tissue and lymphoid tissue, and
cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial
fluid or spinal fluid) or another tissue or cell sample taken from an individual having
such a disorder, relative to the standard gene expression level, i.e., the expression level
15 in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that polynucleotides and polypeptides
corresponding to this gene are useful for used as a diagnostic marker for breast cancer.

FEATURES OF PROTEIN ENCODED BY GENE NO: 39

20 This gene is expressed primarily in brain and to a lesser extent in other tissues.

Therefore, polynucleotides and polypeptides of the invention are useful as
reagents for differential identification of the tissue(s) or cell type(s) present in a
biological sample and for diagnosis of diseases and conditions: neuronal disorders such
as trauma, brain degeneration, and brain tumor. Similarly, polypeptides and antibodies
25 directed to these polypeptides are useful in providing immunological probes for
differential identification of the tissue(s) or cell type(s). For a number of disorders of
the above tissues or cells, particularly of the brain, expression of this gene at
significantly higher or lower levels may be routinely detected in certain tissues and cell
types (e.g., brain and other tissue of the nervous system, and cancerous and wounded
30 tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or
another tissue or cell sample taken from an individual having such a disorder, relative to
the standard gene expression level, i.e., the expression level in healthy tissue or bodily
fluid from an individual not having the disorder.

The tissue distribution indicates that polynucleotides and polypeptides
35 corresponding to this gene are useful for diagnosis and therapeutic treatment of
neuronal disorders.

FEATURES OF PROTEIN ENCODED BY GENE NO: 40

5 This gene is expressed in early stage human embryo, adrenal gland tumor, and immune tissues such as fetal liver, fetal spleen, T-cell, and myeloid progenitor cell line and to a lesser extent in ovary, colon cancer, and a few other tissues.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: tumorigenesis including
10 adrenal gland tumor, colon cancer and various other tumors, developmental and immune disorders. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the cancer tissues, early stage human tissues, and immune system,
15 expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., liver, spleen, blood cells, bone marrow, ovary and other reproductive tissue, and colon, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard
20 gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for diagnosis and therapeutic treatment of immune and developmental disorders, and tumorigenesis.

25

FEATURES OF PROTEIN ENCODED BY GENE NO: 41

This gene is expressed primarily in fetal lung, endothelial cells, liver, thymus and a few other immune tissues.

Therefore, polynucleotides and polypeptides of the invention are useful as
30 reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: immune disorders such as immune deficiency and autoimmune diseases, pulmonary diseases, liver diseases, and tumor matasis. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification
35 of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the fetal lung, liver, endothelial cells, and immune tissues, expression of this gene at significantly higher or lower levels may be routinely detected in certain

tissues and cell types (e.g., lung, endothelial cells, liver, thymus, and other tissue of the immune system, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e.,
5 the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for diagnosis of immune disorders and pulmonary and hepatic diseases. Its promoter may also be used for immune system and lung-
10 specific gene therapies. The expression of this gene in endothelial cells indicates that it may also involve in angiogenesis which therefore may play role in tumor matasis.

FEATURES OF PROTEIN ENCODED BY GENE NO: 42

This gene is expressed primarily in liver, thyroid, parathyroid and to a lesser
15 extent in fetal lung, stomach and early embryos.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: metabolic regulation, obesity, hepatic failure, hepatocellular tumors or thyroiditis and thyroid tumors. Similarly,
20 polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the digestive/endocrine system expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., liver, thyroid, parathyroid, lung,
25 stomach, and embryonic tissue, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

30 The tissue distribution and the extracellular locations indicates that polynucleotides and polypeptides corresponding to this gene are useful for the detection and treatment of digestive/endocrine disorders, including metabolic regulation, hepatic failure, malabsorption, gastritis and neoplasms.

FEATURES OF PROTEIN ENCODED BY GENE NO: 43

This gene is expressed primarily in Schizophrenic adult brain, pituitary, front cortex, hypothalamus and to a lesser extent in retina, adipose and stomach cancer and placenta.

5 Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: schizophrenia and other neurological disorders. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification
10 of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the central nerve system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., retinal tissue, adipose, stomach, and placenta, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or
15 cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful in treatment/detection of disorders in the nerve
20 system, including schizophrenia, neurodegeneration, and neoplasia. Additionally, a secreted protein in brain may serve as an endocrine.

FEATURES OF PROTEIN ENCODED BY GENE NO: 44

The translation product of this gene shares sequence homology with GTP
25 binding proteins which are thought to be important in signal transduction and protein transport.

This gene is expressed primarily in umbilical vein and microvascular endothelial cells, GM-CSF treated macrophage, anergic T cells, osteoblast, osteoclast, CD34+ cells and to a lesser extent in gall bladder.

30 Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: bone formation and growth, osteonecrosis, osteoporosis, angiogenesis and/or hematopoiesis. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing
35 immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the skeletal and hematopoiesis systems, expression of this gene at significantly higher or lower levels

may be routinely detected in certain tissues and cell types (e.g., endothelial cells, blood cells, bone, and gall bladder, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution and homology to GTP binding proteins indicate that polynucleotides and polypeptides corresponding to this gene are useful for treatment/detection of bone formation and growth, osteonecrosis, osteoporosis, and/or hematopoiesis because its involvement in the growth signaling or angiogenesis.

FEATURES OF PROTEIN ENCODED BY GENE NO: 45

The translation product of this gene shares sequence homology with signal sequence receptor gamma subunit which is thought to be important in protein translocation on endoplasmic reticulum.

This gene is expressed primarily in adrenal gland, salivary gland, prostate, and to a lesser extent in endothelial cells and smooth muscle.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: protein secretion. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the secretory organs, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., adrenal gland, salivary gland, prostate, endothelial cells, and smooth muscle, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution and homology to SSR gamma subunit indicate that polynucleotides and polypeptides corresponding to this gene are useful for endocrine disorders, prostate cancer, xerostomia or sialorrhea.

FEATURES OF PROTEIN ENCODED BY GENE NO: 46

This gene is expressed primarily in osteoclastoma cells and to a lesser extent in melanocyte, amygdala, brain, and stomach.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: ossification, osteoporosis, fracture, osteonecrosis, osteosarcoma. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the skeletal systems, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., melanocytes, amygdala, brain and other tissue of the nervous system, and stomach, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful in intervention of ossification, osteoporosis, fracture, osteonecrosis and osteosarcoma.

FEATURES OF PROTEIN ENCODED BY GENE NO: 48

The translation product of this gene shares sequence homology with proline rich proteins which is thought to be important in protein-protein interaction.

This gene is expressed primarily in brain.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: neurological and psychological disorders. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the central nerve system and endocrine system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., brain and other tissue of the nervous system, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution and homology to proline-rich proteins indicate that polynucleotides and polypeptides corresponding to this gene are useful in intervention

and detection of neurological diseases, including trauma, neoplasia, degenerative or metabolic conditions in the central nerve system. Additionally, the gene product may be secreted by the brain as an endocrine.

5 **FEATURES OF PROTEIN ENCODED BY GENE NO: 49**

The translation product of this gene shares sequence homology with the AOCB gene from *Aspergillus nidulans* which is important in asexual development.

This gene is expressed primarily in infant brain and to a lesser extent in the developing embryo, trachea tumors, B-cell lymphoma and synovial sarcoma.

10 Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: neurodegenerative diseases, leukemia and sarcoma's. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential
15 identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the brain and immune system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., embryonic tissue, blood cells, trachea, and synovial tissue, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or
20 spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution in infant brain and sarcoma's and homology to a gene involved in a key step of eukaryotic development (fungal spore formation) indicates
25 that the protein product of this clone could play a role in neurological diseases such as schizophrenia, particularly in infants. The existence of the gene in a B-cell lymphoma indicates the gene may be used in the treatment and detection of leukemia.

FEATURES OF PROTEIN ENCODED BY GENE NO: 50

30 This gene is expressed primarily in fetal lung.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: pulmonary disorders including lung cancer. Similarly, polypeptides and antibodies directed to these
35 polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the pulmonary system, expression of this gene at significantly higher or

lower levels may be routinely detected in certain tissues and cell types (e.g., lung, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution of this gene only in fetal lung indicates that it plays a key role in development of the pulmonary system. This would suggest that misregulation of the expression of this protein product in the adult could lead to lymphoma or sarcoma formation, particularly in the lung. It may also be involved in predisposition to certain pulmonary defects such as pulmonary edema and embolism, bronchitis and cystic fibrosis.

FEATURES OF PROTEIN ENCODED BY GENE NO: 51

This gene is expressed primarily in hematopoietic cell types and fetal cells and to a lesser extent in all tissue types.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: defects in the immune system and hematopoiesis. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune and hematopoietic systems, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., hematopoietic cells, and fetal tissue, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution of this gene predominantly in hematopoietic cells and in the developing embryo indicates that polynucleotides and polypeptides corresponding to this gene are useful for detection and treatment of lymphomas and disease states affecting the immune system or hematopoiesis disorders such as leukemia, AIDS, arthritis and asthma..

FEATURES OF PROTEIN ENCODED BY GENE NO: 52

This gene is expressed primarily in prostate and to a lesser extent in fetal spleen, fetal liver, infant brain and T cell leukemias.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: prostate disorders, prostate cancer, leukemia. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune system, and/or prostate gland expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., thymus, spleen, liver, brain and other tissue of the nervous system, and blood cells, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution of this gene in prostate indicates that polynucleotides and polypeptides corresponding to this gene are useful for detection or treatment of prostate disorders or prostate cancer. Its distribution in fetal liver and fetal spleen indicates it may play a role in the immune system and its misregulation could lead to immune disorders such as leukemia, arthritis and asthma.

20

FEATURES OF PROTEIN ENCODED BY GENE NO: 53

The translation product of this gene shares sequence homology with dynein.

This gene is expressed primarily in brain.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: neuro-degenerative diseases of the brain. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly neuro-degenerative diseases expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., brain and other tissue of the nervous system, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The predominant tissue distribution in the brain and homology to dynein, a microtubule motor protein involved in the positioning of cellular organelles and molecules indicates that polynucleotides and polypeptides corresponding to this gene are useful for detection/treatment of neurodegenerative diseases, such as Alzheimers, 5 Huntingtons, Parkinsons diseases and shizophrenia.

FEATURES OF PROTEIN ENCODED BY GENE NO: 54

The translation product of this gene shares sequence homology with ubiquitin-conjugation protein, an enzyme which is thought to be important in the processing of 10 the Huntingtons Disease causing gene.

This gene is expressed primarily in brain and to a lesser extent in activated macrophages.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a 15 biological sample and for diagnosis of diseases and conditions: neurodegenerative disease states including Huntington's disease. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of brain tissues. For a number of disorders of the above tissues or cells, particularly of the neurological systems expression of this gene at 20 significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., brain and other tissue of the nervous system, and blood cells, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level 25 in healthy tissue or bodily fluid from an individual not having the disorder.

The predominant tissue distribution of this gene in the brain and its homology to a Huntington interacting protein indicates that polynucleotides and polypeptides corresponding to this gene are useful for the regulation of the expression of the Huntington disease gene and other neurodegenerative diseases including 30 spinocerebellar ataxia types I and III, dentatorubropallidoluysian and spinal bulbar muscular atrophy. In addition, the existence of elevated levels of free ubiquitin pools in Alzheimer's disease, Parkinson's disease and amyotrophic lateral sclerosis indicates that the ubiquitin pathway of protein degradation plays a role in these disease states. Thus, considering the gene described here is homologous to a ubiquitin-conjugation 35 protein it may play a general role in neurodegenerative conditions.

FEATURES OF PROTEIN ENCODED BY GENE NO: 56

This gene is expressed primarily in T-cells (anergic T-cells, resting T-Cells, apoptotic T-cells) and lymph node (breast), as well as brain (hypothalamus, hippocampus, pituitary, infant brain, early-stage brain).

- 5 Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: immune (e.g. immunodeficiencies, autoimmunities, inflammation, leukemias & lymphomas) and neurological (e.g. Alzheimer's disease, dementia, schizophrenia) disorders. Similarly,
- 10 polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the central nervous, hematopoietic and immune systems, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., blood
- 15 cells, lymphoid tissue, and brain and other tissue of the nervous system, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.
- 20 The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful in the intervention or detection of pathologies associated with the hematopoietic and immune systems, such as anemias (leukemias). In addition, the expression in brain (including fetal) might suggest a role in developmental brain defects, neuro-degenerative diseases or behavioral abnormalities
- 25 (e.g. schizophrenia, Alzheimer's, dementia, depression, etc.).

FEATURES OF PROTEIN ENCODED BY GENE NO: 57

- This gene is expressed primarily in lung, and to a lesser extent in a variety of other hematological cell types (e.g. Raji cells, bone marrow cell line, activated
- 30 monocytes).

- Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: pulmonary and/or hematological disfunction. Similarly, polypeptides and antibodies directed to these
- 35 polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the vasculo-pulmonary and hematopoietic systems, expression of this

gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., lung and blood cells, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the
5 standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful in the intervention and detection of pathologies associated with the vasculo-pulmonary system. In addition the expression of this gene
10 in a variety of leukocytic cell types and a bone marrow cell line might suggest a role in hematopoietic and immune system disorders, such as leukemias & lymphomas, inflammation, immunodeficiencies and autoimmunities.

FEATURES OF PROTEIN ENCODED BY GENE NO: 58

15 The translation product of this gene shares sequence homology with adenylate kinase isozyme 3 (gil163528 GTP:AMP phosphotransferase (EC 2.7.4.10) [Bos taurus]), which is thought to be important in catalyzing the phosphorylation of AMP to ADP in the presence of ATP or inorganic triphosphate.

This gene is expressed primarily in fetal liver, heart and placenta, and to a lesser
20 extent in many other tissues.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: hepatic, cardiovascular or reproductive disorders. Similarly, polypeptides and antibodies directed to these
25 polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the hepatic, cardiovascular and reproductive systems, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., liver, heart, and placenta, and cancerous and wounded tissues) or
30 bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that polynucleotides and polypeptides
35 corresponding to this gene are useful for the treatment and diagnosis of conditions related to hepatic function and pathogenesis, in particular, those dealing with liver development and the differentiation of hepatocyte progenitor cells.

FEATURES OF PROTEIN ENCODED BY GENE NO: 59

This gene is expressed primarily in CD34 positive cells (Cord Blood).

Therefore, polynucleotides and polypeptides of the invention are useful as
5 reagents for differential identification of the tissue(s) or cell type(s) present in a
biological sample and for diagnosis of diseases and conditions: hematopoietic
differentiation and immune disorders. Similarly, polypeptides and antibodies directed to
these polypeptides are useful in providing immunological probes for differential
10 identification of the tissue(s) or cell type(s). For a number of disorders of the above
tissues or cells, particularly of hematopoietic and immune systems, expression of this
gene at significantly higher or lower levels may be routinely detected in certain tissues
and cell types (e.g., hematopoietic cells, and blood cells, and cancerous and wounded
tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or
15 another tissue or cell sample taken from an individual having such a disorder, relative to
the standard gene expression level, i.e., the expression level in healthy tissue or bodily
fluid from an individual not having the disorder.

The tissue distribution indicates that polynucleotides and polypeptides
corresponding to this gene are useful in the detection and treatment of conditions
associated with CD34-positive cells, and therefore as a marker for cell differentiation in
20 hematopoiesis, as well as immunological disorders.

FEATURES OF PROTEIN ENCODED BY GENE NO: 60

The translation product of the predicted open reading frame of this contig has
sequence identity to the murine gene designated Insulin-Like Growth Factor-Binding
25 Protein (IGFBP)-1 as described by Lee and colleagues (Hepatology 19 (3), 656-665
(1994)).

This gene is expressed exclusively in hemangiopericytoma.

Therefore, polynucleotides and polypeptides of the invention are useful as
reagents for differential identification of the tissue(s) or cell type(s) present in a
30 biological sample and for diagnosis of hemangiopericytoma and other pericyte or
endothelial cell proliferative disorders. Similarly, polypeptides and antibodies directed
to these polypeptides are useful in providing immunological probes for differential
identification of the tissue(s) or cell type(s). For a number of disorders of the above
tissues or cells, particularly of the circulatory and immune systems, expression of this
35 gene at significantly higher or lower levels may routinely be detected in certain tissues
and cell types (e.g., pericyte or endothelial cells, and liver, and cancerous and wounded
tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or

another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

Polynucleotides and polypeptides corresponding to this gene are useful as cell growth regulators since IGFBP-1-like molecules function as modulators of insulin-like growth factor activity. In addition, since IGFBP-1 is expressed at high levels following hepatectomy and during fetal liver development, polynucleotides of the present invention may also be used for the diagnosis of developmental disorders. Further, polypeptides of the present invention may be used therapeutically to treat developmental liver disorders as well as to regulate hepatocyte and supporting cell growth following hepatectomy or to treat liver disorders.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for diagnosis and treatment of hemangiopericytoma and liver disorders.

FEATURES OF PROTEIN ENCODED BY GENE NO: 61

This gene is expressed primarily in schizophrenic frontal cortex.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: nervous system and cognitive disorders. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the frontal cortex and CNS expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., brain and other tissue of the nervous system, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for study, treatment and diagnosis of frontal cortex, neuro-degenerative and CNS disorders

FEATURES OF PROTEIN ENCODED BY GENE NO: 62

This gene is expressed primarily in human adrenal gland tumor, and to a lesser extent in human kidney, medulla and adult pulmonary tissue.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: metabolic, endocrine disorders. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the endocrine and nervous system disorders and neoplasia, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., adrenal gland, kidney, brain and other tissue of the nervous system, pulmonary tissue, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for study, treatment and diagnosis of neurological and endocrine disorders including neoplasia.

FEATURES OF PROTEIN ENCODED BY GENE NO: 63

This gene is expressed primarily in human adipocytes, and to a lesser extent in spleen, 12-week old human, and testes.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: immune, metabolic and growth disorders. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., adipocytes, spleen, and testes and other reproductive tissue, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for study, diagnosis and treatment of immune, developmental and metabolic disorders.

FEATURES OF PROTEIN ENCODED BY GENE NO: 64

One translated product of this clone is homologous to the mouse zinc finger protein PZF. (See Accession No. 453376; see also Gene 152 (2), 233-238 (1995).) Preferred

5 polypeptide fragments correspond to the highly conserved domains shared between mouse and man. For example, preferred polypeptide fragments comprise the amino acid sequence: LQCEICGFTCRQKASLNWHMKKHDADSFYQFSCNICGKKFEKKDSVVAHKAKSH PEV (SEQ ID NO: 621); ITSTDILGTNPESLTQPSD (SEQ ID NO: 622); NSTSGECLLLEAGM SKSY (SEQ ID NO: 623); CSGTERVSLMADGKIFVGSGSSGGTEGLVMNSDILGATTEVLIEDSD

10 SAGP (SEQ ID NO: 624); IQYVRCEMEGCGTVLAHPRYLQHIIKYQHLLKKKYVCPHPSCGRLF RLQKQLLRHAKHHT (SEQ ID NO: 625); DQRDYICEYCARAFKSSHNLAVHRMIHTGEK (SEQ ID NO: 626); RSSRTSVSRHRDTENTRSSRSKTGSLQLICKSEPNTDQLDY (SEQ ID NO: 627); PFKDDPRDETYKPHLERETPKPRRKS (SEQ ID NO: 630); QYVRCEMEGCGTVLAHPRYLQ HHIKYQHLLKKKYVCPHPSCGRLFRLQKQLLRHAKHHTD (SEQ ID NO: 629); or residues

15 151-182 of QRDYICEYCARAFKSSHNLAVHRMIHTGEKHY (SEQ ID NO: 628). Also preferred are polynucleotide fragments encoding these polypeptide fragments.

This gene is expressed primarily in Rhabdomyosarcoma, melanocyte and colon cancer tissue and to a lesser extent in smooth muscle, pancreatic tumor, and apoptotic T-cells.

20 Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions which include, but are not limited to,. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s)

25 or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune and hemopoetic, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., striated muscle, melanocytes, colon, smooth muscle, pancreas, and blood cells, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal

30 fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for study, diagnosis and treatment of cancer and

35 hemopoetic disorders.

FEATURES OF PROTEIN ENCODED BY GENE NO: 65

This gene is expressed primarily in human adipose and salivary gland tissue and to a lesser extent in human bone marrow and fetal kidney.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: metabolic and immune disorders. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the metabolic and hemopoetic systems, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., adipose, salivary gland, bone marrow, and kidney, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for study, diagnosis of metabolic and immune disorders.

FEATURES OF PROTEIN ENCODED BY GENE NO: 66

This translated product of this gene was recently identified as oxytocinase splice variant 1. (See Accession Nos. 2209276 and d1010078.) Preferred polypeptide fragments comprise the amino acid sequence: EMFDSL SYFKGSSLLMLKTYLSEDVFQHAVVLYLHN HSYASIQSDDLWDSFNEVTNQTL DVKRMMKWTWLQKGFLVTVQKKGKELFIQQRFFLNMK PEIQPSDTRYM (SEQ ID NO: 631). Also preferred are polynucleotide fragments encoding this polypeptide fragment.

FEATURES OF PROTEIN ENCODED BY GENE NO: 67

This gene is expressed primarily in hemopoetic cells, particularly apoptotic T-cells, and to lesser extent in primary dendritic cells and adipose tissue.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of apoptotic T-cells, primary dendritic cells, and adipose tissue present in a biological sample and for diagnosis of diseases and conditions: hemopoetic diseases including cancer and general immune disorders. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell

type(s). For a number of disorders of the above tissues or cells, particularly of the oral and intestinal mucosa as well as hemopoetic and immune systems, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., hematopoietic cells, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for treatment of diseases of the immune system, including cancer, hemopoetic and infectious diseases.

FEATURES OF PROTEIN ENCODED BY GENE NO: 68

This gene is expressed primarily in kidney cortex and to a lesser extent in infant brain, heart, uterus, and blood.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of kidney tissue present in a biological sample and for diagnosis of diseases and conditions: soft tissue cancer, inflammation, kidney fibrosis. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the nervous and endocrines systems, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., kidney, brain, and other nervous tissue, heart, uterus, and blood cells, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for study and treatment of cancer and fibroses.

FEATURES OF PROTEIN ENCODED BY GENE NO: 69

The translation product of this gene shares strong sequence homology with vertebrate and invertebrate protein tyrosine phosphatases.

This gene is expressed primarily in endometrial tumors, melanocytes, myeloid progenitors and to a lesser extent in infant brain, adipocytes, and several hematopoietic stem cells.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of transformed hematopoietic and epithelial cells present in a biological sample and for diagnosis of diseases and conditions which include, but are not limited to, of skin and endometrium, leukemia. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the nervous and hemopoietic systems, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., endometrium, melanocytes, bone marrow, adipocytes, hematopoietic cells, and brain and other tissue of the nervous system, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution and sequence similarity with tyrosine phosphatases indicate that polynucleotides and polypeptides corresponding to this gene are useful for study and treatment of cancer and hematopoietic disorders.

20 FEATURES OF PROTEIN ENCODED BY GENE NO: 70

This gene is expressed primarily in osteoclastoma, breast, and infant brain and to a lesser extent in various fetal and transformed bone, ovarian, and neuronal cells.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: degenerative conditions of the brain and skeleton. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the nervous and skeletal system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., bone, mammary tissue, and brain and other tissue of the nervous system, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for study and treatment of degenerative, neurological and skeletal disorders.

5 FEATURES OF PROTEIN ENCODED BY GENE NO: 71

This gene was originally cloned from tumor cell lines. Recently another group has also cloned this gene, calling it the human malignant melanoma metastasis-suppressor (KiSS-1) gene. (See Accession No. U43527.) Preferred polypeptide fragments comprise the amino acid sequence: LEKVASVGNSRPTGQQLSLGLLA (SEQ ID NO: 632); VHREEASCYCQAEPGDL (SEQ ID NO: 633); RPALRQAGGGTREPRQKRWAGL (SEQ ID NO: 634); and AVNFRPQRSQSM (SEQ ID NO: 635). Any frame shifts can easily be resolved using known molecular biology techniques.

This gene is expressed primarily in many types of carcinomas and to a lesser extent in many normal organs.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissues(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions which include, but are not limited to, cancer particularly melanomas, and other hyperproliferative disorders. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of transformed organ tissue, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder. As a tumor suppressor gene, increase amounts of the polypeptide can be used to treat patients having a particular cancer.

The tissue distribution indicates that this gene and the translated product is useful for diagnosing and study of cancer.

FEATURES OF PROTEIN ENCODED BY GENE NO: 72

This gene is expressed primarily in striatum and to a lesser extent in adipocytes and hemangiopericytoma.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of striatal cells present in a biological sample and for diagnosis of diseases and conditions: neurological, fat and lysosomal storage

diseases. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the nervous and immune systems, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., striatal tissue, adipocytes, and vascular tissue, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for diagnosis, study and treatment of neurodegenerative and growth disorders.

15 FEATURES OF PROTEIN ENCODED BY GENE NO: 73

This gene is expressed primarily in bone marrow stromal cells and to a lesser extent in smooth muscle, testes, endothelium, and brain.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of bone marrow present in a biological sample and for diagnosis of diseases and conditions: connective tissue and hematopoietic diseases. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the skeletal and hematopoietic systems, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., bone marrow, stromal cells, smooth muscle, testes and other reproductive tissue, endothelium, brain and other tissue of the nervous system, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for study, diagnosis, and treatment of connective tissue and blood diseases.

FEATURES OF PROTEIN ENCODED BY GENE NO: 74

This gene is expressed primarily in brain, fetal liver and lung and to a lesser extent in retina, spinal chord, activated T-cells and endothelial cells.

Therefore, polynucleotides and polypeptides of the invention are useful as
5 reagents for differential identification of brain and regenerating liver present in a biological sample and for diagnosis of diseases and conditions: CNS and spinal chord injuries, immune disorders. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells,
10 particularly of the nervous and immune system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., brain and other tissue of the nervous system, liver, pulmonary tissue, blood cells, and endothelial cells, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from
15 an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that polynucleotides and polypeptides
20 corresponding to this gene are useful for study and treatment of hematopoietic and neurological conditions.

FEATURES OF PROTEIN ENCODED BY GENE NO: 75

The translation product of this gene shares sequence homology with GTP binding proteins (intracellular).

25 This gene is expressed primarily in bone marrow, brain, and melanocytes and to a lesser extent in various endocrine and hematopoietic tissues.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: hematopoietic and
30 nervous system conditions. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the nervous and immune, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., bone
35 marrow, melanocytes, brain and other tissue of the nervous system, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder,

relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution and homology to nucleotide binding factors indicate that polynucleotides and polypeptides corresponding to this gene are useful for study,
5 diagnosis, and treatment of brain degenerative, skin and blood diseases.

FEATURES OF PROTEIN ENCODED BY GENE NO: 76

This gene is expressed primarily in activated T-cells and to a lesser extent in retina, brain, and fetal bone.

10 Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of activated T-cells and developing brain present in a biological sample and for diagnosis of diseases and conditions: immune deficiencies and skeletal and neuronal growth disorders. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes
15 for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the nervous, immune, and skeletomuscular systems, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., blood cells, brain and other tissue of the nervous system, retinal tissue, and bone, and cancerous and wounded tissues) or
20 bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that polynucleotides and polypeptides
25 corresponding to this gene are useful for diagnosis, study and treatment of cancer, urogenital, and brain degenerative diseases.

FEATURES OF PROTEIN ENCODED BY GENE NO: 77

This gene is expressed primarily in fetal liver, activated monocytes, osteoblasts
30 and to a lesser extent in synovial, brain, and lymphoid tissues.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of myeloid and lymphoid present in a biological sample and for diagnosis of diseases and conditions: inflammation, immune deficiencies, cancer. Similarly, polypeptides and antibodies directed to these
35 polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune system and skeleton, expression of this gene at significantly

higher or lower levels may be routinely detected in certain tissues and cell types (e.g., liver, blood cells, bone, synovial tissue, brain and other tissue of the nervous system, and lymphoid tissue, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample
5 taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for study, diagnosis, and treatment of lymphoid
10 and mesenchymal cancers and nervous system diseases.

FEATURES OF PROTEIN ENCODED BY GENE NO: 78

The translation product of this gene shares sequence homology with polymerase polyprotein precursor which is thought to be important in DNA repair and replication

15 This gene is expressed primarily in infant brain and to a lesser extent in tumors and tumor cell lines

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions which include, but are
20 not limited to, especially of the neural system and developing organs. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the neural system expression of this gene at significantly higher or lower levels may be routinely detected
25 in certain (e.g., brain and other tissue of the nervous system, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

30 The tissue distribution and homology to polymerase polyprotein precursor indicate that polynucleotides and polypeptides corresponding to this gene are useful for diagnosis and treatment of cancers especially of the neural system and developing organs

35 FEATURES OF PROTEIN ENCODED BY GENE NO: 79

This gene is expressed primarily in muscle and endothelial cells and to a lesser extent in brain.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: vascular diseases. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the vascular system, expression of this gene at significantly higher or lower levels may be routinely detected in certain (e.g., muscle, endothelial cells, brain and other tissue of the nervous system, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for treatment and diagnosis of disorders of the vascular and neural system including cardiovascular and endothelial.

FEATURES OF PROTEIN ENCODED BY GENE NO: 80

This gene is expressed primarily in placenta and to a lesser extent in fetal liver

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: developmental disorders and disorder of the haemopoietic system, fetal liver and placenta. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of developmental disorders and disorder of the haemopoietic system, fetal liver and placenta, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., placenta and liver, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for diagnosis and treatment of developmental disorders and disorders of the haemopoietic system, fetal liver and placenta.

FEATURES OF PROTEIN ENCODED BY GENE NO: 81

This gene is expressed primarily in bone marrow, placenta and tissues and organs of the hematopoietic system.

5 Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: disorders of the bone and haemopoietic system. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification
10 of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune, bone and hematopoietic system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., bone marrow, placenta, and hematopoietic cells, and cancerous and
15 wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for diagnosis and treatment of disorders of the
20 immune, bone and hematopoietic system

FEATURES OF PROTEIN ENCODED BY GENE NO: 82

The translation product of this gene shares sequence homology with secretory carrier membrane protein which is thought to be important in protein transport and
25 export. Any frame shifts in coding sequence can be easily resolved using standard molecular biology techniques. Another group recently cloned this gene, calling it SCAMP. (See Accession No. 2232243.)

This gene is expressed primarily in prostate, breast and spleen, and to a lesser extent in several other tissues and organs.

30 Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: disorders of the breast prostate and spleen. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification
35 of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly disorders of the breast prostate and spleen, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell

types (e.g., prostate, mammary tissue, and spleen, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution and homology to secretory carrier membrane protein indicate that polynucleotides and polypeptides corresponding to this gene are useful for diagnosis and treatment of disorders of the breast, prostate and spleen.

10 **FEATURES OF PROTEIN ENCODED BY GENE NO: 83**

This gene is expressed primarily in developing organs and tissue like placenta and infant brain and to a lesser extent in developed organs and tissue like cerebellum and heart.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: neurological diseases. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the neural system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., placenta, heart, brain and other tissue of the nervous system, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for treatment and diagnosis of diseases of the neural system including neurological disorders and cancer.

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FEATURES OF PROTEIN ENCODED BY GENE NO: 84

The translation product of this gene shares sequence homology with ATPase 6 in *Trypanosoma brucei* which is thought to be important in metabolism.

This gene is expressed primarily in tumor and fetal tissues and to a lesser extent in melanocytes, kidney cortex, monocytes and ovary.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a

biological sample and for diagnosis of diseases and conditions: metabolism disorders. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the fetal systems, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., fetal tissues, melanocytes, kidney, blood cells, ovary and other tissue of the reproductive system, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution and homology to ATPase indicate that polynucleotides and polypeptides corresponding to this gene are useful for treatment and diagnosis of metabolism disorders, especially in fetal and tumor tissue growth.

FEATURES OF PROTEIN ENCODED BY GENE NO: 85

The translation product of this gene shares sequence homology with the immunoglobulin superfamily of proteins which are known to be important in immune response and immunity.

This gene is expressed primarily in stromal cells, colon cancer, lung, amygdala, melanocyte and to a lesser extent in a variety of other tissues.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: defects of stromal cell development and cancer. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the stromal cells, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., stromal cells, colon, lung, amygdala, and melanocytes, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution and homology to immunoglobulin indicate that polynucleotides and polypeptides corresponding to this gene are useful for treatment and diagnosis of immune system disorders.

FEATURES OF PROTEIN ENCODED BY GENE NO: 86

The translation product of this gene shares sequence homology with transcription initiation factor eIF-4 gamma which is thought to be important in gene transcription.

This gene is expressed primarily in tumor tissues.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: tumorigenesis.

Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly in tumor tissues, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., endometrium and lung, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution and homology to transcription initiation factor eIF-4 gamma indicate that polynucleotides and polypeptides corresponding to this gene are useful for gene regulation in tumorigenesis.

FEATURES OF PROTEIN ENCODED BY GENE NO: 87

The translation product of this gene shares sequence homology at low level in prolines with secreted basic proline-rich peptide II-2 which is thought to be important in protein structure or inhibiting hydroxyapatite formation in vitro.

This gene is expressed primarily in endometrial tumor and fetal lung.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: endometrial tumors. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the muscular/skeletal and reproductive systems, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., endometrium, and lung, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample

taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution and homology to secreted basic proline-rich peptide II-2 indicate that polynucleotides and polypeptides corresponding to this gene are useful for inhibiting hydroxyapatite formation or establishing cell/tissue structure.

FEATURES OF PROTEIN ENCODED BY GENE NO: 88

This gene is expressed primarily in: amniotic cells induced with TNF in culture; and to a lesser extent in colon tissue from a patient with Crohn's Disease; parathyroid tumor; activated T-cells; cells of the human Caco-2 cell line; adenocarcinoma; colon; corpus colosum; fetal kidney; pancreas tumor; fetal brain; early stage brain, and anergic T-cells.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: tumors. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune system; e.g., tumors, expression of this gene at significantly higher or lower levels may be routinely detected in certain (e.g., amniotic cells, colon, kidney, pancreas, parathyroid, brain and other tissue of the nervous system, blood cells, hematopoietic cells, liver, spleen, bone, testes and other reproductive tissue, brain and other tissue of the nervous system, and epithelial cells, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that the protein product of this clone is useful for modulating tumorigenesis and other immune system conditions such as disorders in immune response.

FEATURES OF PROTEIN ENCODED BY GENE NO: 89

This gene is expressed primarily in fetal liver/spleen and hematopoietic cells and to a lesser extent in brain, osteosarcoma, and testis tumor.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a

biological sample and for diagnosis of diseases and conditions: leukemia and hematopoietic disorders. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the hematopoietic and immune systems, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., hematopoietic cells, liver, spleen, bone, testes, and other reproductive tissue, brain and other tissue of the nervous system, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for diagnosis and treatment of hematopoietic and immune disorders.

FEATURES OF PROTEIN ENCODED BY GENE NO: 90

The translation product of this gene shares weak sequence homology with mouse Gcap1 protein which is developmentally regulated in brain.

This gene is expressed primarily in infant and adult brain and fetal liver/spleen and to a lesser extent in smooth muscle, T cells, and a variety of other tissues.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: neurological or hematopoietic disorders. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the nervous, hematopoietic, immune, and endocrine systems, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., brain and other tissue of the nervous system, blood cells, liver, spleen, and smooth muscle, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution and its homology to Gcap1 protein indicate that polynucleotides and polypeptides corresponding to this gene are useful for treatment and diagnosis of disorders in neuronal, hematopoietic, immune, and endocrine systems.

5 FEATURES OF PROTEIN ENCODED BY GENE NO: 91

This gene is expressed primarily in brain and hematopoietic cells and to a lesser extent in tumor tissues.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: disorder in nervous, hematopoietic, immune systems and tumorigenesis. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the nervous, hematopoietic, immune systems, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., brain and other tissue of the nervous system, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that the protein product of this clone is useful for diagnosis and treatment of disorders in the nervous, hematopoietic, and immune systems.

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FEATURES OF PROTEIN ENCODED BY GENE NO: 92

The translation product of this gene shares sequence homology with neuroendocrine-specific protein A which is thought to be important in neurologic systems.

30 This gene is expressed primarily in brain tissues.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: neural disorders and degeneration disease. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the central or peripheral nervous systems, expression of this gene at

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significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., hematopoietic cells, and brain and other tissue of the nervous system, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having
5 such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution and homology to neuroendocrine-specific protein A indicate that polynucleotides and polypeptides corresponding to this gene are useful for treatment or diagnosis of neural disorders and degeneration disease.

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FEATURES OF PROTEIN ENCODED BY GENE NO: 93

The translation product of this gene shares sequence homology with collagen-like protein and prolin-rich protein which are thought to be important in connective tissue function and tissue structure.

15 This gene is expressed primarily in fetal liver/spleen and brain tissues.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: neuronal or hematopoietic disorders. Similarly, polypeptides and antibodies directed to these
20 polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the nervous and hematopoietic systems, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., liver, spleen, and brain and other tissue of the nervous system, and
25 cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution and homology to collagen-like protein and proline-rich
30 proteins indicate that polynucleotides and polypeptides corresponding to this gene are useful for supporting brain and hematopoietic tissue function and diagnosis and treatment of disorders in these functions.

FEATURES OF PROTEIN ENCODED BY GENE NO: 94

35 This gene is expressed primarily in embryonic tissues and tumor tissues.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a

biological sample and for diagnosis of diseases and conditions which include, but are not limited to,. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of
5 the immune system (e.g., tumors), expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., embryonic tissue and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e.,
10 the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for diagnosis and treatment of cancer.

15 **FEATURES OF PROTEIN ENCODED BY GENE NO: 95**

This gene is expressed primarily in brain tumor, placenta, and melanoma.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: brain tumor or
20 melanoma. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the brain or melanocytes, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., brain and other tissue of
25 the nervous system, placenta, and melanocytes, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

30 The tissue distribution indicates that the translation product of this gene is useful in the diagnosis and treatment of brain tumors and melanoma.

FEATURES OF PROTEIN ENCODED BY GENE NO: 96

The translation product of this gene shares sequence homology with a yeast
35 membrane protein, SUR4, which encodes for APA1 that acts on a glucose-signaling pathway that controls the expression of several genes that are transcriptionally regulated by glucose.

This gene is expressed primarily in fetal liver, and to a lesser extent in placenta and breast tissue.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: defects of fetal liver or defects of glucose-regulated ATPase activities in tissues. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the fetal immune/hematopoietic system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., liver, placenta, and mammary tissue, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution and homology to yeast SUR4 membrane protein indicate that polynucleotides and polypeptides corresponding to this gene are useful for diagnosis and treatment of defects of fetal liver or defects of glucose-regulated ATPase activities.

FEATURES OF PROTEIN ENCODED BY GENE NO: 97

This gene is expressed primarily in fetal liver, brain, and amniotic fluid.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: defects of the fetal immune system and adult brain. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the fetal immune system and adult brain, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., liver, and brain and other tissue of the nervous system, and cancerous and wounded tissues) or bodily fluids (e.g., amniotic fluid, serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that the protein product of this clone is useful for detecting defects of the fetal immune and hematopoietic systems since fetal liver is

the predominant organ responsible for hematopoiesis in the fetus. In addition, the gene product of this gene is thought to be useful for detecting certain neurological defects of the brain.

5 FEATURES OF PROTEIN ENCODED BY GENE NO: 98

The translation product of this gene shares sequence homology with an yolk protein precursor, Vitellogenin which is thought to be important in binding lipids such as phosvitin.

This gene is expressed primarily in amniotic cells and fetal liver.

10 Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: defects in amniotic cells, fetal liver development and the fetal immune system. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes
15 for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the [insert system where a related disease state is likely, e.g., immune], expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., amniotic cells, and liver, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma,
20 urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution and homology to vitellogenin indicate that the protein
25 product of this clone is useful for treatment and diagnosis of defects in amniotic cells, fetal liver development and the fetal immune system.

FEATURES OF PROTEIN ENCODED BY GENE NO: 99

This gene is expressed primarily in placenta, endometrial tumor, osteosarcoma
30 and stromal cells.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: tumor of the endometrium or bone, and osteosarcoma. Similarly, polypeptides and antibodies
35 directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the obstetric system (e.g. placenta,

endometrium) and the bones, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., placenta, endometrium, bone, and stromal cells, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for diagnosis and treatment of tumors and abnormalities of the endometrium, and the bones because of its abundance in the aforementioned tissues..

FEATURES OF PROTEIN ENCODED BY GENE NO: 100

This gene is expressed primarily in hepatocellular tumor.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: hepatocellular tumor. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the liver, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., liver, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that the protein product of this clone is useful for diagnosis and treatment of hepatocellular cancer because of its abundant expression in this tissue.

FEATURES OF PROTEIN ENCODED BY GENE NO: 101

This gene is expressed primarily in Corpus Colosum, fetal lung and infant brain.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: defects of the Corpus Colosum or defects of the fetal lung. Similarly, polypeptides and antibodies directed to

these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the Corpus Colosum and brain in general, and fetal lung, expression of this gene at significantly higher or lower levels may be routinely detected

5 in certain tissues and cell types (e.g., lung, and brain and other tissue of the nervous system, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the

10 disorder.

The tissue distribution indicates that the protein product of this clone is useful for diagnosis and treatment of defects of the Corpus Colosum and brain in general, and defects of fetal lung.

15 **FEATURES OF PROTEIN ENCODED BY GENE NO: 102**

This gene is expressed primarily in T cells and stromal cells, and to a lesser extent in adrenal gland.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a

20 biological sample and for diagnosis of diseases and conditions: defects of T cell immunity and stromal cell development. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune system, expression of this gene at

25 significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., blood cells, stromal cells, and adrenal gland, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily

30 fluid from an individual not having the disorder.

The tissue distribution indicates that the protein product of this clone is useful for diagnosis and treatment of defects of T cell immunity and stromal cell development because of its abundant expression in these tissues.

35 **FEATURES OF PROTEIN ENCODED BY GENE NO: 103**

This gene is expressed primarily in infant brain and placenta.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: defects of the brain and nervous system. Similarly, polypeptides and antibodies directed to these polypeptides
5 are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the nervous system, especially brain, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell
10 types (e.g., brain and other tissue of the nervous system, and placenta, cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that the protein product of this clone is useful
15 for detecting defects of the brain, especially in young children.

FEATURES OF PROTEIN ENCODED BY GENE NO: 105

This gene is expressed primarily in human osteoclastoma and to a lesser extent in human pancreas tumor.

20 Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions which include, but are not limited to, cancer particularly osteoclastoma and pancreatic tumor. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing
25 immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly in transformed tissues, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., bone and pancreas, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or
30 another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that the protein product of this clone is useful for diagnosis and treatment of some types of tumors, particularly pancreatic cancer and
35 osteoclastoma.

FEATURES OF PROTEIN ENCODED BY GENE NO: 106

This gene is expressed primarily in fetal liver/spleen, and to a lesser extent in activated T-Cells.

Therefore, polynucleotides and polypeptides of the invention are useful as
5 reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: immune disorders. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the
10 immune system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., liver, spleen, and blood cells, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the
15 expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for diagnosis or treatment of immune disorders.

20 FEATURES OF PROTEIN ENCODED BY GENE NO: 107

This gene is expressed primarily in human embryo and to a lesser extent in spleen and chronic lymphocytic leukemia.

Therefore, polynucleotides and polypeptides of the invention are useful as
25 reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: leukemia. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune or hemopoietic systems, expression of this gene at significantly higher or lower levels may
30 be routinely detected in certain tissues and cell types (e.g., embryonic tissue, spleen, and blood cells, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the
35 disorder.

The tissue distribution indicates that the protein product of this clone is useful for the diagnosis and treatment of leukemia.

FEATURES OF PROTEIN ENCODED BY GENE NO: 108

This gene is expressed primarily in placenta, and to a lesser extent in early stage human brain and in lung.

5 Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: fetal developmental abnormalities. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s)
10 or cell type(s). For a number of disorders of the above tissues or cells, particularly in fetal and amniotic tissue, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., placenta, brain and other tissue of the nervous system, and lung, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another
15 tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that the protein product of this is useful for production of growth factor(s) associated with fetal development. Preferred
20 polypeptides comprise the full-length polypeptide shown in the sequence listing, truncated however, at the amino terminus and beginning with QTIE.

FEATURES OF PROTEIN ENCODED BY GENE NO: 109

This gene is expressed primarily in fetal spleen, and to a lesser extent in B-Cell
25 lymphoma and T-Cell lymphoma.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: lymphoma. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing
30 immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., spleen and blood cells, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal
35 fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that the protein product of this clone is useful for the treatment and diagnosis of human lymphomas.

FEATURES OF PROTEIN ENCODED BY GENE NO: 110

5 The translation product of this gene shares sequence homology with sarcoma amplified sequence (SAS), a tetraspan receptor which is thought to be important in malignant fibrous histiocyoma and liposarcoma.

This gene is expressed primarily in human osteoclastoma, and to a lesser extent in pineal gland and infant brain.

10 Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: malignant fibrous histiocyoma and liposarcoma. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification
15 of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., bone, pineal gland, and brain and other tissue of the nervous system, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal
20 fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution and homology to sarcoma amplified sequence (SAS) indicate that the protein product of this clone is useful for treatment of, osteosarcoma,
25 malignant fibrous histiocyoma and liposarcoma and related cancers, particularly sarcomas.

FEATURES OF PROTEIN ENCODED BY GENE NO: 111

The translation product of this gene shares sequence homology with 6.8K
30 proteolipid protein, mitochondrial - bovine.

This gene is expressed primarily in Wilm's tumor and to a lesser extent in cerebellum and placenta.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a
35 biological sample and for diagnosis of diseases and conditions: Wilm's tumor. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell

type(s). For a number of disorders of the above tissues or cells, particularly of the immune or renal systems, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., brain and other tissue of the nervous system, and placenta, and cancerous and wounded tissues) or bodily fluids
5 (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution and homology to 6.8K proteolipid protein indicate that
10 the protein product of this clone is useful for diagnostic and therapeutics associated with tumors, particularly Wilm's tumor disease.

FEATURES OF PROTEIN ENCODED BY GENE NO: 112

This gene is expressed primarily in embryonic tissue and to a lesser extent in
15 osteoblasts, endothelial cells, macrophages (GM-CSF treated), and bone marrow.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: immune disorders. Similarly, polypeptides and antibodies directed to these polypeptides are useful in
20 providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., embryonic tissue, bone, endothelial cells, blood cells and bone marrow, and cancerous and wounded tissues) or
25 bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that polynucleotides and polypeptides
30 corresponding to this gene are useful for treatment or diagnosis of immune disorders. Preferred polypeptides encoded by this gene comprise the following amino acid sequence: MITDVQLAIFANMLGVSLFLLVVLHYHVA VNNPKKQE (SEQ ID NO: 636).

FEATURES OF PROTEIN ENCODED BY GENE NO: 113

35 This gene is expressed primarily in hepatocellular tumor, and to a lesser extent in fetal liver/spleen.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: tumors, particularly hepatocellular tumors. Similarly, polypeptides and antibodies directed to these

5 polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the hepatic system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., liver, and spleen, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma,

10 urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that the protein product of this clone is useful

15 for diagnosis and treatment of tumors, particularly hepatocellular tumors.

FEATURES OF PROTEIN ENCODED BY GENE NO: 114

The translation product of this gene exhibits a very high degree of sequence identity with the human Pig8 gene which is thought to be important in p53 mediated

20 apoptosis. The sequence of this gene has since been published by Polyak and colleagues (Nature 389, 300-306 (1997)). In addition, the predicted translation product of this contig exhibits very high sequence homology with a murine gene denoted as EI24 which is also thought to be important in p53 mediated apoptosis.

This gene is expressed primarily in infant brain and activated T-cells and to a

25 lesser extent in bone marrow, fetal liver, and prostate.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions which include, but are not limited to, and tissue damage by radiation and anti-cancer drugs. Similarly,

30 polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the nervous and immune systems, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., brain and other tissue of the

35 nervous system, blood cells, bone marrow, liver, and prostate, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder,

relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution and homology to human Pig8 and murine EI24 genes indicate that polynucleotides and polypeptides corresponding to this gene are useful for preventing apoptosis in patients being treated with anti-oncogenic drugs such as etoposide, hydroperoxycyclophosphamide, and X-irradiation, since this protein product is upregulated in cells undergoing such treatment where p53 was overexpressed. It may also be useful in the treatment of hematopoietic disorders and in boosting numbers of hematopoietic stem cells by interfering with the apoptosis of progenitor cells. The mature polypeptide is predicted to comprise the following amino acid sequence:

EEMADSVKTFQLDARGIKDSIWGICTISKLDARIQQKREEQRRRRASSVLAQRRRAQSIERKQES
EPRIVSRIFQCCA WNGGVFWFSLLLFYRVFIPVLQSVTARIIGDPSLHGDVWSWLEFFLTSIFSA
LWVLPFLVLSKVVNAIWFQDIADLAFEVSGRKPFPFSVKIADMLFNLLLQALFLIQGMFVSL
FPIHLVGQLVSLHMSLLYSLYCFEYRWFNKGIEHQRLSNIERNWPYYFGFGLPLAFLTAMQ
SSYIISGCLFSLFPLFIISANEAKTPGKAYLFQLRFLSLVVFLSNRLFHKTVYLQSALSSSTSAEK
FPSPHSPAKLKATAGH (SEQ ID NO: 637). Accordingly, polypeptides comprising the foregoing amino acid sequence are provided as are polynucleotides encoded such polypeptides.

20 FEATURES OF PROTEIN ENCODED BY GENE NO: 115

This gene is expressed primarily in stromal cells and to a lesser extent in multiple sclerosis.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: affecting the nervous system. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the nervous system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., stromal cells and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for treatment and diagnosis of multiple sclerosis and other autoimmune diseases.

FEATURES OF PROTEIN ENCODED BY GENE NO: 116

This gene is expressed primarily in the gall bladder

Therefore, polynucleotides and polypeptides of the invention are useful as
5 reagents for differential identification of the tissue(s) or cell type(s) present in a
biological sample and for diagnosis of diseases and conditions: gall stones or infection
of the digestive system. Similarly, polypeptides and antibodies directed to these
polypeptides are useful in providing immunological probes for differential identification
10 of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells,
particularly of the digestive system or renal system, expression of this gene at
significantly higher or lower levels may be routinely detected in certain tissues and cell
types (e.g., gall bladder and tissue of the digestive system, and cancerous and wounded
tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or
15 another tissue or cell sample taken from an individual having such a disorder, relative to
the standard gene expression level, i.e., the expression level in healthy tissue or bodily
fluid from an individual not having the disorder.

The tissue distribution indicates that polynucleotides and polypeptides
corresponding to this gene are useful for possible prevention of digestive disorders
where there may be a lack of digestive enzymes produced or in the detection and
20 possible prevention of gall stones.

FEATURES OF PROTEIN ENCODED BY GENE NO: 117

The translation product of this gene shares sequence homology with dystrophin
gene which is thought to be important in building and maintenance of muscles.

25 This gene is expressed primarily in placenta and to a lesser extent in fetal brain
and fetal liver, and spleen.

Therefore, polynucleotides and polypeptides of the invention are useful as
reagents for differential identification of the tissue(s) or cell type(s) present in a
biological sample and for diagnosis of diseases and conditions: muscular dystrophy,
30 Duchenne and Becker's muscular dystrophies. Similarly, polypeptides and antibodies
directed to these polypeptides are useful in providing immunological probes for
differential identification of the tissue(s) or cell type(s). For a number of disorders of
the above tissues or cells, particularly of the skeletal muscle system, expression of this
gene at significantly higher or lower levels may be routinely detected in certain tissues
35 and cell types (e.g., placenta, brain and other tissue of the nervous system, muscle,
liver, and spleen, and cancerous and wounded tissues) or bodily fluids (e.g., serum,
plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from

an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

- 5 The tissue distribution and homology to the dystrophin gene indicate that polynucleotides and polypeptides corresponding to this gene are useful for diseases related the degenerative myopathies that are characterized by the weakness and atrophy of muscles without neural degradation; such as Duchenne and Becker's muscular dystrophies.

10 **FEATURES OF PROTEIN ENCODED BY GENE NO: 118**

This gene is expressed primarily in olfactory tissue and to a lesser extent in cartilage.

- Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: connective tissue diseases; chondrosarcoma. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the connective tissue, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., olfactory tissue and cartilage, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for tumors of connective tissues, osteoarthritis and the treatment and diagnosis of chondrosarcoma.

30 **FEATURES OF PROTEIN ENCODED BY GENE NO: 119**

This gene is expressed primarily in Activated Neutrophils and to a lesser extent in fetal spleen, and CD34 positive cells from cord blood.

- Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: allergies, defects in hematopoiesis and inflammation. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential

identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune system and hematopoiesis system the, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., blood cells, and spleen, and cancerous and
5 wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that polynucleotides and polypeptides
10 corresponding to this gene are useful for reducing the allergic effects felt by allergy suffers by neutralizing the activity of the immune system, especially since neutrophils are abundant in persons suffering from allergies and other inflammatory conditions.

FEATURES OF PROTEIN ENCODED BY GENE NO: 120

15 The translation product of this gene shares sequence homology with poly A binding protein II which is thought to be important in RNA binding for transcription of RNA to DNA

This gene is expressed primarily in colon and to a lesser extent in brain and immune system.

20 Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: colon cancer. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a
25 number of disorders of the above tissues or cells, particularly of the immune and digestive system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., colon, tissue and cells of the immune system, and brain or other tissue of the nervous system, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal
30 fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution and homology to poly A binding protein II indicate that polynucleotides and polypeptides corresponding to this gene are useful for detection
35 and treatment of colon cancer and other disorders of the digestive system..

FEATURES OF PROTEIN ENCODED BY GENE NO: 121

The translation product of this gene shares sequence homology with thymidine diphosphoglucose 4.6 dehydrase which is thought to be important in the metabolism of sugar.

5 This gene is expressed primarily in fetal liver and spleen and to a lesser extent in infant brain.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: diabetes. Similarly,
10 polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the endocrine system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., liver, spleen, and brain and other tissue of the
15 nervous system, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

20 The tissue distribution and homology to thymidine diphosphoglucose 4.6 dehydrase indicate that polynucleotides and polypeptides corresponding to this gene are useful for treatment of persons with diabetes since it appears that this protein is needed in the metabolism of sugar in to its more basic components.

25 FEATURES OF PROTEIN ENCODED BY GENE NO: 122

The translation product of this gene shares sequence homology with ceruloplasmin which is thought to be important in the metabolism and transport of iron and copper. Ceruloplasmin also contains domains with homology to clotting factors V and VIII. Defects in the circulating levels of ceruloplasmin (aceruloplasminemia) have
30 been associated with certain disease conditions such as Wilson disease, and the accompanying hepatolenticular degeneration.

This gene is expressed primarily in brain and retina and to a lesser extent in endothelial cells.

Therefore, polynucleotides and polypeptides of the invention are useful as
35 reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: diseases marked by defects in iron metabolism; aceruloplasminemia not characterized by defects in the

known ceruloplasmin gene locus; nonclassical Wilson disease; movement disorders; and tumors derived from a brain tissue origin. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the brain, retina, and nervous system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., brain and other tissue of the nervous system, retinal tissue, and endothelial cells, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution and homology to ceruloplasmin indicate that polynucleotides and polypeptides corresponding to this gene are useful for treatment of patients with aceruloplasminemia, or other defects in iron and/or copper metabolism. Mutations in this locus could also be diagnostic for patients currently experiencing or predicted to experience aceruloplasminemia.

FEATURES OF PROTEIN ENCODED BY GENE NO: 123

This gene is expressed primarily in brain and B cell lymphoma and to a lesser extent in fetal liver and spleen.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: B cell lymphoma; tumors and diseases of the brain and/or spleen; hematopoietic defects. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the brain and hematopoietic system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., brain and other tissue of the nervous system, blood cells, liver, and spleen, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for treatment of disorders in neuronal,

hematopoietic, and immune systems. It could potentially be useful for neurodegenerative disorders and neuronal and/or hematopoietic cell survival or proliferation.

5 **FEATURES OF PROTEIN ENCODED BY GENE NO: 124**

This gene is expressed primarily in osteoclastoma, dermatofibrosarcoma, and B cell lymphoma and to a lesser extent in endothelial cells.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions which include, but are not limited to, cancer in particular osteoclastoma, dermatofibrosarcoma, and B cell lymphoma. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the bone, immune, and circulatory system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., bone, epidermis, blood cells, and endothelial cells, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for diagnosis and treatment of cancers and lymphoma; osteoporosis; and the control of cell proliferation and/or differentiation.

25 **FEATURES OF PROTEIN ENCODED BY GENE NO: 125**

This gene is expressed primarily in immune tissues and hematopoietic cells, particularly in activated T cells and neutrophils, spleen, and fetal liver, and to a lesser extent in infant adrenal gland.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: defects in T cell activation; hematopoietic disorders; tumors of a hematopoietic and/or adrenal gland origin. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the hematopoietic and/or endocrine systems, expression of this gene at significantly higher

or lower levels may be routinely detected in certain tissues and cell types (e.g., cells and tissues of the immune system, hematopoietic cells, blood cells, liver, and adrenal gland, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual
5 having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for immune and/or hematopoietic disorders;
10 diseases related to proliferation and/or differentiation of hematopoietic cells; defects in T cell and neutrophil activation and responsiveness; and endocrine and/or metabolic disorders, particularly of early childhood.

FEATURES OF PROTEIN ENCODED BY GENE NO: 126

15 This gene is expressed primarily in placenta and endothelial cells and to a lesser extent in melanocytes and embryonic tissues.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: tumors of an endothelial
20 cell origin; angiogenesis associated with tumor development and metastasis. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the vascular system and developing embryo, expression of this gene at significantly higher or lower levels
25 may be routinely detected in certain tissues and cell types (e.g., placenta, endothelial cells, melanocytes, and embryonic tissues, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily
30 fluid from an individual not having the disorder.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for treatment of developmental disorders; inhibition of angiogenesis; and vascular patterning.

35 FEATURES OF PROTEIN ENCODED BY GENE NO: 127

This gene is expressed primarily in endothelial cells and hematopoietic tissues, including spleen, tonsils, leukocytes, and both B- and T-cell lymphomas.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: tumors of an endothelial cell and/or hematopoietic origin; leukemias and lymphomas. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune and vascular systems, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., endothelial cells, hematopoietic cells, spleen, tonsils, and blood cells, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for the manipulation of angiogenesis; the differentiation and morphogenesis of endothelial cells; the proliferation and/or differentiation of hematopoietic cells; and the commitment of hematopoietic cells to distinct cell lineages.

20

FEATURES OF PROTEIN ENCODED BY GENE NO: 128

This gene is expressed primarily in kidney medulla and to a lesser extent in spleen from chronic myelogenous leukemia patients, prostate cancer, and some other tissues.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: tumors of a kidney origin; chronic myelogenous leukemia; prostate cancer. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the kidney and spleen, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., kidney, spleen, and prostate, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for the diagnosis and treatment of kidney disorders and cancer, particularly chronic myelogenous leukemia and prostate cancer. It may also be useful for the enhancement of kidney tubule regeneration in the treatment of acute renal failure.

FEATURES OF PROTEIN ENCODED BY GENE NO: 129

This gene is expressed primarily in adult and infant brain and to a lesser extent in mesenchymal or fibroblast cells, as well as tissues with a mesenchymal origin.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: tumors of a brain and/or mesenchymal origin; neurodegenerative disorders; cancer; fibrosis. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the brain and of mesenchymal cells and tissues, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., brain and other tissue of the nervous system and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for the diagnosis of tumors of a brain and/or mesenchymal origin; neurodegenerative disorders; cancer; and fibrosis, based upon the expression of this gene within those tissues. Fibrosis is considered as mesenchymal cells and fibroblasts are the primary cellular targets involved in this pathological condition.

FEATURES OF PROTEIN ENCODED BY GENE NO: 130

This gene is expressed primarily in hepatocellular cancer and to a lesser extent in fetal tissues as well as testes tumor.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: liver cancer. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing

immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the digestive system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., liver, fetal tissue, and testes and other

5 reproductive tissue, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

10 The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for diagnosis and treatment of liver cancer.

FEATURES OF PROTEIN ENCODED BY GENE NO: 131

This gene is expressed only in infant early brain.

15 Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: development and diseases of the nervous system. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification
20 of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the brain and nervous system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., brain and other tissue of the nervous system and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another
25 tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for treating diseases of the brain in children and in
30 treating nervous system disorders such as Alzheimer's disease, schizophrenia, dementia, depression, etc.

FEATURES OF PROTEIN ENCODED BY GENE NO: 132

This gene is expressed primarily in brain and to a lesser extent in glioblastoma.

35 Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: Alzheimer's disease,

schizophrenia, depression, mania, and dementia. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the brain and nervous system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., brain and other tissue of the nervous system, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for treating brain disorders such as Alzheimer's disease, schizophrenia, depression, mania, and dementia.

15 FEATURES OF PROTEIN ENCODED BY GENE NO: 133

The translation product of this gene shares sequence homology with ribitol dehydrogenase of bacteria which is thought to be important in metabolism of sugars.

This gene is expressed primarily in macrophage and to a lesser extent in T-cell lymphoma and lung.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: tissue destruction in inflammation. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., blood cells and lung, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution and homology to ribitol dehydrogenase indicate that polynucleotides and polypeptides corresponding to this gene are useful for altering macrophage metabolism in diseases such as inflammation where macrophages are causing excess tissue destruction.

FEATURES OF PROTEIN ENCODED BY GENE NO: 134

This gene is expressed primarily in pancreatic tumor and to a lesser extent in synovial sarcoma.

Therefore, polynucleotides and polypeptides of the invention are useful as
5 reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions which include, but are not limited to,. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of
10 the endocrine and connective tissue systems, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., pancreas, and synovial tissue, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene
15 expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for treating and diagnosing various cancers.

20 FEATURES OF PROTEIN ENCODED BY GENE NO: 135

This gene is expressed primarily in T cell lines such as Raji and to a lesser extent in infant brain.

Therefore, polynucleotides and polypeptides of the invention are useful as
25 reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: immune system disorders and inflammation. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune system, expression of this gene at significantly higher or
30 lower levels may be routinely detected in certain tissues and cell types (e.g., blood cells, and brain and other tissue of the nervous system, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily
35 fluid from an individual not having the disorder.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for treating and diagnosing inflammatory diseases

such as rheumatoid arthritis, sepsis, inflammatory bowel disease, and psoriasis, as well as neutropenia.

FEATURES OF PROTEIN ENCODED BY GENE NO: 136

5 The translation product of this gene shares high sequence homology with SAR1 subfamily of GTP-binding proteins which is thought to be important in vesicular transport in mammalian cells.

 This gene is expressed primarily in serum-stimulated smooth muscle cells and to a lesser extent in a T-cell lymphoma.

10 Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: diseases affecting vesicular transport. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification
15 of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the muscular system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., blood cells, and smooth muscle, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample
20 taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

 The tissue distribution and homology to GTP-binding proteins indicate that polynucleotides and polypeptides corresponding to this gene are useful for gene therapy
25 in treating the large number of diseases involved in defective vesicular transport within cells..

FEATURES OF PROTEIN ENCODED BY GENE NO: 137

 The translation product of this gene shares sequence homology with a protein
30 found in *C. elegans* cosmid F25B5.

 This gene is expressed primarily in a fetal tissues and to a lesser extent in melanocytes.

 Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a
35 biological sample and for diagnosis of diseases and conditions: abnormal fetal development, especially of the pulmonary system. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes

for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the fetal pulmonary system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., fetal tissue, pulmonary tissue, and melanocytes, and
5 cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that polynucleotides and polypeptides
10 corresponding to this gene are useful for treatment and diagnosis of diseases affecting the pulmonary system, such as emphysema.

FEATURES OF PROTEIN ENCODED BY GENE NO: 138

This gene is expressed primarily in gall bladder and to a lesser extent in smooth
15 muscle.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: digestive system disease and gall bladder problems. Similarly, polypeptides and antibodies directed to these
20 polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the digestive system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., gall bladder and tissue of the digestive system, and smooth muscle, and cancerous and
25 wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that polynucleotides and polypeptides
30 corresponding to this gene are useful for treating diseases of the digestive system.

FEATURES OF PROTEIN ENCODED BY GENE NO: 139

This gene is expressed primarily in placenta and to a lesser extent in brain.

Therefore, polynucleotides and polypeptides of the invention are useful as
35 reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: abnormal fetal development. Similarly, polypeptides and antibodies directed to these polypeptides are

- useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of developing tissues, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., placenta, and brain and other
- 5 tissue of the nervous system, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.
- 10 The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for treating and diagnosing abnormal fetal development.

FEATURES OF PROTEIN ENCODED BY GENE NO: 140

- 15 This gene is expressed primarily in smooth muscle and to a lesser extent in ovary, prostate cancer, and activated monocytes.
- Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: hypertension and
- 20 atherosclerosis. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the circulatory system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., smooth
- 25 muscle, ovary and other reproductive tissue, prostate, and blood cells, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.
- 30 The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for treating diseases of the circulatory system, such as hypertension, atherosclerosis, etc.

FEATURES OF PROTEIN ENCODED BY GENE NO: 141

- 35 This gene is expressed primarily in fetal spleen and to a lesser extent in placenta and bone marrow.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: anemia and other diseases affecting blood cells. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the circulatory and pulmonary systems, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., spleen, placenta, bone marrow, and blood cells, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for the generation of red and white blood cells and for the diagnosis of disease of these cells.

FEATURES OF PROTEIN ENCODED BY GENE NO: 142

The predicted translation product of this contig is a human homolog of the murine tetracycline/sugar transporter molecule recently reported by Matsuo and colleagues (Biochem. Biophys. Res. Commun. 238 (1), 126-129 (1997)).

This gene is expressed primarily in synovium and to a lesser extent in endothelial cells.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: rheumatoid arthritis and inflammation. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune and lymphatic systems, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., synovial tissue, and endothelial cells, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for treatment and diagnosis of inflammatory diseases, such as rheumatoid arthritis, leukemia, neutropenia, inflammatory bowel disease, psoriasis, sepsis, and the like.

5

FEATURES OF PROTEIN ENCODED BY GENE NO: 143

This gene is expressed primarily in placenta and to a lesser extent in melanocyte, fetal liver and spleen, and bone marrow.

Therefore, polynucleotides and polypeptides of the invention are useful as
10 reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: abnormal early development. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, lower levels
15 may be routinely detected in certain tissues and cell types (e.g., placenta, melanocytes, liver, spleen, and bone marrow, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an
20 individual not having the disorder.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for the treatment and diagnosis of abnormal early development phenomena and diseases.

25 FEATURES OF PROTEIN ENCODED BY GENE NO: 144

This gene is expressed primarily in fetal liver and spleen.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: anemia and neutropenia.
30 Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune and blood systems, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., liver and spleen,
35 and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the

expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful in hematopoiesis and bone marrow regeneration as it is most abundant in fetal tissues responsible for the generation of hematopoietic cells.

FEATURES OF PROTEIN ENCODED BY GENE NO: 145

The translation product of this gene shares sequence homology with protein tyrosine phosphatase which is thought to be important in transducing signal to activate cells such as T cell, B cell and other cell types.

This gene is expressed primarily in T cells and tissues in early stages of development and to a lesser extent in cancers.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: immuno-related diseases and cancer. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune system expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., embryonic and fetal tissue, undifferentiated cells, and blood cells, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution and homology to the protein tyrosine phosphatase family indicate that polynucleotides and polypeptides corresponding to this gene are useful for modulating the immune system.

FEATURES OF PROTEIN ENCODED BY GENE NO: 146

This gene is expressed primarily in T cell and to a lesser extent in B cell, macrophages and tumor tissues.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: immuno-disorders. Similarly, polypeptides and antibodies directed to these polypeptides are useful in

providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., blood cells, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for regulating the immune system therefore can be used in treating diseases such as autoimmune diseases and cancers.

FEATURES OF PROTEIN ENCODED BY GENE NO: 147

This gene is expressed primarily in placenta and to a lesser extent in endothelial cells, testis tumor, ovarian cancer, uterine cancer.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions which include, but are not limited to cancer. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., placenta, endothelial cells, testis and ovary and other reproductive tissue, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for diagnosis and treatment of cancers.

FEATURES OF PROTEIN ENCODED BY GENE NO: 148

This sequence has significant homology to mouse torsin A. Recently, another group cloned the human Torsin A gene. (See, Accession No. 2358279; see also Nature Genet. 17, 40-48 (1997).)

This gene is expressed primarily in osteoclastoma, T-cell, and placenta and to a lesser extent in fetal lung, fetal liver, fetal brain, adult brain and tumor tissues

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: disease conditions in hematopoiesis and cancers. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the hematopoiesis system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., blood cells, bone, placenta, lung, liver, and brain and other tissues of the nervous system, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for treating blood related diseases such as deficiencies in red blood cell, white blood cell, platelet and other hematopoiesis cells.

FEATURES OF PROTEIN ENCODED BY GENE NO: 149

This gene is expressed primarily in T cell, prostate and prostate cancer, endothelial cells and to a lesser extent in monocyte, dendritic cell, bone marrow, salivary gland, colon cancer, stomach cancer, pancreatic tumor, uterine cancer, fetal spleen and osteoclastoma.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: immuno-related diseases and cancers. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., blood cells, prostate, endothelial cells, dendritic cells, bone marrow, salivary gland, colon, stomach, pancreas, uterus, spleen and bone, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for treatment of cancers.

FEATURES OF PROTEIN ENCODED BY GENE NO: 150

- 5 This gene was recently cloned by another group, calling it eIF3-p66. (See Accession No. 2351378.) This gene plays a role in RNA binding and macromolecular assembly, and therefore, any mutations in this gene would likely result in a diseased phenotype. Preferred polypeptide fragments comprise the amino acid sequence:
- 10 MAKFMTPIQDNPSGWGPCAVPEQFRDMPYQPFSGDRLGKVADWTGATYQDKRYTNKYSS
QFGGGSQYAYFHEEDESFLVDTARTQKTAYQRNRMFAQRNLRRDKDRRNMLQFNLQILP
KSAKQKERERIRLQKKFQKQFGVRQKWDQKSQKPRDSSVEVRSDWEVKEEMDFPQLMKMRY
LEVSEPDIECCGALEYDYDKAFDRITRSEKPLRXXKRIFHTVTTTTDDPVIRKLAKTQGNVFATD
AILATLMSCTRSVYSWDIVVQRVGSKLFFDKRDNSDFDLLTVSETANEPQDEGNSFNSPRNL
AMEATYINHNFSQQCLRMGKERYNFPNPNPFVEDMDKNEIASVAYRYSRGLGDDIDLIVRC
15 EHDGVMGTGANGEVSFINIKTLNEWDSRHCVGVDWRQKLDSQRGAVIATELKNNSYKLARWTC
CALLAGSEYLKLGYSRYHVKDSSRHVILGTQQFKPNEFASQINLSVENAWGILRCVIDICMKL
EEGKYLLKDPNKQVIRVYSLPDGTFSS (SEQ ID NO: 638), as well as N-terminal and C-terminal deletions of this polypeptide fragment.

- 20 This gene is expressed primarily in T cell, bone marrow, embryo and endothelial cells and to a lesser extent in testis tumor and endometrial tumor.

- Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: immune diseases and tumors. Similarly, polypeptides and antibodies directed to these polypeptides are useful
- 25 in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune system and reproductive system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial
- 30 fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for immune disorders and cancers.

FEATURES OF PROTEIN ENCODED BY GENE NO: 151

This gene is expressed primarily in testis and to a lesser extent in T cell, spinal cord, placenta, neutrophil and monocyte.

Therefore, polynucleotides and polypeptides of the invention are useful as
5 reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: male reproductive and endocrine disorders. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells,
10 particularly of the reproductive, immune and endocrine systems, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., testis and other reproductive tissue, blood cells, tissue of the nervous system, and placenta, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell
15 sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that polynucleotides and polypeptides
corresponding to this gene are useful for regulating immune and reproductive functions.
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FEATURES OF PROTEIN ENCODED BY GENE NO: 152

The translation product of this gene shares sequence homology with tyrosyl-tRNA synthetase which is thought to be important in cell growth.

This gene is expressed primarily in brain, liver, keratinocytes, tonsils, and
25 heart.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions which include, but are not limited to, cancer autoimmune diseases. Similarly, polypeptides and antibodies
30 directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the brain, liver, keratinocytes, tonsils, heart expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., brain and other tissues of the nervous system,
35 liver, keratinocytes, tonsils and heart, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard

gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution and homology to tyrosyl-tRNA synthetase indicate that polynucleotides and polypeptides corresponding to this gene are useful for modulating cell growth.

FEATURES OF PROTEIN ENCODED BY GENE NO: 153

This gene is homologous to the *Drosophila* transcriptional regulator dre4. (See Accession No. 2511745.) Dre4 is a gene required for steroidogenesis in *Drosophila melanogaster* and encodes a developmentally expressed homologue of the yeast transcriptional regulator CDC68. Preferred polypeptide fragments comprise the amino acid sequence: KKRHTDVQFYTEVGEITDLGKHQMHDRDDLYAEQMEREMRHKLKTAFTKN FIEKVEALTKEELEFEVPPFDLGFNGAPYRSTCLLQPTSSALVNATEWPPFVVTLDVELIHFXR VQFHLKNFDMVIVYKDYSKKVTMINAIPVASLDPIKEWLNNSCDLKYTEGVQSLNWTIMKTIVD DPEGFEEQGGWSFL (SEQ ID NO: 639), as well as N-terminal and C-terminal deletions of this fragments. Also preferred are polynucleotide fragments encoding this polypeptide fragment.

This gene is expressed primarily in fetal liver, spleen, placenta, lung, T cell, thyroid, testes.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: brain tumor, heart and liver diseases. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the fetal liver, spleen, placenta, lung, T cell, thyroid, testes expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., liver, spleen, placenta, lung, blood cells, thyroid, and testes and other reproductive tissue, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

FEATURES OF PROTEIN ENCODED BY GENE NO: 154

This gene is expressed primarily in brain and to a lesser extent in fetal heart, testis, spleen, lung.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: heart, liver and spleen diseases, immunological diseases. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the brain, fetal heart, testis, spleen, lung expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., brain and other tissue of the nervous system, heart, testes and other reproductive tissue, spleen, and lung, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

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FEATURES OF PROTEIN ENCODED BY GENE NO: 155

Activation of T cells through the T cell antigen receptor (TCR) results in the rapid tyrosine phosphorylation of a number of cellular proteins, one of the earliest being a 100 kDa protein. This gene is the human equivalent of murine valosin containing protein (VCP). VCP is a member of a family of ATP binding, homo-oligomeric proteins, and the mammalian homolog of *Saccharomyces cerevisiae* cdc48p, a protein essential to the completion of mitosis in yeast. Both endogenous and expressed murine VCP are tyrosine phosphorylated in response to T cell activation. Thus we have identified a novel component of the TCR mediated tyrosine kinase activation pathway that may provide a link between TCR activation and cell cycle control.

25

This gene is expressed primarily in brain, liver, spleen, placenta.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions which include, but are not limited to, cancer immunological disorders. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the brain, liver, spleen, placenta expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., brain and other tissue of the nervous system, liver, spleen, and placenta, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from

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an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

5 The tissue distribution and homology to VCR indicate that polynucleotides and polypeptides corresponding to this gene are useful for treating cancer.

FEATURES OF PROTEIN ENCODED BY GENE NO: 156

10 The translation product of this gene shares sequence homology with rat growth response protein which is thought to be important in cell growth. A group recently cloned the human homolog of this gene, calling it insulin induced protein 1. (See Accession No. 2358269, see also, Genomics 43 (3), 278-284 (1997).) Preferred polypeptide fragments comprise the amino acid sequence: RSGLGLGITIAFLATLITQF LVYNGVYQYTSPDFLYIRSWLPCIFFSGGVTVGNIGRQLAMGVPEKPHSD (SEQ ID NO: 640), as well as N-terminal and C-terminal deletions of this polypeptide fragment. Also
15 preferred are polynucleotide fragments encoding these polypeptide fragments.

This gene is expressed primarily in brain, liver, placenta, heart, spleen, lymphoma.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a
20 biological sample and for diagnosis of diseases and conditions which include, but are not limited to, cancer immunological disorders. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the brain, liver, placenta, heart, spleen.
25 expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., brain and other tissue of the nervous system, liver, placenta, heart, spleen, and lymphoid tissue, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the
30 standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution and homology to growth-response protein indicate that polynucleotides and polypeptides corresponding to this gene are useful for modulating cell growth.

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FEATURES OF PROTEIN ENCODED BY GENE NO: 157

This gene is expressed primarily in Glioblastoma, endometrial tumor, lymphoma and pancreas tumor.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: Glioblastoma, Endometrial tumor, lymphoma and pancreas tumor. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., endometrium, lymphoid tissue, pancreas, and tissue of the nervous system, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

FEATURES OF PROTEIN ENCODED BY GENE NO: 158

The translation product of this gene shares sequence homology with IGE receptor which is thought to be important in allergy and asthma.

This gene is expressed primarily in T cell, and fetal liver.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: allergy and asthma and other immunological disorders. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., blood cells, and liver, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution and homology to IgE receptor indicate that polynucleotides and polypeptides corresponding to this gene are useful for allergy and asthma.

5 **FEATURES OF PROTEIN ENCODED BY GENE NO: 159**

The translation product of this gene shares sequence homology with immunoglobulin heavy chain which is thought to be important in immune response to the antigen.

10 This gene is expressed primarily in activated neutrophil and to a lesser extent in activated T cell, monocyte and heart.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: infection, inflammation and cancer. Similarly, polypeptides and antibodies directed to these polypeptides are
15 useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., blood cells, and heart, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial
20 fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution and homology to immunoglobulin heavy chain variable region indicate that polynucleotides and polypeptides corresponding to this gene are
25 useful for making the ligand to block specific antigen which cause certain disease.

FEATURES OF PROTEIN ENCODED BY GENE NO: 160

The translation product of this gene shares sequence homology with mouse X inactive specific transcript protein which is thought to be important in X chromosome
30 inactivation.

This gene is expressed primarily in HSA172 cell and to a lesser extent in normal ovary tissue, ovarian cancer, frontal cortex and brain.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a
35 biological sample and for diagnosis of diseases and conditions: ovarian tumor, schizophrenia and other neurological disorders. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for

differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune and neural system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., ovary and other reproductive tissue, and brain and other
5 tissue of the nervous system, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

- 10 The tissue distribution and homology to X inactive specific transcript protein indicate that polynucleotides and polypeptides corresponding to this gene are useful for diagnosis and treatment of reproductive system tumors and CNS tumors.

FEATURES OF PROTEIN ENCODED BY GENE NO: 161

- 15 This gene is expressed primarily in adipose cell and to a lesser extent in liver and prostate.

- Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: obesity and liver
20 disorder. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the adipose cell, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., adipose cells, liver, and
25 prostate, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

- 30 The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for treatment of obesity and liver disorder.

FEATURES OF PROTEIN ENCODED BY GENE NO: 162

- The translation product of this gene shares sequence homology with yeast
35 ubiquitin activating enzyme homolog which is thought to be important in protein posttraslation processing.

This gene is expressed primarily in stromal cell and to a lesser extent in retina, H. Atrophic Endometrium, colon carcinoma and myeloid progenitor cell.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: defects of stromal cell development, neuronal growth disorders and tumors. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune and neural system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., retinal cells, endometrium, colon, and bone marrow, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution and homology to ubiquitin-activating enzyme homolog indicate that polynucleotides and polypeptides corresponding to this gene are useful for diagnosis or treatment of some type of tumors, fucosidosis and neuronal growth disorders.

FEATURES OF PROTEIN ENCODED BY GENE NO: 163

This gene is expressed primarily in primary breast cancer and hemangiopericytoma and to a lesser extent in adult brain and cerebellum.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: breast cancer, leukemia and cerebellum disorders. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune system and neural system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., mammary tissue, brain and other tissue of the nervous system, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for diagnosis or treatment of various tumors and disease involved in neural system.

5 **FEATURES OF PROTEIN ENCODED BY GENE NO: 164**

The translation product of this gene shares sequence homology with proline rich proteins. Recently, another group has also cloned this gene, calling it CD84 leukocyte antigen, a new member of the Ig superfamily. (See Accession No. U82988, see also, Blood 90 (6), 2398-2405 (1997).)

10 This gene is expressed primarily in Weizmann olfactory tissue and osteoclastoma and to a lesser extent in anergic T-cell.

 Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: ostsis and immune
15 disease. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., olfactory tissue, bone, and
20 blood cells, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

25 The tissue distribution and homology to the Ig superfamily indicate that the protein product of this clone is useful for treatment of osteoporosis, autoimmune disease, and other immune disorders.

FEATURES OF PROTEIN ENCODED BY GENE NO: 165

30 This gene is expressed primarily in atrophic endometrium and colon cancer and to a lesser extent in some fetal tissues.

 Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: tumors. Similarly,
35 polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune system,

expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., endometrium, colon, and fetal tissue, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having
5 such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for diagnosis and treatment of tumors, specifically endometrium and colon tumors.

10

FEATURES OF PROTEIN ENCODED BY GENE NO: 166

This gene is expressed primarily in human primary breast cancer and to a lesser extent in activated monocyte. Although the predicted signal sequence is identified in Table 1, other upstream sequences are also relevant. Preferred polypeptide fragments comprise
15 the amino acid sequence: VTQPKHLSASMGGSV EIPFSFYYPWELAXXPXVRISWRRGHFHG QSFYSTRPPSIHKDYVNRLFLNWTEGQESGFLRISNLRKEDQSVYFCRVELDTRRSG (SEQ ID NO: 641), as well as N-terminal and C-terminal deletions. Also preferred are polynucleotide fragments encoding these polypeptide fragments.

Therefore, polynucleotides and polypeptides of the invention are useful as
20 reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: breast cancer. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune system,
25 expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., mammary tissue, and blood cells, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in
30 healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that polynucleotides and polypeptides corresponding to this gene are useful for diagnosis of breast cancer.

FEATURES OF PROTEIN ENCODED BY GENE NO: 167

35 This gene is expressed primarily in fetal tissues and to a lesser extent in adult lung. This gene has also been mapped to chromosomal location 9q34, and thus, can be used as a marker for linkage analysis for chromosome 9.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the embryo tissues, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., fetal tissues, and lung, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

FEATURES OF PROTEIN ENCODED BY GENE NO: 168

The translation product of this gene shares sequence homology with Ig Heavy Chain which is thought to be important in immune response.

This gene is expressed primarily in prostate cancer tissue specifically

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: prostate cancer. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the prostate, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., prostate, tissue and cells of the immune system, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

FEATURES OF PROTEIN ENCODED BY GENE NO: 169

The translation product of this gene shares sequence homology with cytosolic acyl coenzyme-A hydrolase, which is thought to be important in neuron-specific fatty acid metabolism. The gene represented by this contig has since been published by Hajra and colleagues (GenBank Accession No. U91316).

This gene is expressed primarily in human pituitary gland and to a lesser extent in colorectal cancer tissue. This gene has also been observed in the LNCAP cell line.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: hyperlipidemias of familial and/or idiopathic origins. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly blood, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., pituitary and colon, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution and homology to rat cytosolic acyl coenzyme-A hydrolase indicate that polynucleotides and polypeptides corresponding to this gene are useful for the detection or treatment of hyperlipidemia disease states by virtue of the ability of specific drugs to activate the enzyme.

FEATURES OF PROTEIN ENCODED BY GENE NO: 170

The translation product of this gene shares sequence homology with a *Caenorhabditis elegans* gene which is thought to be important in organism development.

This gene is expressed primarily in human synovial sarcoma tissue, bone marrow, and to a lesser extent in human brain.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions which include, but are not limited to, of bone, specifically synovial sarcoma. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the bone, connective tissues and possibly immune system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., synovial tissue, bone marrow, brain and other tissue of the nervous system, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another

tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

5 The tissue distribution and homology to *Caenorhabditis elegans* indicate that polynucleotides and polypeptides corresponding to this gene are useful as a diagnostic and/or therapeutic modality directed at the detection and/or treatment of connective tissue sarcomas or other related bone diseases.

FEATURES OF PROTEIN ENCODED BY GENE NO: 171

10 The translation product of this gene shares sequence homology with beta1-6GlcNAc transferase which is thought to be important in the transfer and metabolism of beta1-6, N-acetylglucosamine. This gene product has previously been shown to suppress melanoma lung metastasis in both syngeneic and nude mice, decreased invasiveness into the matrigel, and inhibition of cell attachment to collagen and laminin
15 without affecting cell growth.

This gene is expressed primarily in human testes and prostate tissues, and to a lesser extent in kidney, medulla, and pancreas.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a
20 biological sample and for diagnosis of diseases and conditions which include, but are not limited to, cancer particularly melanoma. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune system, expression of this gene at
25 significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., testes and other reproductive tissue, prostate, kidney, pancreas, brain and other tissue of the nervous system, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard
30 gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution and homology to beta1-6GlcNAc transferase indicate that the protein product of this clone is useful for the development of diagnostic and/or therapeutic modalities directed at the detection and/or treatment of cancer, the metastasis
35 of malignant tissue or cells. Defects in this potentially secreted enzyme may play a role in metastasis.

FEATURES OF PROTEIN ENCODED BY GENE NO: 172

This gene is expressed primarily in fetal spleen and liver.

Therefore, polynucleotides and polypeptides of the invention are useful as
5 reagents for differential identification of the tissue(s) or cell type(s) present in a
biological sample and for diagnosis of diseases and conditions: immune disorders,
Wilm's tumor disease, hepatic disorders, and hematopoietic disorders. Similarly,
polypeptides and antibodies directed to these polypeptides are useful in providing
immunological probes for differential identification of the tissue(s) or cell type(s). For a
10 number of disorders of the above tissues or cells, particularly of the hematopoiesis and
immune systems, expression of this gene at significantly higher or lower levels may be
routinely detected in certain tissues and cell types (e.g., spleen and liver, and cancerous
and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or
spinal fluid) or another tissue or cell sample taken from an individual having such a
15 disorder, relative to the standard gene expression level, i.e., the expression level in
healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that polynucleotides and polypeptides
corresponding to this gene are useful for the treatment and identification of fetal defects
along with correcting diseases that affect hematopoiesis and the immune system.

20

FEATURES OF PROTEIN ENCODED BY GENE NO: 173

The translation product of this gene shares sequence homology with ret II
oncogene which is thought to be important in Hirschsprung disease and many types of
cancers.

25 This gene is expressed in multiple tissues including the lymphatic system, brain,
and thyroid.

Therefore, polynucleotides and polypeptides of the invention are useful as
reagents for identification of the tissue(s) or cell type(s) present in a biological sample
and for diagnosis of diseases and conditions: Hirschsprung disease and multiple
30 cancers. Similarly, polypeptides and antibodies directed to these polypeptides are useful
in providing immunological probes for identification of the tissue(s) or cell type(s). For
a number of disorders of the above tissues or cells, particularly of the immune and
central nervous system, expression of this gene at significantly higher or lower levels
may be routinely detected in certain tissues and cell types (e.g., lymphoid tissue,
35 thyroid, and brain and other tissue of the nervous system, and cancerous and wounded
tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or
another tissue or cell sample taken from an individual having such a disorder, relative to

the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution and homology to ret II oncogene indicate that polynucleotides and polypeptides corresponding to this gene are useful for diagnosis and treatment of various cancers. It would also be useful for the diagnosis and treatment of Hirschsprung disease. Preferred polypeptides of the invention comprise the amino acid sequence: MEAQQVNEAESAREQLQXLHDQIAGQKASKQELETelerLKQEFHYIEEDLY RTKNTLQSRIDRDEEIQLRNQLTNKTLSSSQSELENRLHQLTETLIQKQTMLESLSSTEKNSL VFQLERLEQQMNSASGSSSNGSSINMSGIDNGEGTRLRNVPVLFNDTETNLAGMYGKVRKAAS
 10 SIDQFSIRLGIFLRRYPIARVFVIYIMALLHLWVMIVLLTYTPEM HHDQPYGK (SEQ ID NO: 642).

FEATURES OF PROTEIN ENCODED BY GENE NO: 174

The translation product of this gene shares sequence homology with testis enhanced gene transcript which is thought to be important in regulation of human development.

This gene is expressed primarily in infant brain and to a lesser extent in a variety of other tissues and cell types, including the prostate, testes, monocytes, macrophages, dendritic cells, keratinocytes, and adipocytes.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: neurological, developmental, immune and inflammation disorders. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the brain and immune systems, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., brain and other tissue of the nervous system, prostate, testes and other reproductive tissue, blood cells, keratinocytes, and adipocytes, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution and homology to testis enhanced gene transcript indicate that the protein product of this clone is useful for diagnosis and treatment of disorders involving the developing brain and the immune system.

FEATURES OF PROTEIN ENCODED BY GENE NO: 175

This gene is expressed primarily in prostate and to a lesser extent in various other tissues, including placenta.

5 Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions which include, but are not limited to, cancers, especially of the prostate. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for
10 differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the prostate, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., prostate and placenta, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell
15 sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

 The tissue distribution indicates that the protein product of this clone is useful for diagnosis and treatment of prostate disorders and cancer. It may also be useful for
20 the diagnosis and treatment of endocrine disorders.

FEATURES OF PROTEIN ENCODED BY GENE NO: 176

 The translation product of this gene shares sequence homology with *Sacchomyces cerevisiae* YNT20 gene which is thought to be important in
25 mitochondrial function.

 This gene is expressed at a particularly high level in muscle tissue.

 Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases related to such tissues and cell types
30 including: muscle wasting diseases. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the neuromuscular system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell
35 types (e.g., muscle and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e.,

the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution and homology to the YNT20 gene indicate that this protein is useful for treatment and detection of neuromuscular diseases caused by loss of mitochondrial function. For example this gene or its protein product could be used in replacement therapy for such diseases.

FEATURES OF PROTEIN ENCODED BY GENE NO: 177

This gene is expressed primarily in the brain and to a lesser extent in kidney, placenta, smooth muscle, heart and lung.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: neuromuscular diseases, degenerative diseases of the central nervous system, and heart disease. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the neuromuscular system, central nervous system, and heart, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., brain and other tissue of the nervous system, kidney, placenta, muscle, heart and lung, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

This gene or its protein product could also be used for replacement therapy for the above mentioned diseases.

FEATURES OF PROTEIN ENCODED BY GENE NO: 178

The translation product of this gene shares sequence homology with caldesmon which is thought to be important in the cellular response to changes in glucose levels.

This gene is expressed primarily in multiple tissues including brain and retina.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: central nervous system disorders and retinopathy. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for identification of the tissue(s) or cell

type(s). For a number of disorders of the above tissues or cells, particularly of the CNS disorders and retinopathy, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., brain and other tissue of the nervous system, and retinal tissue, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution and homology to caldesmon indicate that polynucleotides and polypeptides corresponding to this gene are useful for treatment of retinopathies.

FEATURES OF PROTEIN ENCODED BY GENE NO: 179

The translation product of this gene shares sequence homology with mouse fibrosin protein which is thought to be important in regulation of fibrinogenesis in certain chronic inflammatory diseases.

This gene is expressed primarily in amniotic cells and breast tissue.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of breast cancer and abnormal embryo development. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the reproductive system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., amniotic cells, and mammary tissue, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution and homology to fibrosin indicate that the protein product of this clone is useful for treatment of breast cancer. This gene or its protein product could be used in replacement therapy for breast cancer. In addition the protein product of this gene is useful in the treatment of chronic inflammatory diseases.

FEATURES OF PROTEIN ENCODED BY GENE NO: 180

This gene is expressed several infant tissues including brain and liver and various adult tissues including brain, lung, liver, testes, and prostate.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions which include, but are not limited to, brain cancer, lung cancer, liver cancer and cancers of the reproductive system. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the central nervous system, hepatic system, and reproductive system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., brain and other tissue of the nervous system, lung, liver, testes and other reproductive tissue, and prostate, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution of this gene product indicates that the protein product of this clone is involved in growth regulation and could be used as a growth factor or growth blocker in a variety of settings including treatment of cancers.

20 FEATURES OF PROTEIN ENCODED BY GENE NO: 181

This gene is expressed primarily in activated monocytes and to a lesser extent in melanocytes and dendritic cells.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of immune system diseases and cancer. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the immune system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., blood cells, melanocytes, and dendritic cells, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The tissue distribution indicates that the protein product of this clone could be involved in growth regulation and could be used as a growth factor or growth blocker in a variety of settings including treatment of cancers.

FEATURES OF PROTEIN ENCODED BY GENE NO: 182

This gene is expressed primarily in placenta and several tumors of various tissue origin and to a lesser extent in normal tissues including liver, lung, brain, and skin,

5 Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of cancers of all kinds. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders
10 of the above tissues or cells, particularly of the central nervous system, respiratory system and skin, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., liver, lung, brain and other tissues of the nervous system, and skin, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or
15 cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The high expression of this gene in multiple tumors indicates that the protein product of the clone may be involved in cell growth control and therefore would be
20 useful for treatment of certain cancers. Likewise molecules developed to block the activity of the protein product of this clone could be used to block its potential role in tumor growth promotion.

FEATURES OF PROTEIN ENCODED BY GENE NO: 183

25 The translation product of this gene shares sequence homology with the mouse Ndr1 gene which is thought to be important in cancer progression.

This gene is expressed multiple cell types and tissues including brain, lung, kidney, bone marrow, liver, and spleen.

Therefore, polynucleotides and polypeptides of the invention are useful as
30 reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of all types of cancers. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the nervous, immune, and endocrine
35 systems, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., brain and other tissue of the nervous system, lung, kidney, bone marrow, liver and spleen, and cancerous and wounded

tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

- 5 The tissue distribution and homology to Ndr1 gene, which is thought to be involved in cancer progression, indicate that polynucleotides and polypeptides corresponding to this gene are useful for treatment of certain cancers. Likewise molecules developed to block the activity of the protein product of this clone could be used to block its potential role in tumor growth promotion.

10

FEATURES OF PROTEIN ENCODED BY GENE NO: 184

This gene is expressed primarily in early stage human brain and liver and to a lesser extent in several other fetal tissues.

- 15 Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of diseases and conditions: brain and liver cancers. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the
- 20 central nervous system and immune system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., brain and other tissue of the nervous system, liver, and fetal tissue, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder,
- 25 relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The expression of this gene in embryonic tissues indicates that the protein could be involved in growth regulation and could be used as a growth factor or growth blocker in a variety of settings including treatment of cancers.

30

FEATURES OF PROTEIN ENCODED BY GENE NO: 185

This gene is expressed primarily in infant and embryonic brain.

- 35 Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of degenerative nervous system disorders and brain cancer. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell

type(s). For a number of disorders of the above tissues or cells, particularly of the central nervous system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., embryonic tissue, brain and other tissue of the nervous system, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The expression of this gene in embryonic tissues indicates that the protein could be involved in growth regulation and could be used as a growth factor or growth blocker in a variety of settings including treatment of cancers.

FEATURES OF PROTEIN ENCODED BY GENE NO: 186

This gene is expressed primarily in multiple tissues including placenta, fetal lung, fetal liver, and brain.

Therefore, polynucleotides and polypeptides of the invention are useful as reagents for differential identification of the tissue(s) or cell type(s) present in a biological sample and for diagnosis of all types of cancers including liver, brain and lung. Similarly, polypeptides and antibodies directed to these polypeptides are useful in providing immunological probes for differential identification of the tissue(s) or cell type(s). For a number of disorders of the above tissues or cells, particularly of the central nervous system, pulmonary system, and hepatic system, expression of this gene at significantly higher or lower levels may be routinely detected in certain tissues and cell types (e.g., placenta, lung, liver, and brain and other tissue of the nervous system, and cancerous and wounded tissues) or bodily fluids (e.g., serum, plasma, urine, synovial fluid or spinal fluid) or another tissue or cell sample taken from an individual having such a disorder, relative to the standard gene expression level, i.e., the expression level in healthy tissue or bodily fluid from an individual not having the disorder.

The expression of this gene in embryonic tissues indicates that the protein could be involved in growth regulation and could be used as a growth factor or growth blocker in a variety of settings including treatment of cancers.

Gene No.	cDNA Clone ID	ATCC Deposit No: Z and Date	Vector	NT SEQ ID NO: X	Total NT Seq.	5' NT of Clone Seq.	3' NT of Clone Seq.	5' NT of Start Codon	5' NT of First AA of Signal Pep	AA SEQ ID NO: Y	First AA of Sig Pep	Last AA of Sig Pep	Predicted First AA of Secreted Portion	Last AA of ORF
1	HTTEZ21	97897 02/26/97 209043 05/15/97	Uni-ZAP XR	11	582	1	582	177	177	313	1	18	19	22
1	HTTEZ21	97897 02/26/97 209043 05/15/97	Uni-ZAP XR	197	1020	296	830	442	442	499	1	18	19	22
2	HBGBW52	97897 02/26/97 209043 05/15/97	Uni-ZAP XR	12	465	1	465	81	81	314	1	30	31	128
2	HBGBW52	97897 02/26/97 209043 05/15/97	Uni-ZAP XR	198	524	229	343		196	500	1	20	21	33
3	HCUFM41	97897 02/26/97 209043 05/15/97	ZAP Express	13	474	1	474	1	1	315	1	24	25	28
3	HCUFM41	97897 02/26/97 209043 05/15/97	ZAP Express	199	332	1	319	35	35	501	1	24	25	28

Gene No.	cDNA Clone ID	ATCC Deposit No: Z and Date	Vector	NT SEQ ID NO: X	Total NT Seq.	5' NT of Clone Seq.	3' NT of Clone Seq.	5' NT of Start Codon	5' NT of First AA of Signal Pep	AA SEQ ID NO: Y	First AA of Sig Pep	Last AA of Sig Pep	Predicted First AA of Secreted Portion	Last AA of ORF
4	HCUFQ22	97897 02/26/97 209043 05/15/97	ZAP Express	14	314	1	298	122	122	316	1	34	35	64
5	HCUFV01	97897 02/26/97 209043 05/15/97	ZAP Express	15	613	1	613	30	30	317	1	18	19	21
6	HCUGA50	97897 02/26/97 209043 05/15/97	ZAP Express	16	356	1	356	239	239	318	1	22	23	39
7	HCUIM14	97897 02/26/97 209043 05/15/97	ZAP Express	17	414	185	414	278	278	319	1	26	27	33
8	HLD0U93	97897 02/26/97 209043 05/15/97	pCMVSPORT 3.0	18	469	1	469	77	77	320	1	44	45	88
9	HEIAX07	97897 02/26/97 209043 05/15/97	Uni-ZAP XR	19	550	1	550	129	129	321	1	21	22	23

Gene No.	cDNA Clone ID	ATCC Deposit No: Z and Date	Vector	NT SEQ ID NO: X	Total NT Seq.	5' NT of Clone Seq.	5' NT of Clone Seq.	5' NT of First AA of Signal Pep	AA SEQ ID NO: Y	First AA of Sig Pep	Last AA of Sig Pep	Predicted First AA of Secreted Portion	Last AA of ORF
9	HEIAX07	97897 02/26/97 209043 05/15/97	Uni-ZAP XR	200	376	9	376	1	502	1	8	9	15
10	HSAXR76	97897 02/26/97 209043 05/15/97	Uni-ZAP XR	20	741	55	741	190	322	1			27
11	HNGJJ68	97897 02/26/97 209043 05/15/97	Uni-ZAP XR	21	991	1	991	62	323	1	30	31	64
11	HNGJJ68	97897 02/26/97 209043 05/15/97	Uni-ZAP XR	201	1192	253	1137	409	503	1			19
12	HCFAW04	97897 02/26/97 209043 05/15/97	pSport1	22	653	1	653	64	324	1	30	31	196
12	HCFAW04	97897 02/26/97 209043 05/15/97	pSport1	202	589	1	513	109	504	1			29

Gene No.	cDNA Clone ID	ATCC Deposit No: Z and Date	Vector	NT SEQ ID NO: X	Total NT Seq.	5' NT of Clone Seq.	3' NT of Clone Seq.	5' NT of Start Codon	5' NT of First AA of Signal Pep	AA SEQ ID NO: Y	First AA of Sig Pep	Last AA of Sig Pep	Predicted First AA of Secreted Portion	Last AA of AA ORF
13	HLMAV65	97897 02/26/97 209043 05/15/97	Uni-ZAP XR	23	1486	596	1418	102	102	325	1	54	55	252
13	HLMAV65	97897 02/26/97 209043 05/15/97	Uni-ZAP XR	203	847	1	839	87	87	505	1	30	31	75
13	HLMAV65	97897 02/26/97 209043 05/15/97	Uni-ZAP XR	204	852	75	850		690	506	1			10
13	HTXEF04	209235 09/04/97	Uni-ZAP XR	205	1354	54	1354	100	100	507	1	33	34	207
14	HPMFD84	97897 02/26/97 209043 05/15/97	Uni-ZAP XR	24	2323	1017	2059	1242	1242	326	1	21	22	68
14	HPMFD84	97897 02/26/97 209043 05/15/97	Uni-ZAP XR	206	1378	113	1226	303	303	508	1	25	26	36
15	HE6DB26	97897 02/26/97 209043 05/15/97	Uni-ZAP XR	25	683	1	683	304	304	327	1	30	31	84

Gene No.	cDNA Clone ID	ATCC Deposit No: Z and Date	Vector	NT SEQ ID NO: X	Total NT Seq.	5' NT of Clone Seq.	3' NT of Clone Seq.	5' NT of Start Codon	5' NT of First AA of Signal Pep	AA SEQ ID NO: Y	First AA of Sig Pep	Last AA of Sig Pep	Predicted First AA of Secreted Portion	Last AA of ORF
15	HE6DB26	97897 02/26/97 209043 05/15/97	Uni-ZAP XR	207	1166	281	884	567	567	509	1	18	19	19
16	HFFFL33	97897 02/26/97 209043 05/15/97	Uni-ZAP XR	26	2036	14	1959	214	214	328	1	20	21	36
17	HODBD33	97897 02/26/97 209043 05/15/97	Uni-ZAP XR	27	717	1	717	70	70	329	1	30	31	63
17	HODBD33	97897 02/26/97 209043 05/15/97	Uni-ZAP XR	208	697	2	697	33	33	510	1	31	32	32
18	HMDAE90	97897 02/26/97 209043 05/15/97	Uni-ZAP XR	28	495	1	495	39	39	330	1	24	25	35
19	HOUAW01	97897 02/26/97 209043 05/15/97	Uni-ZAP XR	29	556	1	556	116	116	331	1	19	20	23

Gene No.	cDNA Clone ID	ATCC Deposit No: Z and Date	Vector	NT SEQ ID NO: X	Total NT Seq.	5' NT of Clone Seq.	5' NT of Clone Seq.	5' NT of Start Codon	5' NT of First AA of Signal Pep	AA SEQ ID NO: Y	First AA of Sig Pep	Last AA of Sig Pep	Predicted First AA of Secreted Portion	Last AA of ORF
20	HBJAE44	97897 02/26/97 209043 05/15/97	Uni-ZAP XR	30	434	1	434	78	78	332	1	35	36	40
21	HCFME41	97897 02/26/97 209043 05/15/97	pSport1	31	715	1	715	87	87	333	1	30	31	111
21	HCFME41	97897 02/26/97 209043 05/15/97	pSport1	209	932	274	932	387	387	511	1	27	28	28
22	HOGCO71	97897 02/26/97 209043 05/15/97	pCMVSPORT 2.0	32	486	1	486	137	137	334	1	21	22	106
23	HOSEX08	97897 02/26/97 209043 05/15/97	Uni-ZAP XR	33	725	1	725	436	436	335	1	30	31	50
23	HOSEX08	97897 02/26/97 209043 05/15/97	Uni-ZAP XR	210	661	1	647	81	81	512	1	25	26	26

Gene No.	cDNA Clone ID	ATCC Deposit No: Z and Date	Vector	NT SEQ ID NO: X	Total NT Seq.	5' NT of Clone Seq.	3' NT of Clone Seq.	5' NT of Start Codon	5' NT of First AA of Signal Pep	AA SEQ ID NO: Y	First AA of Sig Pep	Last AA of Sig Pep	Predicted First AA of Secreted Portion	Last AA of ORF
24	HSKNJ72	97897 02/26/97 209043 05/15/97	pBluescript	34	437	1	437	85	85	336	1	30	31	48
25	HEBEB69	97898 02/26/97 209044 05/15/97	Uni-ZAP XR	35	943	1	943	196	196	337	1	30	31	41
25	HEBEB69	97898 02/26/97 209044 05/15/97	Uni-ZAP XR	211	592	1	534	72	72	513	1	24	25	33
26	HE6EH18	97898 02/26/97 209044 05/15/97	Uni-ZAP XR	36	604	1	604	375	375	338	1	20	21	76
26	HE6EH18	97898 02/26/97 209044 05/15/97	Uni-ZAP XR	212	938	1	509		17	514	1	30	31	47
27	HSAUZ47	97898 02/26/97 209044 05/15/97	Uni-ZAP XR	37	349	1	349		201	339	1	20	21	31

Gene No.	cDNA Clone ID	ATCC Deposit No: Z and Date	Vector	NT SEQ ID NO: X	Total NT Seq.	5' NT of Clone Seq.	3' NT of Clone Seq.	5' NT of Start Codon	5' NT of First AA of Signal Pep	AA SEQ ID NO: Y	First AA of Sig Pep	Last AA of Sig Pep	Predicted First AA of Secreted Portion	Last AA of ORF
28	HSSDM73	97898 02/26/97 209044 05/15/97	Uni-ZAP XR	38	672	1	672	22	22	340	1	38	39	42
29	HBMVK68	97898 02/26/97 209044 05/15/97	Uni-ZAP XR	39	1908	135	1908	309	309	341	1	20	21	26
30	HMKDC66	97898 02/26/97 209044 05/15/97	pSport1	40	458	93	458	147	147	342	1	24	25	26
31	HMKCU94	97898 02/26/97 209044 05/15/97	pSport1	41	1153	500	1153	427	427	343	1	30	31	157
31	HMKCU94	97898 02/26/97 209044 05/15/97	pSport1	213	1079	502	896		739	515	1	23	24	43
32	HRDEW41	97898 02/26/97 209044 05/15/97	Uni-ZAP XR	42	1983	1092	1983	27	27	344	1	11	12	520

Gene No.	cDNA Clone ID	ATCC Deposit No: Z and Date	Vector	NT SEQ ID NO: X	Total NT Seq.	5' NT of Clone Seq.	3' NT of Clone Seq.	5' NT of Start Codon	5' NT of First AA of Signal Pep	AA SEQ ID NO: Y	First AA of Sig Pep	Last AA of Sig Pep	Predicted First AA of Secreted Portion	Last AA of ORF
32	HRDEW41	97898 02/26/97 209044 05/15/97	Uni-ZAP XR	214	3791	2757	3357		2030	516	1			3
33	HTOJN06	97898 02/26/97 209044 05/15/97	Uni-ZAP XR	43	1406	1	695		19	345	1	19	20	39
34	HBGDA21	97898 02/26/97 209044 05/15/97	Uni-ZAP XR	44	1391	851	1153	74	74	346	1	30	31	234
34	HBGDA21	97898 02/26/97 209044 05/15/97	Uni-ZAP XR	215	1334	822	1036		638	517	1	18	19	174
35	HFGAK75	97898 02/26/97 209044 05/15/97	Uni-ZAP XR	45	1569	768	1569	14	14	347	1	19	20	169
35	HFGAK75	97898 02/26/97 209044 05/15/97	Uni-ZAP XR	216	1511	770	1404	844	844	518	1	32	33	43

Gene No.	cDNA Clone ID	ATCC Deposit No: Z and Date	Vector	NT SEQ ID NO: X	Total NT Seq.	5' NT of Clone Seq.	3' NT of Clone Seq.	5' NT of Start Codon	5' NT of First AA of Signal Pep	AA SEQ ID NO: Y	First AA of Sig Pep	Last AA of Sig Pep	Predicted First AA of Secreted Portion	Last AA of ORF
36	HHPBD40	97898 02/26/97 209044 05/15/97	Uni-ZAP XR	46	1924	1	1681	62	62	348	1	19	20	43
37	HOVCL83	97898 02/26/97 209044 05/15/97	pSport1	47	475	252	396	141	141	349	1	37	38	78
38	HBCAY62	97898 02/26/97 209044 05/15/97	Uni-ZAP XR	48	346	1	346	61	61	350	1	19	20	24
39	HBICM48	97898 02/26/97 209044 05/15/97	Uni-ZAP XR	49	1366	882	1300	177	177	351	1	30	31	274
39	HBICM48	97898 02/26/97 209044 05/15/97	Uni-ZAP XR	217	642	192	581	448	448	519	1			13
40	HLTCL35	97898 02/26/97 209044 05/15/97	Uni-ZAP XR	50	1405	110	1404	61	61	352	1	30	31	47

Gene No.	cDNA Clone ID	ATCC Deposit No: Z and Date	Vector	NT SEQ ID NO: X	Total NT Seq.	5' NT3' NT of Clone Seq.	5' NT of Start Codon	5' NT of First AA of Signal Pep	AA SEQ ID NO: Y	First AA of Sig Pep	Last AA of Sig Pep	Predicted First AA of Secreted Portion	Last AA of ORF
40	HLTCL35	97898 02/26/97 209044 05/15/97	Uni-ZAP XR	218	1241	1	1241	172	520	1	21	22	30
41	HLHCK50	97898 02/26/97 209044 05/15/97	Uni-ZAP XR	51	504	207	485	222	353	1			3
42	HRSAN45	97899 02/26/97 209045 05/15/97	ZAP Express	52	777	1	214	113	354	1	24	25	52
43	HSNBB14	97899 02/26/97 209045 05/15/97	Uni-ZAP XR	53	602	1	419	41	355	1	59	60	132
43	HSNBB14	97899 02/26/97 209045 05/15/97	Uni-ZAP XR	219	1080	186	686	399	521	1	26	27	47
44	HMABL38	97899 02/26/97 209045 05/15/97	Uni-ZAP XR	54	1749	222	1749	166	356	1	30	31	204

Gene No.	cDNA Clone ID	ATCC Deposit No: Z and Date	Vector	NT SEQ ID NO: X	Total NT Seq.	5' NT of Clone Seq.	5' NT of Start Codon	5' NT of First AA of Signal Pep	AA SEQ ID NO: Y	First AA of Sig Pep	Last AA of Sig Pep	Predicted First AA of Secreted Portion	Last AA of ORF
44	HMA3L38	97899 02/26/97 209045 05/15/97	Uni-ZAP XR	220	1258	149	1190	254	522	1	18	19	26
45	HSKDK47	97899 02/26/97 209045 05/15/97	Uni-ZAP XR	55	1896	596	1614	650	357	1	33	34	47
46	HOSFH03	97899 02/26/97 209045 05/15/97	Uni-ZAP XR	56	1753	555	1753	414	358	1	18	19	73
46	HOSFH03	97899 02/26/97 209045 05/15/97	Uni-ZAP XR	221	1693	554	1693	526	523	1	25	26	58
47	HOGAV75	97899 02/26/97 209045 05/15/97	pCMVSPORT 2.0	57	1220	690	1024	128	359	1	30	31	102
47	HOGAV75	97899 02/26/97 209045 05/15/97	pCMVSPORT 2.0	222	1196	712	1163	1097	524	1			19

Gene No.	cDNA Clone ID	ATCC Deposit No: Z and Date	Vector	NT SEQ ID NO: X	Total NT Seq.	5' NT of Clone Seq.	3' NT of Clone Seq.	5' NT of Start Codon	5' NT of First AA of Signal Pep	AA SEQ ID NO: Y	First AA of Sig Pep	Last AA of Sig Pep	Predicted First AA of Secreted Portion	Last AA of ORF
48	HFCA174	97899 02/26/97 209045 05/15/97	Uni-ZAP XR	58	1049	362	1049	335	335	360	1	33	34	48
49	HAGBI17	97899 02/26/97 209045 05/15/97	Uni-ZAP XR	59	1776	854	1737	189	189	361	1	30	31	179
49	HAGBI17	97899 02/26/97 209045 05/15/97	Uni-ZAP XR	223	1791	979	1791	1164	1164	525	1	18	19	40
50	HLFBC91	97899 02/26/97 209045 05/15/97	pBluescript SK-	60	443	1	443	164	164	362	1	21	22	25
51	HPRCA31	97899 02/26/97 209045 05/15/97	Uni-ZAP XR	61	2888	1909	2888	90	90	363	1	30	31	224
51	HPRCA31	97899 02/26/97 209045 05/15/97	Uni-ZAP XR	224	2517	1597	2517	1953	1953	526	1	18	19	57

Gene No.	cDNA Clone ID	ATCC Deposit No: Z and Date	Vector	NT SEQ ID NO: X	Total NT Seq.	5' NT of Clone Seq.	5' NT of Clone Seq.	5' NT of Start Codon	5' NT of First AA of Signal Pep	AA SEQ ID NO: Y	First AA of Sig Pep	Last AA of Sig Pep	Predicted First AA of Secreted Portion	Last AA of ORF
52	HPRCE95	97899 02/26/97 209045 05/15/97	Uni-ZAP XR	62	1851	1568	1736	139	139	364	1	30	31	349
52	HPRCE95	97899 02/26/97 209045 05/15/97	Uni-ZAP XR	225	2424	299	2309		530	527	1	17	18	21
53	HHTLC66	97899 02/26/97 209045 05/15/97	ZAP Express	63	3542	883	3492	964	964	365	1	25	26	467
54	HMADI02	97899 02/26/97 209045 05/15/97	Uni-ZAP XR	64	883	237	883	229	229	366	1	30	31	152
54	HMADI02	97899 02/26/97 209045 05/15/97	Uni-ZAP XR	226	1080	242	1033	436	436	528	1	24	25	39
55	HPRCU93	97899 02/26/97 209045 05/15/97	Uni-ZAP XR	65	1541	1	1541	236	236	367	1	30	31	373

Gene No.	cDNA Clone ID	ATCC Deposit No: Z and Date	Vector	NT SEQ ID NO: X	Total NT Seq.	5' NT of Clone Seq.	3' NT of Clone Seq.	5' NT of Start Codon	5' NT of First AA of Signal Pep	AA SEQ ID NO: Y	First AA of Sig Pep	Last AA of Sig Pep	Predicted First AA of Secreted Portion	Last AA of ORF
55	HPRCU93	97899 02/26/97 209045 05/15/97	Uni-ZAP XR	227	1336	4	1336	946	946	529	1	25	26	128
56	HSAXS65	97899 02/26/97 209045 05/15/97	Uni-ZAP XR	66	732	41	698	163	163	368	1	18	19	83
56	HSAXS65	97899 02/26/97 209045 05/15/97	Uni-ZAP XR	228	2043	1133	1756	1262	1262	530	1	20	21	82
57	HKTAG35	209011 04/28/97	Uni-ZAP XR	67	629	1	629	264	264	369	1			21
57	HMEFX42	97899 02/26/97 209045 05/15/97	Lambda ZAP II	229	540	25	536	227	227	531	1			20
58	HHFHN61	97899 02/26/97 209045 05/15/97	Uni-ZAP XR	68	1751	375	1751	95	95	370	1	19	20	227
59	HCWEF90	97899 02/26/97 209045 05/15/97	ZAP Express	69	508	1	508	22	22	371	1	30	31	79

Gene No.	cDNA Clone ID	ATCC Deposit No: Z and Date	Vector	NT SEQ ID NO: X	Total NT Seq.	5' NT of Clone Seq.	3' NT of Clone Seq.	5' NT of Start Codon	5' NT of First AA of Signal Pep	AA SEQ ID NO: Y	First AA of Sig Pep	Last AA of Sig Pep	Predicted First AA of Secreted Portion	Last AA of ORF
59	HCWEF90	97899 02/26/97 209045 05/15/97	ZAP Express	230	448	9	448		1	532	1	22	23	75
60	HHGCM20	97899 02/26/97 209045 05/15/97	Lambda ZAP II	70	245	1	245	93	93	372	1	1	2	51
61	HFRAU10	97900 02/26/97 209046 05/15/97	Uni-ZAP XR	71	361	1	361	1	1	373	1	30	31	61
61	HFRAU10	97900 02/26/97 209046 05/15/97	Uni-ZAP XR	231	407	1	407	210	210	533	1	17	18	60
62	HATDT67	97900 02/26/97 209046 05/15/97	Uni-ZAP XR	72	713	8	713	169	169	374	1	30	31	40
62	HATDT67	97900 02/26/97 209046 05/15/97	Uni-ZAP XR	232	830	190	580	329	329	534	1	28	29	39

Gene No.	cDNA Clone ID	ATCC Deposit No.: Z and Date	Vector	NT SEQ ID NO: X	Total NT Seq.	5' NT of Clone Seq.	5' NT 3' NT of Clone Seq.	5' NT of Start Codon	5' NT of First AA of Signal Pep	AA SEQ ID NO: Y	First AA of Sig Pep	Last AA of Sig Pep	Predicted First AA of Secreted Portion	Last AA of ORF
63	HOUBG93	97900 02/26/97 209046 05/15/97	Uni-ZAP XR	73	862	1	862	67	67	375	1	30	31	44
63	HOUBG93	97900 02/26/97 209046 05/15/97	Uni-ZAP XR	233	932	138	905	287	287	535	1			2
64	HMWEX24	97900 02/26/97 209046 05/15/97	Uni-Zap XR	74	4602	4162	4525	730	730	376	1	30	31	203
64	HMWEX24	97900 02/26/97 209046 05/15/97	Uni-Zap XR	234	2786	2406	2739	2577	2577	536	1	22	23	36
65	HSGBA84	97900 02/26/97 209046 05/15/97	Uni-ZAP XR	75	1255	1	1195	112	112	377	1	28	29	29
66	HTOCD52	97900 02/26/97 209046 05/15/97	Uni-ZAP XR	76	475	1	475	13	13	378	1	30	31	136

Gene No.	cDNA Clone ID	ATCC Deposit No: Z and Date	Vector	NT SEQ ID NO: X	Total NT Seq.	5' NT of Clone Seq.	3' NT of Clone Seq.	5' NT of Start Codon	5' NT of First AA of Signal Pep	AA SEQ ID NO: Y	First AA of Sig Pep	Last AA of Sig Pep	Predicted First AA of Secreted Portion	Last AA of ORF
66	HTOCD52	97900 02/26/97 209046 05/15/97	Uni-ZAP XR	235	458	1	458	26	26	537	1			14
67	HTGCP16	97900 02/26/97 209046 05/15/97	Uni-ZAP XR	77	465	25	299	74	74	379	1	33	34	41
68	HKIXR69	97900 02/26/97 209046 05/15/97	pBluescript	78	1907	1627	1730	26	26	380	1	30	31	468
68	HKIXR69	97900 02/26/97 209046 05/15/97	pBluescript	236	591	1	444	251	251	538	1			18
69	HETGJ09	97900 02/26/97 209046 05/15/97	Uni-ZAP XR	79	1168	136	1168	267	267	381	1	20	21	29
70	HOBNC61	97900 02/26/97 209046 05/15/97	Uni-ZAP XR	80	1285	132	1285	292	292	382	1	27	28	29

Gene No.	cDNA Clone ID	ATCC Deposit No: Z and Date	Vector	NT SEQ ID NO: X	Total NT Seq.	5' NT of Clone Seq.	3' NT of Clone Seq.	5' NT of Start Codon	5' NT of First AA of Signal Pep	AA SEQ ID NO: Y	First AA of Sig Pep	Last AA of Sig Pep	Predicted First AA of Secreted Portion	Last AA of ORF
71	HFFAH94	97900 02/26/97 209046 05/15/97	Lambda ZAP II	81	1290	768	1054	701	701	383	1	21	22	138
72	HBIAB195	97900 02/26/97 209046 05/15/97	Uni-ZAP XR	82	684	1	684	119	119	384	1	30	31	74
73	HSQEL25	97900 02/26/97 209046 05/15/97	Uni-ZAP XR	83	2024	1609	1953	200	200	385	1	30	31	521
73	HSQEL25	97900 02/26/97 209046 05/15/97	Uni-ZAP XR	237	1286	391	959		1204	539	1	9	10	11
74	HEBEG68	97900 02/26/97 209046 05/15/97	Uni-ZAP XR	84	931	14	537	85	85	386	1	25	26	137
75	HBIAB39	97900 02/26/97 209046 05/15/97	Uni-ZAP XR	85	825	59	802	66	66	387	1	30	31	186

Gene No.	cDNA Clone ID	ATCC Deposit No: Z and Date	Vector	NT SEQ ID NO: X	Total NT Seq.	5' NT of Clone Seq.	3' NT of Clone Seq.	5' NT of Start Codon	5' NT of First AA of Signal Pep	AA SEQ ID NO: Y	First AA of Sig Pep	Last AA of Sig Pep	Predicted First AA of Secreted Portion	Last AA of ORF
75	HBIAB39	97900 02/26/97 209046 05/15/97	Uni-ZAP XR	238	734	1	734	1	1	540	1	37	38	108
75	HBIAB39	97900 02/26/97 209046 05/15/97	Uni-ZAP XR	239	809	80	794		294	541	1	15	16	106
76	HTXDU73	97900 02/26/97 209046 05/15/97	Uni-ZAP XR	86	1238	36	918	17	17	388	1			1
77	HOEAS24	97900 02/26/97 209046 05/15/97	Uni-ZAP XR	87	1460	9	1458	166	166	389	1	53	54	299
77	HOEAS24	97900 02/26/97 209046 05/15/97	Uni-ZAP XR	240	2201	841	2080	507	507	542	1	43	44	136
77	HOEAS24	97900 02/26/97 209046 05/15/97	Uni-ZAP XR	241	1661	311	1520	390	390	543	1	35	36	424

Gene No.	cDNA Clone ID	ATCC Deposit No: Z and Date	Vector	NT SEQ ID NO: X	Total NT Seq.	5' NT of Clone Seq.	3' NT of Clone Seq.	5' NT of Start Codon	5' NT of First AA of Signal Pep	AA SEQ ID NO: Y	First AA of Sig Pep	Last AA of Sig Pep	Predicted First AA of Secreted Portion	Last AA of ORF
78	HTEIY30	97900 02/26/97 209046 05/15/97	Uni-ZAP XR	88	1395	567	1395	639	639	390	1	36	37	49
79	HSKNE46	97900 02/26/97 209046 05/15/97	pBluescript	89	1186	352	1186	540	540	391	1	49	50	61
79	HSKNE46	97900 02/26/97 209046 05/15/97	pBluescript	242	1146	329	1146	564	564	544	1	21	22	39
80	HPMFL27	97900 02/26/97 209046 05/15/97	Uni-ZAP XR	90	1821	1203	1614	1503	1503	392	1	30	31	79
81	HMWDN32	97900 02/26/97 209046 05/15/97	Uni-Zap XR	91	862	253	862	359	359	393	1	32	33	36
82	HPRAX55	97900 02/26/97 209046 05/15/97	Uni-ZAP XR	92	696	349	696	98	98	394	1	30	31	180

Gene No.	cDNA Clone ID	ATCC Deposit No: Z and Date	Vector	NT SEQ ID NO: X	Total NT Seq.	5' NT of Clone Seq.	3' NT of Clone Seq.	5' NT of Start Codon	5' NT of First AA of Signal Pep	AA SEQ ID NO: Y	First AA of Sig Pep	Last AA of Sig Pep	Predicted First AA of Secreted Portion	Last AA of ORF
82	HPRAX55	97900 02/26/97 209046 05/15/97	Uni-ZAP XR	243	1350	265	1230	348	348	545	1	32	33	58
83	HHFFW36	97900 02/26/97 209046 05/15/97	Uni-ZAP XR	93	1886	1	1759	197	197	395	1			21
84	HE2PL77	97901 02/26/97 209047 05/15/97	Uni-ZAP XR	94	1774	742	1772	785	785	396	1	21	22	60
85	HSDFV29	209076 05/22/97	Uni-ZAP XR	95	2503	1	1648	206	206	397	1	32	33	152
85	HCQAV53	97901 02/26/97 209047 05/15/97	Lambda ZAP II	244	1529	72	911	191	191	546	1	20	21	33
86	HTPEG42	97901 02/26/97 209047 05/15/97	Uni-ZAP XR	96	2801	418	2801	234	234	398	1	30	31	480
86	HTPEG42	97901 02/26/97 209047 05/15/97	Uni-ZAP XR	245	1537	1	1537	125	125	547	1	21	22	367

Gene No.	cDNA Clone ID	ATCC Deposit No: Z and Date	Vector	NT SEQ ID NO: X	Total NT Seq.	5' NT of Clone Seq.	3' NT of Clone Seq.	5' NT of Start Codon	5' NT of First AA of Signal Pep	AA SEQ ID NO: Y	First AA of Sig Pep	Last AA of Sig Pep	Predicted First AA of Secreted Portion	Last AA of ORF
87	HLHDR57	97901 02/26/97 209047 05/15/97	Uni-ZAP XR	97	1631	916	1631	1	1	399	1	1	2	423
88	HAUAV32	97901 02/26/97 209047 05/15/97	Uni-ZAP XR	98	504	26	504	197	197	400	1	23	24	78
88	HAUAV32	97901 02/26/97 209047 05/15/97	Uni-ZAP XR	246	506	1	499	183	183	548	1	32	33	77
89	HNEBI60	97901 02/26/97 209047 05/15/97	Uni-ZAP XR	99	1416	145	1416	456	456	401	1	18	19	74
89	HNEBI60	97901 02/26/97 209047 05/15/97	Uni-ZAP XR	247	1348	84	1348	363	363	549	1	21	22	47
90	HSJC116	97901 02/26/97 209047 05/15/97	Uni-ZAP XR	100	2847	1	2847		2	402	1			20

Gene No.	cDNA Clone ID	ATCC Deposit No: Z and Date	Vector	NT SEQ ID NO: X	Total NT Seq.	5' NT of Clone Seq.	3' NT of Clone Seq.	5' NT of Start Codon	5' NT of First AA of Signal Pep	AA SEQ ID NO: Y	First AA of Sig Pep	Last AA of Sig Pep	Predicted First AA of Secreted Portion	Last AA of ORF
91	HTSEL31	97901 02/26/97 209047 05/15/97	pBluescript	101	1394	608	1346	602	602	403	1	23	24	87
92	HAUBL57	97901 02/26/97 209047 05/15/97	Uni-ZAP XR	102	794	1	794	518	518	404	1	30	31	92
92	HAUBL57	97901 02/26/97 209047 05/15/97	Uni-ZAP XR	248	1766	42	1766	356	356	550	1	30	31	168
92	HAUBL57	97901 02/26/97 209047 05/15/97	Uni-ZAP XR	249	2664	47	1708		147	551	1	18	19	124
93	HODAS59	97901 02/26/97 209047 05/15/97	Uni-ZAP XR	103	1544	898	1531	975	975	405	1			21
94	HE6CT48	97901 02/26/97 209047 05/15/97	Uni-ZAP XR	104	871	106	871	248	248	406	1	34	35	174

Gene No.	cDNA Clone ID	ATCC Deposit No: Z and Date	Vector	NT SEQ ID NO: X	Total NT Seq.	5' NT of Clone Seq.	3' NT of Clone Seq.	5' NT of Start Codon	5' NT of First AA of Signal Pep	AA SEQ ID NO: Y	First AA of Sig Pep	Last AA of Sig Pep	Predicted First AA of Secreted Portion	Last AA of ORF
94	HE6CT48	97901 02/26/97 209047 05/15/97	Uni-ZAP XR	250	865	97	865	258	258	552	1	19	20	177
95	HMDAA61	97901 02/26/97 209047 05/15/97	Uni-ZAP XR	105	404	1	404	16	16	407	1	21	22	64
95	HMDAA61	97901 02/26/97 209047 05/15/97	Uni-ZAP XR	251	2082	852	2074	829	829	553	1	22	23	72
96	HAQBK61	97901 02/26/97 209047 05/15/97	Uni-ZAP XR	106	1542	506	1542	122	122	408	1	51	52	280
96	HAQBK61	97901 02/26/97 209047 05/15/97	Uni-ZAP XR	252	1482	508	1482		633	554	1	15	16	45
96	HCUHB01	209215 08/21/97	ZAP Express	253	834	1	834	82	82	555	1	40	41	251
97	HAQBF73	97901 02/26/97 209047 05/15/97	Uni-ZAP XR	107	2327	1528	2327	465	465	409	1	30	31	284

Gene No.	cDNA Clone ID	ATCC Deposit No: Z and Date	Vector	NT SEQ ID NO: X	Total NT Seq.	5' NT of Clone Seq.	3' NT of Clone Seq.	5' NT of Start Codon	5' NT of First AA of Signal Pep	AA SEQ ID NO: Y	First AA of Sig Pep	Last AA of Sig Pep	Predicted First AA of Secreted Portion	Last AA of AA of ORF
97	HAQBF73	97901 02/26/97 209047 05/15/97	Uni-ZAP XR	254	1508	885	1508		988	556	1			19
98	HAQBT94	97901 02/26/97 209047 05/15/97	Uni-ZAP XR	108	1062	157	1062	172	172	410	1	28	29	187
99	HETHE07	97901 02/26/97 209047 05/15/97	Uni-ZAP XR	109	2539	275	2501	903	903	411	1	30	31	237
99	HETHE07	97901 02/26/97 209047 05/15/97	Uni-ZAP XR	255	2514	592	2431	176	176	557	1	30	31	217
99	HETHE07	97901 02/26/97 209047 05/15/97	Uni-ZAP XR	256	2357	465	2288		1151	558	1	12	13	82
100	HLQAB52	97901 02/26/97 209047 05/15/97	Lambda ZAP II	110	1751	969	1751	4	4	412	1	46	47	192

Gene No.	cDNA Clone ID	ATCC Deposit No: Z and Date	Vector	NT SEQ ID NO: X	Total NT Seq.	5' NT of Clone Seq.	3' NT of Clone Seq.	5' NT of Start Codon	5' NT of First AA of Signal Pep	AA SEQ ID NO: Y	First AA of Sig Pep	Last AA of Sig Pep	Predicted First AA of Secreted Portion	Last AA of ORF
100	HLQAB52	97901 02/26/97 209047 05/15/97	Lambda ZAP II	257	689	218	655	314	314	559	1	18	19	95
100	HEONN58	209119 06/12/97	pSport1	258	2377	5	2377	25	25	560	1	28	29	54
101	HCRAM28	97901 02/26/97 209047 05/15/97	Uni-ZAP XR	111	1117	1	1117		1	413	1	19	20	21
101	HIBEK16	209627 02/12/98	Other	259	1193	69	1135	242	242	561	1	24	25	108
102	HE2BG03	97901 02/26/97 209047 05/15/97	Uni-ZAP XR	112	1313	128	1313	271	271	414	1	30	31	51
102	HE2BG03	97901 02/26/97 209047 05/15/97	Uni-ZAP XR	260	1262	26	1262	35	35	562	1	35	36	50
103	HEBDJ82	97901 02/26/97 209047 05/15/97	Uni-ZAP XR	113	1654	553	1654	709	709	415	1			32

Gene No.	cDNA Clone ID	ATCC Deposit No: Z and Date	Vector	NT SEQ ID NO: X	Total NT Seq.	5' NT3' NT of Clone Seq.	5' NT of Clone Seq.	5' NT of First AA of Signal Pep	AA SEQ ID NO: Y	First AA of Sig Pep	Last AA of Sig Pep	Predicted First AA of Secreted Portion	Last AA of ORF
104	HCUBC79	97901 02/26/97 209047 05/15/97	ZAP Express	114	1171	540	1171	337	416	1	30	31	163
104	HCUBC79	97901 02/26/97 209047 05/15/97	ZAP Express	261	1179	626	1161	335	563	1	30	31	253
104	HCUBC79	97901 02/26/97 209047 05/15/97	ZAP Express	262	1162	629	1131	942	564	1			18
105	HSVAF07	97901 02/26/97 209047 05/15/97	Uni-ZAP XR	115	842	373	800	100	417	1	65	66	174
105	HSVAF07	97901 02/26/97 209047 05/15/97	Uni-ZAP XR	263	735	290	735		565	1			
105	HSVAF07	97901 02/26/97 209047 05/15/97	Uni-ZAP XR	264	783	416	783	413	566	1	33	34	73

Gene No.	cDNA Clone ID	ATCC Deposit No.: Z and Date	Vector	NT SEQ ID NO: X	Total NT Seq.	5' NT of Clone Seq.	3' NT of Clone Seq.	5' NT of Start Codon	5' NT of First AA of Signal Pep	AA SEQ ID NO: Y	First AA of Sig Pep	Last AA of Sig Pep	Predicted First AA of Secreted Portion	Last AA of ORF
106	HT3AM65	97901 02/26/97 209047 05/15/97	Uni-ZAP XR	116	1640	187	1470	581	581	418	1	30	31	50
106	HT3AM65	97901 02/26/97 209047 05/15/97	Uni-ZAP XR	265	1638	301	1405	119	119	567	1	30	31	263
106	HT3AM65	97901 02/26/97 209047 05/15/97	Uni-ZAP XR	266	1455	148	1188	438	438	568	1	24	25	70
107	HE6DK18	97901 02/26/97 209047 05/15/97	Uni-ZAP XR	117	952	418	906	499	499	419	1	28	29	120
108	HEBEK93	97901 02/26/97 209047 05/15/97	Uni-ZAP XR	118	1256	21	1079	301	301	420	1	30	31	159
108	HEBEK93	97901 02/26/97 209047 05/15/97	Uni-ZAP XR	267	1086	25	1050	227	227	569	1	23	24	34

Gene No.	cDNA Clone ID	ATCC Deposit No: Z and Date	Vector	NT SEQ ID NO: X	Total NT Seq.	5' NT of Clone Seq.	3' NT of Clone Seq.	5' NT of Start Codon	5' NT of First AA of Signal Pep	AA SEQ ID NO: Y	First AA of Sig Pep	Last AA of Sig Pep	Predicted First AA of Secreted Portion	Last AA of ORF
109	HJPCM10	97901 02/26/97 209047 05/15/97	Uni-ZAP XR	119	1143	171	1051	175	175	421	1	50	51	154
109	HJPCM10	97901 02/26/97 209047 05/15/97	Uni-ZAP XR	268	1003	21	1003	115	115	570	1	34	35	104
109	HJPCM10	97901 02/26/97 209047 05/15/97	Uni-ZAP XR	269	1234	174	1015	232	232	571	1	27	28	132
110	HSXBL78	97901 02/26/97 209047 05/15/97	Uni-ZAP XR	120	1782	1	1720	138	138	422	1	32	33	204
111	HOEAW81	97901 02/26/97 209047 05/15/97	Uni-ZAP XR	121	610	18	609	50	50	423	1	30	31	67
111	HOEAW81	97901 02/26/97 209047 05/15/97	Uni-ZAP XR	270	574	1	566	337	337	572	1	27	28	32

Gene No.	cDNA Clone ID	ATCC Deposit No: Z and Date	Vector	NT SEQ ID NO: X	Total NT Seq.	5' NT of Clone Seq.	3' NT of Clone Seq.	5' NT of Start Codon	5' NT of First AA of Signal Pep	AA SEQ ID NO: Y	First AA of Sig Pep	Last AA of Sig Pep	Predicted First AA of Secreted Portion	Last AA of ORF
112	HOEAP41	97901 02/26/97 209047 05/15/97	Uni-ZAP XR	122	526	185	375	143	143	424	1	21	22	25
113	HEAAR60	97901 02/26/97 209047 05/15/97	Uni-ZAP XR	123	2081	1179	1976	48	48	425	1	30	31	299
113	HEAAR60	97901 02/26/97 209047 05/15/97	Uni-ZAP XR	271	1731	889	1626	886	886	573	1	18	19	28
114	HTXGS75	97902 02/26/97 209048 05/15/97	Uni-ZAP XR	124	1717	764	1640	76	76	426	1			13
115	HOVBA03	97902 02/26/97 209048 05/15/97	pSport1	125	804	1	804	145	145	427	1	15	16	198
115	HOVBA03	97902 02/26/97 209048 05/15/97	pSport1	272	1320	77	637	280	280	574	1	22	23	40

Gene No.	cDNA Clone ID	ATCC Deposit No: Z and Date	Vector	NT SEQ ID NO: X	Total NT Seq.	5' NT of Clone Seq.	5' NT of Clone Seq.	5' NT of AA of Signal Pep	AA SEQ ID NO: Y	First AA of Sig Pep	Last AA of Sig Pep	Predicted First AA of Secreted Portion	Last AA of ORF
116	HGBGK76	97902 02/26/97 209048 05/15/97	Uni-ZAP XR	126	431	1	431	73	428	1	38	39	47
116	HGBGK76	97902 02/26/97 209048 05/15/97	Uni-ZAP XR	273	515	1	515	43	575	1	20	21	30
117	HBMUW78	97902 02/26/97 209048 05/15/97	Uni-ZAP XR	127	3752	3465	3752	748	429	1	30	31	370
117	HBMUW78	97902 02/26/97 209048 05/15/97	Uni-ZAP XR	274	2995	2738	2995	2777	576	1	18	19	29
118	HASAS24	97902 02/26/97 209048 05/15/97	Uni-ZAP XR	128	1144	669	1144	896	430	1			30
119	HSIDN55	97902 02/26/97 209048 05/15/97	Uni-ZAP XR	129	1830	1234	1830	1265	431	1			24

Gene No.	cDNA Clone ID	ATCC Deposit No: Z and Date	Vector	NT SEQ ID NO: X	Total NT Seq.	5' NT of Clone Seq.	3' NT of Clone Seq.	5' NT of AA of Signal Pep	AA SEQ ID NO: Y	First AA of Sig Pep	Last AA of Sig Pep	Predicted First AA of Secreted Portion	Last AA of ORF
120	HGBGZ64	97902 02/26/97 209048 05/15/97	Uni-ZAP XR	130	1864	1505	1741	1578	432	1	37	38	53
121	H6EBJ64	97902 02/26/97 209048 05/15/97	Uni-ZAP XR	131	2041	1	1214	46	433	1	35	36	176
121	H6EBJ64	97902 02/26/97 209048 05/15/97	Uni-ZAP XR	275	1990	8	1128	71	577	1	16	17	92
122	HOECP43	97902 02/26/97 209048 05/15/97	Uni-ZAP XR	132	2012	853	1986	1127	434	1	22	23	77
123	H2CBV31	97902 02/26/97 209048 05/15/97	pBluescript SK-	133	1669	670	1632	962	435	1	25	26	32
124	HPCAD23	97902 02/26/97 209048 05/15/97	Uni-ZAP XR	134	1565	281	1565	274	436	1	25	26	30

Gene No.	cDNA Clone ID	ATCC Deposit No: Z and Date	Vector	NT SEQ ID NO: X	Total NT Seq.	5' NT3' NT of Clone Seq.	5' NT of Start Codon	5' NT of First AA of Signal Pep	AA SEQ ID NO: Y	First AA of Sig Pep	Last AA of Sig Pep	Predicted First AA of Secreted Portion	Last AA of ORF
125	HSPAG15	97902 02/26/97 209048 05/15/97	pSport1	135	2007	1101 2007	1124	1124	437	1	39	40	69
126	HELGH31	97902 02/26/97 209048 05/15/97	Uni-ZAP XR	136	1291	1 1180	107	107	438	1			19
127	HUSHH48	97902 02/26/97 209048 05/15/97	Lambda ZAP II	137	1906	1 1906	184	184	439	1	30	31	43
127	HUSHH48	97902 02/26/97 209048 05/15/97	Lambda ZAP II	276	2436	572 2436	726	726	578	1	30	31	42
128	HLYAU95	97902 02/26/97 209048 05/15/97	pSport1	138	1935	1044 1794	1183	1183	440	1	18	19	33
129	HHSCV65	97902 02/26/97 209048 05/15/97	Uni-ZAP XR	139	1446	572 1347	585	585	441	1	25	26	53

Gene No.	cDNA Clone ID	ATCC Deposit No: Z and Date	Vector	NT SEQ ID NO: X	Total NT Seq.	5' NT of Clone Seq.	3' NT of Clone Seq.	5' NT of Start Codon	5' NT of First AA of Signal Pep	AA SEQ ID NO: Y	First AA of Sig Pep	Last AA of Sig Pep	Predicted First AA of Secreted Portion	Last AA of ORF
130	HTTAD57	97902 02/26/97 209048 05/15/97	Uni-ZAP XR	140	1109	639	1109	676	676	442	1	24	25	64
131	HEBGA37	97902 02/26/97 209048 05/15/97	Uni-ZAP XR	141	497	9	497	95	95	443	1			34
132	HEBFU93	97902 02/26/97 209048 05/15/97	Uni-ZAP XR	142	269	1	269	1	1	444	1	30	31	89
132	HEBFU93	97902 02/26/97 209048 05/15/97	Uni-ZAP XR	277	782	408	781		571	579	1	31	32	70
133	HSGSC60	97902 02/26/97 209048 05/15/97	Lambda ZAP II	143	1269	55	1262	55	55	445	1	25	26	350
134	HPMGD24	97902 02/26/97 209048 05/15/97	Uni-ZAP XR	144	1944	97	1871	306	306	446	1	16	17	49

Gene No.	cDNA Clone ID	ATCC Deposit No: Z and Date	Vector	NT SEQ ID NO: X	Total NT Seq.	5' NT of Clone Seq.	3' NT of Clone Seq.	5' NT of Start Codon	5' NT of First AA of Signal Pep	AA SEQ ID NO: Y	First AA of Sig Pep	Last AA of Sig Pep	Predicted First AA of Secreted Portion	Last AA of ORF
135	HPTVC60	97902 02/26/97 209048 05/15/97	pBluescript	145	1021	526	1021	74	74	447	1	30	31	278
135	HPTVC60	97902 02/26/97 209048 05/15/97	pBluescript	278	961	524	961	545	545	580	1	23	24	110
136	HSKNE18	97902 02/26/97 209048 05/15/97	pBluescript	146	1285	5	1285	116	116	448	1	30	31	199
136	HSKNE18	97902 02/26/97 209048 05/15/97	pBluescript	279	1228	9	1228	324	324	581	1	26	27	30
137	HMWIF35	97902 02/26/97 209048 05/15/97	Uni-Zap XR	147	1386	169	1272	165	165	449	1	30	31	258
137	HMWIF35	97902 02/26/97 209048 05/15/97	Uni-Zap XR	280	1327	169	1208	160	160	582	1	23	24	71

Gene No.	cDNA Clone ID	ATCC Deposit No: Z and Date	Vector	NT SEQ ID NO: X	Total NT Seq.	5' NT of Clone Seq.	3' NT of Clone Seq.	5' NT of Start Codon	5' NT of First AA of Signal Pep	AA SEQ ID NO: Y	First AA of Sig Pep	Last AA of Sig Pep	Predicted First AA of Secreted Portion	Last AA of ORF
138	HMWGI25	97902 02/26/97 209048 05/15/97	Uni-Zap XR	148	2098	721	2044	784	784	450	1	18	19	87
139	HSKGF03	97902 02/26/97 209048 05/15/97	pBluescript	149	1847	1689	1847	241	241	451	1	33	34	315
139	HSKGF03	97902 02/26/97 209048 05/15/97	pBluescript	281	799	1	799		243	583	1	12	13	47
140	HMSKE75	97902 02/26/97 209048 05/15/97	Uni-ZAP XR	150	1569	113	1517	417	417	452	1	21	22	52
141	HCMSH30	97902 02/26/97 209048 05/15/97	Uni-ZAP XR	151	1540	538	1540	48	48	453	1	30	31	383
141	HCMSH30	97902 02/26/97 209048 05/15/97	Uni-ZAP XR	282	2196	270	2196	294	294	584	1	32	33	39

Gene No.	cDNA Clone ID	ATCC Deposit No: Z and Date	Vector	NT SEQ ID NO: X	Total NT Seq.	5' NT of Clone Seq.	3' NT of Clone Seq.	5' NT of Start Codon	5' NT of AA of Signal Pep	AA SEQ ID NO: Y	First AA of Sig Pep	Last AA of Sig Pep	Predicted First AA of Secreted Portion	Last AA of ORF
142	HTWCB92	97902 02/26/97 209048 05/15/97	pSport1	152	1719	690	1575	6	6	454	1	52	53	186
143	HBMDM46	97902 02/26/97 209048 05/15/97	pBluescript	153	863	1	863	195	195	455	1	26	27	163
143	HBMDM46	97902 02/26/97 209048 05/15/97	pBluescript	283	1185	277	1166	621	621	585	1			19
144	HFAMG13	97902 02/26/97 209048 05/15/97	Uni-ZAP XR	154	1101	1	512	40	40	456	1	21	22	46
145	HFXHL79	97903 02/26/97 209049 05/15/97	Lambda ZAP II	155	2031	669	2031	411	411	457	1	23	24	105
145	HFXHL79	97903 02/26/97 209049 05/15/97	Lambda ZAP II	284	1634	615	1485	878	878	586	1	20	21	23

Gene No.	cDNA Clone ID	ATCC Deposit No: Z and Date	Vector	NT SEQ ID NO: X	Total NT Seq.	5' NT of Clone Seq.	5' NT of Clone Seq.	5' NT of Start Codon	5' NT of First AA of Signal Pep	AA SEQ ID NO: Y	First AA of Sig Pep	Last AA of Sig Pep	Predicted First AA of Secreted Portion	Last AA of ORF
146	HSNAK17	97903 02/26/97 209049 05/15/97	Uni-ZAP XR	156	1981	1458	1809	1592	1592	458	1	23	24	70
146	HSNAK17	97903 02/26/97 209049 05/15/97	Uni-ZAP XR	285	1795	1458	1749	1562	1562	587	1	33	34	69
147	HCFBC03	97903 02/26/97 209049 05/15/97	pSport1	157	915	45	912	22	22	459	1	22	23	155
147	HCFBC03	97903 02/26/97 209049 05/15/97	pSport1	286	858	46	858	224	224	588	1	30	31	77
147	HSJAP03	209139 07/03/97	Uni-ZAP XR	287	915	1	915	22	22	589	1	22	23	155
148	HSKGO26	97903 02/26/97 209049 05/15/97	pBluescript	158	2117	51	1422	32	32	460	1	23	24	332
149	HCQAV96	97903 02/26/97 209049 05/15/97	Lambda ZAP II	159	2395	1509	2382	1440	1440	461	1			5

Gene No.	cDNA Clone ID	ATCC Deposit No: Z and Date	Vector	NT SEQ ID NO: X	Total NT Seq.	5' NT3' NT of Clone Seq.	5' NT of Start Codon	5' NT of First AA of Signal Pep	AA SEQ ID NO: Y	First AA of Sig Pep	Last AA of Sig Pep	Predicted First AA of Secreted Portion	Last AA of ORF
150	HSHCC16	97903 02/26/97 209049 05/15/97	Uni-ZAP XR	160	2120	1223 2108	1416	1416	462	1			14
151	HTLEF62	97903 02/26/97 209049 05/15/97	Uni-ZAP XR	161	900	482 900	46	46	463	1	30	31	285
151	HTLEF62	97903 02/26/97 209049 05/15/97	Uni-ZAP XR	288	1517	783 1517	1062	1062	590	1			24
152	HTLAD94	97903 02/26/97 209049 05/15/97	Uni-ZAP XR	162	1003	1 1003	288	288	464	1	30	31	80
152	HTLAD94	97903 02/26/97 209049 05/15/97	Uni-ZAP XR	289	3865	217 1195	281	281	591	1	16	17	38
153	HTSFQ12	97903 02/26/97 209049 05/15/97	pBluescript	163	2196	1607 2180	1611	1611	465	1	30	31	47

Gene No.	cDNA Clone ID	ATCC Deposit No: Z and Date	Vector	NT SEQ ID NO: X	Total NT Seq.	5' NT of Clone Seq.	3' NT of Clone Seq.	5' NT of Start Codon	5' NT of First AA of Signal Pep	AA SEQ ID NO: Y	First AA of Sig Pep	Last AA of Sig Pep	Predicted First AA of Secreted Portion	Last AA of ORF
154	HE6FL83	97903 02/26/97 209049 05/15/97	Uni-ZAP XR	164	1945	271	1840	299	299	466	1	63	64	96
154	HE6FL83	97903 02/26/97 209049 05/15/97	Uni-ZAP XR	290	1910	279	1818	355	355	592	1	39	40	69
155	HTXFJ55	97903 02/26/97 209049 05/15/97	Uni-ZAP XR	165	2933	489	2871	258	258	467	1	30	31	399
155	HTXFJ55	97903 02/26/97 209049 05/15/97	Uni-ZAP XR	291	3276	486	2838		525	593	1	45	46	308
156	HJPCJ76	97903 02/26/97 209049 05/15/97	Uni-ZAP XR	166	2243	343	2221		341	468	1			1
157	HLTED27	97903 02/26/97 209049 05/15/97	Uni-ZAP XR	167	1816	1130	1816	284	284	469	1	31	32	273

Gene No.	cDNA Clone ID	ATCC Deposit No: Z and Date	Vector	NT SEQ ID NO: X	Total NT Seq.	5' NT of Clone Seq.	5' NT of Clone Seq.	5' NT of First AA of Signal Pep	AA SEQ ID NO: Y	First AA of Sig Pep	Last AA of Sig Pep	Predicted First AA of Secreted Portion	Last AA of ORF
157	HLTED27	97903 02/26/97 209049 05/15/97	Uni-ZAP XR	292	1695	1098	1548	1306	594	1			22
158	HMKBA64	97903 02/26/97 209049 05/15/97	pSport1	168	945	1	787	208	470	1	18	19	192
159	HNFIP24	97903 02/26/97 209049 05/15/97	pBluescript	169	902	46	816	19	471	1	26	27	234
160	HCELB21	97903 02/26/97 209049 05/15/97	Uni-ZAP XR	170	1883	798	1869	1001	472	1	45	46	105
160	HCELB21	97903 02/26/97 209049 05/15/97	Uni-ZAP XR	293	1501	438	1501	510	595	1			24
161	HAWBA28	97903 02/26/97 209049 05/15/97	pBluescript SK-	171	2100	1642	2100	1722	473	1	23	24	32

Gene No.	cDNA Clone ID	ATCC Deposit No: Z and Date	Vector	NT SEQ ID NO: X	Total NT Seq.	5' NT of Clone Seq.	5' NT of Clone Seq.	5' NT of AA of Signal Pep	AA SEQ ID NO: Y	First AA of Sig Pep	Last AA of Sig Pep	Predicted First AA of Secreted Portion	Last AA of ORF
162	HSAAS44	97903 02/26/97 209049 05/15/97	pBluescript SK-	172	1930	187	1930	65	474	1	30	31	571
162	HSAAS44	97903 02/26/97 209049 05/15/97	pBluescript SK-	294	2683	183	2683	431	596	1			24
163	HAFAL73	97903 02/26/97 209049 05/15/97	pBluescript SK-	173	1509	962	1451	122	475	1	30	31	312
163	HAFAL73	97903 02/26/97 209049 05/15/97	pBluescript SK-	295	1454	961	1420	976	597	1			1
164	HSAWF26	97903 02/26/97 209049 05/15/97	Uni-ZAP XR	174	3173	2197	2972	51	476	1	21	22	329
164	HSAWF26	97903 02/26/97 209049 05/15/97	Uni-ZAP XR	296	828	52	828	305	598	1			8

Gene No.	cDNA Clone ID	ATCC Deposit No: Z and Date	Vector	NT SEQ ID NO: X	Total NT Seq.	5' NT of Clone Seq.	3' NT of Clone Seq.	5' NT of Start Codon	5' NT of First AA of Signal Pep	AA SEQ ID NO: Y	First AA of Sig Pep	Last AA of Sig Pep	Predicted First AA of Secreted Portion	Last AA of ORF
165	HEAAL31	97903 02/26/97 209049 05/15/97	Uni-ZAP XR	175	991	374	970	60	60	477	1	24	25	178
165	HEAAL31	97903 02/26/97 209049 05/15/97	Uni-ZAP XR	297	2416	1387	2413	1473	1473	599	1	18	19	25
166	HFKFX55	97903 02/26/97 209049 05/15/97	Uni-ZAP XR	176	1290	499	1290		688	478	1	25	26	52
167	H2LAO11	97903 02/26/97 209049 05/15/97	pBluescript SK-	177	2290	1	2290	173	173	479	1	22	23	62
168	HPFDZ95	97903 02/26/97 209049 05/15/97	Uni-ZAP XR	178	549	1	549	11	11	480	1	21	22	27
168	HPFDZ95	97903 02/26/97 209049 05/15/97	Uni-ZAP XR	298	545	1	545	17	17	600	1	21	22	27

Gene No.	cDNA Clone ID	ATCC Deposit No: Z and Date	Vector	NT SEQ ID NO: X	Total NT Seq.	5' NT of Clone Seq.	3' NT of Clone Seq.	5' NT of Start Codon	5' NT of First AA of Signal Pep	AA SEQ ID NO: Y	First AA of Sig Pep	Last AA of Sig Pep	Predicted First AA of Secreted Portion	Last AA of ORF
169	HPTTU11	97904 02/26/97 209050 05/15/97	Uni-ZAP XR	179	1509	294	1352	92	92	481	1	30	31	339
169	HPTTU11	97904 02/26/97 209050 05/15/97	Uni-ZAP XR	299	1530	385	1530	562	562	601	1	23	24	61
170	HCFAE79	97904 02/26/97 209050 05/15/97	pSport1	180	1316	985	1250	995	995	482	1	26	27	32
171	HTEDJ34	97904 02/26/97 209050 05/15/97	Uni-ZAP XR	181	777	1	777	51	51	483	1	30	31	48
171	HTEDJ34	97904 02/26/97 209050 05/15/97	Uni-ZAP XR	300	997	244	997	300	300	602	1	23	24	29
172	HODCW06	97904 02/26/97 209050 05/15/97	Uni-ZAP XR	182	791	1	791	14	14	484	1	29	30	38

Gene No.	cDNA Clone ID	ATCC Deposit No: Z and Date	Vector	NT SEQ ID NO: X	Total NT Seq.	5' NT of Clone Seq.	3' NT of Clone Seq.	5' NT of Start Codon	5' NT of First AA of Signal Pep	AA SEQ ID NO: Y	First AA of Sig Pep	Last AA of Sig Pep	Predicted First AA of Secreted Portion	Last AA of ORF
173	HFTAR26	97904 02/26/97 209050 05/15/97	Uni-ZAP XR	183	1405	346	1405	575	575	485	1	20	21	61
174	H2MBF44	97904 02/26/97 209050 05/15/97	pBluescript SK-	184	1596	75	1596	131	131	486	1	24	25	346
174	H2MBF44	97904 02/26/97 209050 05/15/97	pBluescript SK-	301	2345	75	2345	233	233	603	1	56	57	69
175	HE8BI92	97904 02/26/97 209050 05/15/97	Uni-ZAP XR	185	2293	355	2288	67	67	487	1	30	31	237
175	HE8BI92	97904 02/26/97 209050 05/15/97	Uni-ZAP XR	302	2369	2	1946		60	604	1	9	10	24
176	HFTBR48	97904 02/26/97 209050 05/15/97	Uni-ZAP XR	186	1212	462	1180	257	257	488	1	30	31	200

Gene No.	cDNA Clone ID	ATCC Deposit No: Z and Date	Vector	NT SEQ ID NO: X	Total NT Seq.	5' NT of Clone Seq.	3' NT of Clone Seq.	5' NT of Start Codon	5' NT of First AA of Signal Pep	AA SEQ ID NO: Y	First AA of Sig Pep	Last AA of Sig Pep	Predicted First AA of Secreted Portion	Last AA of ORF
176	HFTBR48	97904 02/26/97 209050 05/15/97	Uni-ZAP XR	303	1181	424	1149	663	663	605	1	23	24	35
177	HE9CM64	97904 02/26/97 209050 05/15/97	Uni-ZAP XR	187	1605	770	1554	166	166	489	1	30	31	351
177	HE9CM64	97904 02/26/97 209050 05/15/97	Uni-ZAP XR	304	1537	719	1515		787	606	1	43	44	130
178	HATAV51	97904 02/26/97 209050 05/15/97	Uni-ZAP XR	188	1516	960	1516	8	8	490	1	30	31	265
178	HATAV51	97904 02/26/97 209050 05/15/97	Uni-ZAP XR	305	1493	1	1261	54	54	607	1	18	19	23
179	HAQAF27	97904 02/26/97 209050 05/15/97	Uni-ZAP XR	189	681	287	681		401	491	1			25

Gene No.	cDNA Clone ID	ATCC Deposit No: Z and Date	Vector	NT SEQ ID NO: X	Total NT Seq.	5' NT of Clone Seq.	3' NT of Clone Seq.	5' NT of Start Codon	5' NT of First AA of Signal Pep	AA SEQ ID NO: Y	First AA of Sig Pep	Last AA of Sig Pep	Predicted First AA of Secreted Portion	Last AA of ORF
180	HCEEK08	97904 02/26/97 209050 05/15/97	Uni-ZAP XR	190	1014	703	1014	360	360	492	1	30	31	159
180	HCEEK08	97904 02/26/97 209050 05/15/97	Uni-ZAP XR	306	577	1	577	175	608	1	1			6
181	HAFUAU18	97904 02/26/97 209050 05/15/97	pBluescript SK-	191	2779	2207	2630	1153	1153	493	1	30	31	279
181	HAFUAU18	97904 02/26/97 209050 05/15/97	pBluescript SK-	307	2860	163	2860	21	21	609	1	30	31	232
181	HAFUAU18	97904 02/26/97 209050 05/15/97	pBluescript SK-	308	876	275	876	302	302	610	1	32	33	34
182	HETBY74	97904 02/26/97 209050 05/15/97	Uni-ZAP XR	192	1923	30	1923	45	45	494	1	33	34	193

Gene No.	cDNA Clone ID	ATCC Deposit No: Z and Date	Vector	NT SEQ ID NO: X	Total NT Seq.	5' NT of Clone Seq.	3' NT of Clone Seq.	5' NT of Start Codon	5' NT of First AA of Signal Pep	AA SEQ ID NO: Y	First AA of Sig Pep	Last AA of Sig Pep	Predicted First AA of Secreted Portion	Last AA of ORF
183	HTOAF35	97904 02/26/97 209050 05/15/97	Uni-ZAP XR	193	2346	1160	2286	178	178	495	1	30	31	205
183	HTOAF35	97904 02/26/97 209050 05/15/97	Uni-ZAP XR	309	2025	840	2025	971	971	611	1	18	19	21
184	HCRBX32	97904 02/26/97 209050 05/15/97	Uni-ZAP XR	194	3054	2004	3054	434	434	496	1	11	12	147
184	HCRBX32	97904 02/26/97 209050 05/15/97	Uni-ZAP XR	310	3026	1966	3026		2131	612	1			9
185	HEBGB80	97904 02/26/97 209050 05/15/97	Uni-ZAP XR	195	907	152	907	297	297	497	1	30	31	64
185	HEBGB80	97904 02/26/97 209050 05/15/97	Uni-ZAP XR	311	712	67	712	107	107	613	1	18	19	29

Gene No.	cDNA Clone ID	ATCC Deposit No: Z and Date	Vector	NT SEQ ID NO: X	Total NT Seq.	5' NT of Clone Seq.	3' NT of Clone Seq.	5' NT of Start Codon	5' NT of First AA of Signal Pep	AA SEQ ID NO: Y	First AA of Sig Pep	Last AA of Sig Pep	Predicted First AA of Secreted Portion	Last AA of ORF
186	HFAMH74	97904 02/26/97 209050 05/15/97	Uni-ZAP XR	196	1290	84	809	225	225	498	1	30	31	94
186	HFAMH74	97904 02/26/97 209050 05/15/97	Uni-ZAP XR	312	1289	785	1289	927	927	614	1	28	29	30

Table 1 summarizes the information corresponding to each "Gene No." described above. The nucleotide sequence identified as "NT SEQ ID NO:X" was assembled from partially homologous ("overlapping") sequences obtained from the "cDNA clone ID" identified in Table 1 and, in some cases, from additional related DNA clones. The overlapping sequences were assembled into a single contiguous sequence of high redundancy (usually three to five overlapping sequences at each nucleotide position), resulting in a final sequence identified as SEQ ID NO:X.

The cDNA Clone ID was deposited on the date and given the corresponding deposit number listed in "ATCC Deposit No:Z and Date." Some of the deposits contain multiple different clones corresponding to the same gene. "Vector" refers to the type of vector contained in the cDNA Clone ID.

"Total NT Seq." refers to the total number of nucleotides in the contig identified by "Gene No." The deposited clone may contain all or most of these sequences, reflected by the nucleotide position indicated as "5' NT of Clone Seq." and the "3' NT of Clone Seq." of SEQ ID NO:X. The nucleotide position of SEQ ID NO:X of the putative start codon (methionine) is identified as "5' NT of Start Codon." Similarly, the nucleotide position of SEQ ID NO:X of the predicted signal sequence is identified as "5' NT of First AA of Signal Pep."

The translated amino acid sequence, beginning with the methionine, is identified as "AA SEQ ID NO:Y," although other reading frames can also be easily translated using known molecular biology techniques. The polypeptides produced by these alternative open reading frames are specifically contemplated by the present invention.

The first and last amino acid position of SEQ ID NO:Y of the predicted signal peptide is identified as "First AA of Sig Pep" and "Last AA of Sig Pep." The predicted first amino acid position of SEQ ID NO:Y of the secreted portion is identified as "Predicted First AA of Secreted Portion." Finally, the amino acid position of SEQ ID NO:Y of the last amino acid in the open reading frame is identified as "Last AA of ORF."

SEQ ID NO:X and the translated SEQ ID NO:Y are sufficiently accurate and otherwise suitable for a variety of uses well known in the art and described further below. For instance, SEQ ID NO:X is useful for designing nucleic acid hybridization probes that will detect nucleic acid sequences contained in SEQ ID NO:X or the cDNA contained in the deposited clone. These probes will also hybridize to nucleic acid molecules in biological samples, thereby enabling a variety of forensic and diagnostic methods of the invention. Similarly, polypeptides identified from SEQ ID NO:Y may be used to generate antibodies which bind specifically to the secreted proteins encoded by the cDNA clones identified in Table 1.

Nevertheless, DNA sequences generated by sequencing reactions can contain sequencing errors. The errors exist as misidentified nucleotides, or as insertions or deletions of nucleotides in the generated DNA sequence. The erroneously inserted or deleted nucleotides cause frame shifts in the reading frames of the predicted amino acid sequence. In these cases, the predicted amino acid sequence diverges from the actual amino acid sequence, even though the generated DNA sequence may be greater than 99.9% identical to the actual DNA sequence (for example, one base insertion or deletion in an open reading frame of over 1000 bases).

Accordingly, for those applications requiring precision in the nucleotide sequence or the amino acid sequence, the present invention provides not only the generated nucleotide sequence identified as SEQ ID NO:X and the predicted translated amino acid sequence identified as SEQ ID NO:Y, but also a sample of plasmid DNA containing a human cDNA of the invention deposited with the ATCC, as set forth in Table 1. The nucleotide sequence of each deposited clone can readily be determined by sequencing the deposited clone in accordance with known methods. The predicted amino acid sequence can then be verified from such deposits. Moreover, the amino acid sequence of the protein encoded by a particular clone can also be directly determined by peptide sequencing or by expressing the protein in a suitable host cell containing the deposited human cDNA, collecting the protein, and determining its sequence.

The present invention also relates to the genes corresponding to SEQ ID NO:X, SEQ ID NO:Y, or the deposited clone. The corresponding gene can be isolated in accordance with known methods using the sequence information disclosed herein. Such methods include preparing probes or primers from the disclosed sequence and identifying or amplifying the corresponding gene from appropriate sources of genomic material.

Also provided in the present invention are species homologs. Species homologs may be isolated and identified by making suitable probes or primers from the sequences provided herein and screening a suitable nucleic acid source for the desired homologue.

The polypeptides of the invention can be prepared in any suitable manner. Such polypeptides include isolated naturally occurring polypeptides, recombinantly produced polypeptides, synthetically produced polypeptides, or polypeptides produced by a combination of these methods. Means for preparing such polypeptides are well understood in the art.

The polypeptides may be in the form of the secreted protein, including the mature form, or may be a part of a larger protein, such as a fusion protein (see below).

It is often advantageous to include an additional amino acid sequence which contains secretory or leader sequences, pro-sequences, sequences which aid in purification, such as multiple histidine residues, or an additional sequence for stability during recombinant production.

5 The polypeptides of the present invention are preferably provided in an isolated form, and preferably are substantially purified. A recombinantly produced version of a polypeptide, including the secreted polypeptide, can be substantially purified by the one-step method described in Smith and Johnson, *Gene* 67:31-40 (1988). Polypeptides of the invention also can be purified from natural or recombinant sources
10 using antibodies of the invention raised against the secreted protein in methods which are well known in the art.

Signal Sequences

Methods for predicting whether a protein has a signal sequence, as well as the
15 cleavage point for that sequence, are available. For instance, the method of McGeoch, *Virus Res.* 3:271-286 (1985), uses the information from a short N-terminal charged region and a subsequent uncharged region of the complete (uncleaved) protein. The method of von Heinje, *Nucleic Acids Res.* 14:4683-4690 (1986) uses the information
20 from the residues surrounding the cleavage site, typically residues -13 to +2, where +1 indicates the amino terminus of the secreted protein. The accuracy of predicting the cleavage points of known mammalian secretory proteins for each of these methods is in the range of 75-80%. (von Heinje, *supra*.) However, the two methods do not always produce the same predicted cleavage point(s) for a given protein.

In the present case, the deduced amino acid sequence of the secreted polypeptide
25 was analyzed by a computer program called SignalP (Henrik Nielsen et al., *Protein Engineering* 10:1-6 (1997)), which predicts the cellular location of a protein based on the amino acid sequence. As part of this computational prediction of localization, the methods of McGeoch and von Heinje are incorporated. The analysis of the amino acid sequences of the secreted proteins described herein by this program provided the results
30 shown in Table 1.

As one of ordinary skill would appreciate, however, cleavage sites sometimes vary from organism to organism and cannot be predicted with absolute certainty. Accordingly, the present invention provides secreted polypeptides having a sequence shown in SEQ ID NO:Y which have an N-terminus beginning within 5 residues (i.e., +
35 or - 5 residues) of the predicted cleavage point. Similarly, it is also recognized that in some cases, cleavage of the signal sequence from a secreted protein is not entirely

uniform, resulting in more than one secreted species. These polypeptides, and the polynucleotides encoding such polypeptides, are contemplated by the present invention.

Moreover, the signal sequence identified by the above analysis may not necessarily predict the naturally occurring signal sequence. For example, the naturally occurring signal sequence may be further upstream from the predicted signal sequence. However, it is likely that the predicted signal sequence will be capable of directing the secreted protein to the ER. These polypeptides, and the polynucleotides encoding such polypeptides, are contemplated by the present invention.

10 **Polynucleotide and Polypeptide Variants**

"Variant" refers to a polynucleotide or polypeptide differing from the polynucleotide or polypeptide of the present invention, but retaining essential properties thereof. Generally, variants are overall closely similar, and, in many regions, identical to the polynucleotide or polypeptide of the present invention.

15 "Identity" per se has an art-recognized meaning and can be calculated using published techniques. (See, e.g.: (COMPUTATIONAL MOLECULAR BIOLOGY, Lesk, A.M., ed., Oxford University Press, New York, (1988); BIOCOMPUTING: INFORMATICS AND GENOME PROJECTS, Smith, D.W., ed., Academic Press, New York, (1993); COMPUTER ANALYSIS OF SEQUENCE DATA, PART I, Griffin, A.M., and Griffin, H.G., eds., Humana Press, New Jersey, (1994); SEQUENCE ANALYSIS IN MOLECULAR BIOLOGY, von Heinje, G., Academic Press, (1987); and SEQUENCE ANALYSIS PRIMER, Gribskov, M. and Devereux, J., eds., M Stockton Press, New York, (1991).) While there exists a number of methods to measure identity between two polynucleotide or polypeptide sequences, the term "identity" is well known to skilled artisans. (Carillo, H., and Lipton, D., SIAM J Applied Math 48:1073 (1988).) Methods commonly employed to determine identity or similarity between two sequences include, but are not limited to, those disclosed in "Guide to Huge Computers," Martin J. Bishop, ed., Academic Press, San Diego, (1994), and Carillo, H., and Lipton, D., SIAM J Applied Math 48:1073 (1988). Methods for aligning polynucleotides or polypeptides are codified in computer programs, including the GCG program package (Devereux, J., et al., Nucleic Acids Research (1984) 12(1):387 (1984)), BLASTP, BLASTN, FASTA (Atschul, S.F. et al., J. Molec. Biol. 215:403 (1990), Bestfit program (Wisconsin Sequence Analysis Package, Version 8 for Unix, Genetics Computer Group, University Research Park, 575 Science Drive, Madison, WI 53711 (using the local homology algorithm of Smith and Waterman, Advances in Applied Mathematics 2:482-489 (1981).)

When using any of the sequence alignment programs to determine whether a particular sequence is, for instance, 95% identical to a reference sequence, the parameters are set so that the percentage of identity is calculated over the full length of the reference polynucleotide and that gaps in identity of up to 5% of the total number of nucleotides in the reference polynucleotide are allowed.

A preferred method for determining the best overall match between a query sequence (a sequence of the present invention) and a subject sequence, also referred to as a global sequence alignment, can be determined using the FASTDB computer program based on the algorithm of Brutlag et al. (Comp. App. Biosci. 6:237-245 (1990).) The term "sequence" includes nucleotide and amino acid sequences. In a sequence alignment the query and subject sequences are either both nucleotide sequences or both amino acid sequences. The result of said global sequence alignment is in percent identity. Preferred parameters used in a FASTDB search of a DNA sequence to calculate percent identity are: Matrix=Unitary, k-tuple=4, Mismatch Penalty=1, Joining Penalty=30, Randomization Group Length=0, and Cutoff Score=1, Gap Penalty=5, Gap Size Penalty 0.05, and Window Size=500 or query sequence length in nucleotide bases, whichever is shorter. Preferred parameters employed to calculate percent identity and similarity of an amino acid alignment are: Matrix=PAM 150, k-tuple=2, Mismatch Penalty=1, Joining Penalty=20, Randomization Group Length=0, Cutoff Score=1, Gap Penalty=5, Gap Size Penalty=0.05, and Window Size=500 or query sequence length in amino acid residues, whichever is shorter.

As an illustration, a polynucleotide having a nucleotide sequence of at least 95% "identity" to a sequence contained in SEQ ID NO:X or the cDNA contained in the deposited clone, means that the polynucleotide is identical to a sequence contained in SEQ ID NO:X or the cDNA except that the polynucleotide sequence may include up to five point mutations per each 100 nucleotides of the total length (not just within a given 100 nucleotide stretch). In other words, to obtain a polynucleotide having a nucleotide sequence at least 95% identical to SEQ ID NO:X or the deposited clone, up to 5% of the nucleotides in the sequence contained in SEQ ID NO:X or the cDNA can be deleted, inserted, or substituted with other nucleotides. These changes may occur anywhere throughout the polynucleotide.

Further embodiments of the present invention include polynucleotides having at least 85% identity, more preferably at least 90% identity, and most preferably at least 95%, 96%, 97%, 98% or 99% identity to a sequence contained in SEQ ID NO:X or the cDNA contained in the deposited clone. Of course, due to the degeneracy of the genetic code, one of ordinary skill in the art will immediately recognize that a large number of the polynucleotides having at least 85%, 90%, 95%, 96%, 97%, 98%, or 99% identity

will encode a polypeptide identical to an amino acid sequence contained in SEQ ID NO:Y or the expressed protein produced by the deposited clone.

Similarly, by a polypeptide having an amino acid sequence having at least, for example, 95% "identity" to a reference polypeptide, is intended that the amino acid sequence of the polypeptide is identical to the reference polypeptide except that the polypeptide sequence may include up to five amino acid alterations per each 100 amino acids of the total length of the reference polypeptide. In other words, to obtain a polypeptide having an amino acid sequence at least 95% identical to a reference amino acid sequence, up to 5% of the amino acid residues in the reference sequence may be deleted or substituted with another amino acid, or a number of amino acids up to 5% of the total amino acid residues in the reference sequence may be inserted into the reference sequence. These alterations of the reference sequence may occur at the amino or carboxy terminal positions of the reference amino acid sequence or anywhere between those terminal positions, interspersed either individually among residues in the reference sequence or in one or more contiguous groups within the reference sequence.

Further embodiments of the present invention include polypeptides having at least 80% identity, more preferably at least 85% identity, more preferably at least 90% identity, and most preferably at least 95%, 96%, 97%, 98% or 99% identity to an amino acid sequence contained in SEQ ID NO:Y or the expressed protein produced by the deposited clone. Preferably, the above polypeptides should exhibit at least one biological activity of the protein.

In a preferred embodiment, polypeptides of the present invention include polypeptides having at least 90% similarity, more preferably at least 95% similarity, and still more preferably at least 96%, 97%, 98%, or 99% similarity to an amino acid sequence contained in SEQ ID NO:Y or the expressed protein produced by the deposited clone.

The variants may contain alterations in the coding regions, non-coding regions, or both. Especially preferred are polynucleotide variants containing alterations which produce silent substitutions, additions, or deletions, but do not alter the properties or activities of the encoded polypeptide. Nucleotide variants produced by silent substitutions due to the degeneracy of the genetic code are preferred. Moreover, variants in which 5-10, 1-5, or 1-2 amino acids are substituted, deleted, or added in any combination are also preferred. Polynucleotide variants can be produced for a variety of reasons, e.g., to optimize codon expression for a particular host (change codons in the human mRNA to those preferred by a bacterial host such as *E. coli*).

Naturally occurring variants are called "allelic variants," and refer to one of several alternate forms of a gene occupying a given locus on a chromosome of an

organism. (Genes II, Lewin, B., ed., John Wiley & Sons, New York (1985).) These allelic variants can vary at either the polynucleotide and/or polypeptide level. Alternatively, non-naturally occurring variants may be produced by mutagenesis techniques or by direct synthesis.

5 Using known methods of protein engineering and recombinant DNA technology, variants may be generated to improve or alter the characteristics of the polypeptides of the present invention. For instance, one or more amino acids can be deleted from the N-terminus or C-terminus of the secreted protein without substantial loss of biological function. The authors of Ron et al., J. Biol. Chem. 268: 2984-2988
10 (1993), reported variant KGF proteins having heparin binding activity even after deleting 3, 8, or 27 amino-terminal amino acid residues. Similarly, Interferon gamma exhibited up to ten times higher activity after deleting 8-10 amino acid residues from the carboxy terminus of this protein. (Dobeli et al., J. Biotechnology 7:199-216 (1988).)

Moreover, ample evidence demonstrates that variants often retain a biological
15 activity similar to that of the naturally occurring protein. For example, Gayle and coworkers (J. Biol. Chem 268:22105-22111 (1993)) conducted extensive mutational analysis of human cytokine IL-1a. They used random mutagenesis to generate over 3,500 individual IL-1a mutants that averaged 2.5 amino acid changes per variant over the entire length of the molecule. Multiple mutations were examined at every possible
20 amino acid position. The investigators found that "[m]ost of the molecule could be altered with little effect on either [binding or biological activity]." (See, Abstract.) In fact, only 23 unique amino acid sequences, out of more than 3,500 nucleotide sequences examined, produced a protein that significantly differed in activity from wild-type.

25 Furthermore, even if deleting one or more amino acids from the N-terminus or C-terminus of a polypeptide results in modification or loss of one or more biological functions, other biological activities may still be retained. For example, the ability of a deletion variant to induce and/or to bind antibodies which recognize the secreted form will likely be retained when less than the majority of the residues of the secreted form
30 are removed from the N-terminus or C-terminus. Whether a particular polypeptide lacking N- or C-terminal residues of a protein retains such immunogenic activities can readily be determined by routine methods described herein and otherwise known in the art.

Thus, the invention further includes polypeptide variants which show
35 substantial biological activity. Such variants include deletions, insertions, inversions, repeats, and substitutions selected according to general rules known in the art so as have little effect on activity. For example, guidance concerning how to make

phenotypically silent amino acid substitutions is provided in Bowie, J. U. et al., Science 247:1306-1310 (1990), wherein the authors indicate that there are two main strategies for studying the tolerance of an amino acid sequence to change.

5 The first strategy exploits the tolerance of amino acid substitutions by natural selection during the process of evolution. By comparing amino acid sequences in different species, conserved amino acids can be identified. These conserved amino acids are likely important for protein function. In contrast, the amino acid positions where substitutions have been tolerated by natural selection indicates that these positions are not critical for protein function. Thus, positions tolerating amino acid
10 substitution could be modified while still maintaining biological activity of the protein.

The second strategy uses genetic engineering to introduce amino acid changes at specific positions of a cloned gene to identify regions critical for protein function. For example, site directed mutagenesis or alanine-scanning mutagenesis (introduction of single alanine mutations at every residue in the molecule) can be used. (Cunningham
15 and Wells, Science 244:1081-1085 (1989).) The resulting mutant molecules can then be tested for biological activity.

As the authors state, these two strategies have revealed that proteins are surprisingly tolerant of amino acid substitutions. The authors further indicate which amino acid changes are likely to be permissive at certain amino acid positions in the
20 protein. For example, most buried (within the tertiary structure of the protein) amino acid residues require nonpolar side chains, whereas few features of surface side chains are generally conserved. Moreover, tolerated conservative amino acid substitutions involve replacement of the aliphatic or hydrophobic amino acids Ala, Val, Leu and Ile; replacement of the hydroxyl residues Ser and Thr; replacement of the acidic residues
25 Asp and Glu; replacement of the amide residues Asn and Gln, replacement of the basic residues Lys, Arg, and His; replacement of the aromatic residues Phe, Tyr, and Trp, and replacement of the small-sized amino acids Ala, Ser, Thr, Met, and Gly.

Besides conservative amino acid substitution, variants of the present invention include (i) substitutions with one or more of the non-conserved amino acid residues,
30 where the substituted amino acid residues may or may not be one encoded by the genetic code, or (ii) substitution with one or more of amino acid residues having a substituent group, or (iii) fusion of the mature polypeptide with another compound, such as a compound to increase the stability and/or solubility of the polypeptide (for example, polyethylene glycol), or (iv) fusion of the polypeptide with additional amino
35 acids, such as an IgG Fc fusion region peptide, or leader or secretory sequence, or a sequence facilitating purification. Such variant polypeptides are deemed to be within the scope of those skilled in the art from the teachings herein.

For example, polypeptide variants containing amino acid substitutions of charged amino acids with other charged or neutral amino acids may produce proteins with improved characteristics, such as less aggregation. Aggregation of pharmaceutical formulations both reduces activity and increases clearance due to the aggregate's immunogenic activity. (Pinckard et al., Clin. Exp. Immunol. 2:331-340 (1967); Robbins et al., Diabetes 36: 838-845 (1987); Cleland et al., Crit. Rev. Therapeutic Drug Carrier Systems 10:307-377 (1993).)

Polynucleotide and Polypeptide Fragments

In the present invention, a "polynucleotide fragment" refers to a short polynucleotide having a nucleic acid sequence contained in the deposited clone or shown in SEQ ID NO:X. The short nucleotide fragments are preferably at least about 15 nt, and more preferably at least about 20 nt, still more preferably at least about 30 nt, and even more preferably, at least about 40 nt in length. A fragment "at least 20 nt in length," for example, is intended to include 20 or more contiguous bases from the cDNA sequence contained in the deposited clone or the nucleotide sequence shown in SEQ ID NO:X. These nucleotide fragments are useful as diagnostic probes and primers as discussed herein. Of course, larger fragments (e.g., 50, 150, 500, 600, 2000 nucleotides) are preferred.

Moreover, representative examples of polynucleotide fragments of the invention, include, for example, fragments having a sequence from about nucleotide number 1-50, 51-100, 101-150, 151-200, 201-250, 251-300, 301-350, 351-400, 401-450, 451-500, 501-550, 551-600, 651-700, and 701 to the end of SEQ ID NO:X or the cDNA contained in the deposited clone. In this context "about" includes the particularly recited ranges, larger or smaller by several (5, 4, 3, 2, or 1) nucleotides, at either terminus or at both termini. Preferably, these fragments encode a polypeptide which has biological activity.

In the present invention, a "polypeptide fragment" refers to a short amino acid sequence contained in SEQ ID NO:Y or encoded by the cDNA contained in the deposited clone. Protein fragments may be "free-standing," or comprised within a larger polypeptide of which the fragment forms a part or region, most preferably as a single continuous region. Representative examples of polypeptide fragments of the invention, include, for example, fragments from about amino acid number 1-20, 21-40, 41-60, 61-80, 81-100, 102-120, 121-140, 141-160, and 161 to the end of the coding region. Moreover, polypeptide fragments can be about 20, 30, 40, 50, 60, 70, 80, 90, 100, 110, 120, 130, 140, or 150 amino acids in length. In this context "about"

includes the particularly recited ranges, larger or smaller by several (5, 4, 3, 2, or 1) amino acids, at either extreme or at both extremes.

Preferred polypeptide fragments include the secreted protein as well as the mature form. Further preferred polypeptide fragments include the secreted protein or the mature form having a continuous series of deleted residues from the amino or the carboxy terminus, or both. For example, any number of amino acids, ranging from 1-60, can be deleted from the amino terminus of either the secreted polypeptide or the mature form. Similarly, any number of amino acids, ranging from 1-30, can be deleted from the carboxy terminus of the secreted protein or mature form. Furthermore, any combination of the above amino and carboxy terminus deletions are preferred. Similarly, polynucleotide fragments encoding these polypeptide fragments are also preferred.

Also preferred are polypeptide and polynucleotide fragments characterized by structural or functional domains, such as fragments that comprise alpha-helix and alpha-helix forming regions, beta-sheet and beta-sheet-forming regions, turn and turn-forming regions, coil and coil-forming regions, hydrophilic regions, hydrophobic regions, alpha amphipathic regions, beta amphipathic regions, flexible regions, surface-forming regions, substrate binding region, and high antigenic index regions. Polypeptide fragments of SEQ ID NO:Y falling within conserved domains are specifically contemplated by the present invention. Moreover, polynucleotide fragments encoding these domains are also contemplated.

Other preferred fragments are biologically active fragments. Biologically active fragments are those exhibiting activity similar, but not necessarily identical, to an activity of the polypeptide of the present invention. The biological activity of the fragments may include an improved desired activity, or a decreased undesirable activity.

Epitopes & Antibodies

In the present invention, "epitopes" refer to polypeptide fragments having antigenic or immunogenic activity in an animal, especially in a human. A preferred embodiment of the present invention relates to a polypeptide fragment comprising an epitope, as well as the polynucleotide encoding this fragment. A region of a protein molecule to which an antibody can bind is defined as an "antigenic epitope." In contrast, an "immunogenic epitope" is defined as a part of a protein that elicits an antibody response. (See, for instance, Geysen et al., Proc. Natl. Acad. Sci. USA 81:3998-4002 (1983).)

Fragments which function as epitopes may be produced by any conventional means. (See, e.g., Houghten, R. A., Proc. Natl. Acad. Sci. USA 82:5131-5135 (1985) further described in U.S. Patent No. 4,631,211.)

5 In the present invention, antigenic epitopes preferably contain a sequence of at least seven, more preferably at least nine, and most preferably between about 15 to about 30 amino acids. Antigenic epitopes are useful to raise antibodies, including monoclonal antibodies, that specifically bind the epitope. (See, for instance, Wilson et al., Cell 37:767-778 (1984); Sutcliffe, J. G. et al., Science 219:660-666 (1983).)

10 Similarly, immunogenic epitopes can be used to induce antibodies according to methods well known in the art. (See, for instance, Sutcliffe et al., supra; Wilson et al., supra; Chow, M. et al., Proc. Natl. Acad. Sci. USA 82:910-914; and Bittle, F. J. et al., J. Gen. Virol. 66:2347-2354 (1985).) A preferred immunogenic epitope includes the secreted protein. The immunogenic epitopes may be presented together with a carrier protein, such as an albumin, to an animal system (such as rabbit or mouse) or, if
15 it is long enough (at least about 25 amino acids), without a carrier. However, immunogenic epitopes comprising as few as 8 to 10 amino acids have been shown to be sufficient to raise antibodies capable of binding to, at the very least, linear epitopes in a denatured polypeptide (e.g., in Western blotting.)

20 As used herein, the term "antibody" (Ab) or "monoclonal antibody" (Mab) is meant to include intact molecules as well as antibody fragments (such as, for example, Fab and F(ab')₂ fragments) which are capable of specifically binding to protein. Fab and F(ab')₂ fragments lack the Fc fragment of intact antibody, clear more rapidly from the circulation, and may have less non-specific tissue binding than an intact antibody. (Wahl et al., J. Nucl. Med. 24:316-325 (1983).) Thus, these fragments are preferred,
25 as well as the products of a FAB or other immunoglobulin expression library. Moreover, antibodies of the present invention include chimeric, single chain, and humanized antibodies.

Fusion Proteins

30 Any polypeptide of the present invention can be used to generate fusion proteins. For example, the polypeptide of the present invention, when fused to a second protein, can be used as an antigenic tag. Antibodies raised against the polypeptide of the present invention can be used to indirectly detect the second protein by binding to the polypeptide. Moreover, because secreted proteins target cellular
35 locations based on trafficking signals, the polypeptides of the present invention can be used as targeting molecules once fused to other proteins.

Examples of domains that can be fused to polypeptides of the present invention include not only heterologous signal sequences, but also other heterologous functional regions. The fusion does not necessarily need to be direct, but may occur through linker sequences.

5 Moreover, fusion proteins may also be engineered to improve characteristics of the polypeptide of the present invention. For instance, a region of additional amino acids, particularly charged amino acids, may be added to the N-terminus of the polypeptide to improve stability and persistence during purification from the host cell or subsequent handling and storage. Also, peptide moieties may be added to the
10 polypeptide to facilitate purification. Such regions may be removed prior to final preparation of the polypeptide. The addition of peptide moieties to facilitate handling of polypeptides are familiar and routine techniques in the art.

 Moreover, polypeptides of the present invention, including fragments, and specifically epitopes, can be combined with parts of the constant domain of
15 immunoglobulins (IgG), resulting in chimeric polypeptides. These fusion proteins facilitate purification and show an increased half-life in vivo. One reported example describes chimeric proteins consisting of the first two domains of the human CD4-polypeptide and various domains of the constant regions of the heavy or light chains of mammalian immunoglobulins. (EP A 394,827; Traunecker et al., Nature 331:84-86
20 (1988).) Fusion proteins having disulfide-linked dimeric structures (due to the IgG) can also be more efficient in binding and neutralizing other molecules, than the monomeric secreted protein or protein fragment alone. (Fountoulakis et al., J. Biochem. 270:3958-3964 (1995).)

 Similarly, EP-A-O 464 533 (Canadian counterpart 2045869) discloses fusion
25 proteins comprising various portions of constant region of immunoglobulin molecules together with another human protein or part thereof. In many cases, the Fc part in a fusion protein is beneficial in therapy and diagnosis, and thus can result in, for example, improved pharmacokinetic properties. (EP-A 0232 262.) Alternatively, deleting the Fc part after the fusion protein has been expressed, detected, and purified,
30 would be desired. For example, the Fc portion may hinder therapy and diagnosis if the fusion protein is used as an antigen for immunizations. In drug discovery, for example, human proteins, such as hIL-5, have been fused with Fc portions for the purpose of high-throughput screening assays to identify antagonists of hIL-5. (See, D. Bennett et al., J. Molecular Recognition 8:52-58 (1995); K. Johanson et al., J. Biol.
35 Chem. 270:9459-9471 (1995).)

 Moreover, the polypeptides of the present invention can be fused to marker sequences, such as a peptide which facilitates purification of the fused polypeptide. In

preferred embodiments, the marker amino acid sequence is a hexa-histidine peptide, such as the tag provided in a pQE vector (QIAGEN, Inc., 9259 Eton Avenue, Chatsworth, CA, 91311), among others, many of which are commercially available. As described in Gentz et al., Proc. Natl. Acad. Sci. USA 86:821-824 (1989), for instance, hexa-histidine provides for convenient purification of the fusion protein. Another peptide tag useful for purification, the "HA" tag, corresponds to an epitope derived from the influenza hemagglutinin protein. (Wilson et al., Cell 37:767 (1984).)

Thus, any of these above fusions can be engineered using the polynucleotides or the polypeptides of the claimed invention.

Vectors, Host Cells, and Protein Production

The present invention also relates to vectors containing the polynucleotide of the present invention, host cells, and the production of polypeptides by recombinant techniques. The vector may be, for example, a phage, plasmid, viral, or retroviral vector. Retroviral vectors may be replication competent or replication defective. In the latter case, viral propagation generally will occur only in complementing host cells.

The polynucleotides may be joined to a vector containing a selectable marker for propagation in a host. Generally, a plasmid vector is introduced in a precipitate, such as a calcium phosphate precipitate, or in a complex with a charged lipid. If the vector is a virus, it may be packaged in vitro using an appropriate packaging cell line and then transduced into host cells.

The polynucleotide insert should be operatively linked to an appropriate promoter, such as the phage lambda PL promoter, the E. coli lac, trp, phoA and tac promoters, the SV40 early and late promoters and promoters of retroviral LTRs, to name a few. Other suitable promoters will be known to the skilled artisan. The expression constructs will further contain sites for transcription initiation, termination, and, in the transcribed region, a ribosome binding site for translation. The coding portion of the transcripts expressed by the constructs will preferably include a translation initiating codon at the beginning and a termination codon (UAA, UGA or UAG) appropriately positioned at the end of the polypeptide to be translated.

As indicated, the expression vectors will preferably include at least one selectable marker. Such markers include dihydrofolate reductase, G418 or neomycin resistance for eukaryotic cell culture and tetracycline, kanamycin or ampicillin resistance genes for culturing in E. coli and other bacteria. Representative examples of appropriate hosts include, but are not limited to, bacterial cells, such as E. coli, Streptomyces and Salmonella typhimurium cells; fungal cells, such as yeast cells; insect cells such as Drosophila S2 and Spodoptera Sf9 cells; animal cells such as CHO, COS,

293, and Bowes melanoma cells; and plant cells. Appropriate culture mediums and conditions for the above-described host cells are known in the art.

Among vectors preferred for use in bacteria include pQE70, pQE60 and pQE-9, available from QIAGEN, Inc.; pBluescript vectors, Phagescript vectors, pNH8A, pNH16a, pNH18A, pNH46A, available from Stratagene Cloning Systems, Inc.; and ptrc99a, pKK223-3, pKK233-3, pDR540, pRIT5 available from Pharmacia Biotech, Inc. Among preferred eukaryotic vectors are pWLNEO, pSV2CAT, pOG44, pXT1 and pSG available from Stratagene; and pSVK3, pBPV, pMSG and pSVL available from Pharmacia. Other suitable vectors will be readily apparent to the skilled artisan.

Introduction of the construct into the host cell can be effected by calcium phosphate transfection, DEAE-dextran mediated transfection, cationic lipid-mediated transfection, electroporation, transduction, infection, or other methods. Such methods are described in many standard laboratory manuals, such as Davis et al., Basic Methods In Molecular Biology (1986). It is specifically contemplated that the polypeptides of the present invention may in fact be expressed by a host cell lacking a recombinant vector.

A polypeptide of this invention can be recovered and purified from recombinant cell cultures by well-known methods including ammonium sulfate or ethanol precipitation, acid extraction, anion or cation exchange chromatography, phosphocellulose chromatography, hydrophobic interaction chromatography, affinity chromatography, hydroxylapatite chromatography and lectin chromatography. Most preferably, high performance liquid chromatography ("HPLC") is employed for purification.

Polypeptides of the present invention, and preferably the secreted form, can also be recovered from: products purified from natural sources, including bodily fluids, tissues and cells, whether directly isolated or cultured; products of chemical synthetic procedures; and products produced by recombinant techniques from a prokaryotic or eukaryotic host, including, for example, bacterial, yeast, higher plant, insect, and mammalian cells. Depending upon the host employed in a recombinant production procedure, the polypeptides of the present invention may be glycosylated or may be non-glycosylated. In addition, polypeptides of the invention may also include an initial modified methionine residue, in some cases as a result of host-mediated processes. Thus, it is well known in the art that the N-terminal methionine encoded by the translation initiation codon generally is removed with high efficiency from any protein after translation in all eukaryotic cells. While the N-terminal methionine on most proteins also is efficiently removed in most prokaryotes, for some proteins, this prokaryotic removal process is inefficient, depending on the nature of the amino acid to which the N-terminal methionine is covalently linked.

Uses of the Polynucleotides

Each of the polynucleotides identified herein can be used in numerous ways as reagents. The following description should be considered exemplary and utilizes
5 known techniques.

The polynucleotides of the present invention are useful for chromosome identification. There exists an ongoing need to identify new chromosome markers, since few chromosome marking reagents, based on actual sequence data (repeat polymorphisms), are presently available. Each polynucleotide of the present invention
10 can be used as a chromosome marker.

Briefly, sequences can be mapped to chromosomes by preparing PCR primers (preferably 15-25 bp) from the sequences shown in SEQ ID NO:X. Primers can be selected using computer analysis so that primers do not span more than one predicted exon in the genomic DNA. These primers are then used for PCR screening of somatic
15 cell hybrids containing individual human chromosomes. Only those hybrids containing the human gene corresponding to the SEQ ID NO:X will yield an amplified fragment.

Similarly, somatic hybrids provide a rapid method of PCR mapping the polynucleotides to particular chromosomes. Three or more clones can be assigned per day using a single thermal cycler. Moreover, sublocalization of the polynucleotides can
20 be achieved with panels of specific chromosome fragments. Other gene mapping strategies that can be used include in situ hybridization, prescreening with labeled flow-sorted chromosomes, and preselection by hybridization to construct chromosome specific-cDNA libraries.

Precise chromosomal location of the polynucleotides can also be achieved using
25 fluorescence in situ hybridization (FISH) of a metaphase chromosomal spread. This technique uses polynucleotides as short as 500 or 600 bases; however, polynucleotides 2,000-4,000 bp are preferred. For a review of this technique, see Verma et al., "Human Chromosomes: a Manual of Basic Techniques," Pergamon Press, New York (1988).

For chromosome mapping, the polynucleotides can be used individually (to
30 mark a single chromosome or a single site on that chromosome) or in panels (for marking multiple sites and/or multiple chromosomes). Preferred polynucleotides correspond to the noncoding regions of the cDNAs because the coding sequences are more likely conserved within gene families, thus increasing the chance of cross
35 hybridization during chromosomal mapping.

Once a polynucleotide has been mapped to a precise chromosomal location, the physical position of the polynucleotide can be used in linkage analysis. Linkage

analysis establishes coinheritance between a chromosomal location and presentation of a particular disease. (Disease mapping data are found, for example, in V. McKusick, Mendelian Inheritance in Man (available on line through Johns Hopkins University Welch Medical Library) .) Assuming 1 megabase mapping resolution and one gene per 20 kb, a cDNA precisely localized to a chromosomal region associated with the disease could be one of 50-500 potential causative genes.

Thus, once coinheritance is established, differences in the polynucleotide and the corresponding gene between affected and unaffected individuals can be examined. First, visible structural alterations in the chromosomes, such as deletions or translocations, are examined in chromosome spreads or by PCR. If no structural alterations exist, the presence of point mutations are ascertained. Mutations observed in some or all affected individuals, but not in normal individuals, indicates that the mutation may cause the disease. However, complete sequencing of the polypeptide and the corresponding gene from several normal individuals is required to distinguish the mutation from a polymorphism. If a new polymorphism is identified, this polymorphic polypeptide can be used for further linkage analysis.

Furthermore, increased or decreased expression of the gene in affected individuals as compared to unaffected individuals can be assessed using polynucleotides of the present invention. Any of these alterations (altered expression, chromosomal rearrangement, or mutation) can be used as a diagnostic or prognostic marker.

In addition to the foregoing, a polynucleotide can be used to control gene expression through triple helix formation or antisense DNA or RNA. Both methods rely on binding of the polynucleotide to DNA or RNA. For these techniques, preferred polynucleotides are usually 20 to 40 bases in length and complementary to either the region of the gene involved in transcription (triple helix - see Lee et al., Nucl. Acids Res. 6:3073 (1979); Cooney et al., Science 241:456 (1988); and Dervan et al., Science 251:1360 (1991)) or to the mRNA itself (antisense - Okano, J. Neurochem. 56:560 (1991); Oligodeoxy-nucleotides as Antisense Inhibitors of Gene Expression, CRC Press, Boca Raton, FL (1988).) Triple helix formation optimally results in a shut-off of RNA transcription from DNA, while antisense RNA hybridization blocks translation of an mRNA molecule into polypeptide. Both techniques are effective in model systems, and the information disclosed herein can be used to design antisense or triple helix polynucleotides in an effort to treat disease.

Polynucleotides of the present invention are also useful in gene therapy. One goal of gene therapy is to insert a normal gene into an organism having a defective gene, in an effort to correct the genetic defect. The polynucleotides disclosed in the

present invention offer a means of targeting such genetic defects in a highly accurate manner. Another goal is to insert a new gene that was not present in the host genome, thereby producing a new trait in the host cell.

The polynucleotides are also useful for identifying individuals from minute biological samples. The United States military, for example, is considering the use of restriction fragment length polymorphism (RFLP) for identification of its personnel. In this technique, an individual's genomic DNA is digested with one or more restriction enzymes, and probed on a Southern blot to yield unique bands for identifying personnel. This method does not suffer from the current limitations of "Dog Tags" which can be lost, switched, or stolen, making positive identification difficult. The polynucleotides of the present invention can be used as additional DNA markers for RFLP.

The polynucleotides of the present invention can also be used as an alternative to RFLP, by determining the actual base-by-base DNA sequence of selected portions of an individual's genome. These sequences can be used to prepare PCR primers for amplifying and isolating such selected DNA, which can then be sequenced. Using this technique, individuals can be identified because each individual will have a unique set of DNA sequences. Once an unique ID database is established for an individual, positive identification of that individual, living or dead, can be made from extremely small tissue samples.

Forensic biology also benefits from using DNA-based identification techniques as disclosed herein. DNA sequences taken from very small biological samples such as tissues, e.g., hair or skin, or body fluids, e.g., blood, saliva, semen, etc., can be amplified using PCR. In one prior art technique, gene sequences amplified from polymorphic loci, such as DQa class II HLA gene, are used in forensic biology to identify individuals. (Erlich, H., PCR Technology, Freeman and Co. (1992).) Once these specific polymorphic loci are amplified, they are digested with one or more restriction enzymes, yielding an identifying set of bands on a Southern blot probed with DNA corresponding to the DQa class II HLA gene. Similarly, polynucleotides of the present invention can be used as polymorphic markers for forensic purposes.

There is also a need for reagents capable of identifying the source of a particular tissue. Such need arises, for example, in forensics when presented with tissue of unknown origin. Appropriate reagents can comprise, for example, DNA probes or primers specific to particular tissue prepared from the sequences of the present invention. Panels of such reagents can identify tissue by species and/or by organ type. In a similar fashion, these reagents can be used to screen tissue cultures for contamination.

In the very least, the polynucleotides of the present invention can be used as molecular weight markers on Southern gels, as diagnostic probes for the presence of a specific mRNA in a particular cell type, as a probe to "subtract-out" known sequences in the process of discovering novel polynucleotides, for selecting and making oligomers for attachment to a "gene chip" or other support, to raise anti-DNA antibodies using DNA immunization techniques, and as an antigen to elicit an immune response.

Uses of the Polypeptides

Each of the polypeptides identified herein can be used in numerous ways. The following description should be considered exemplary and utilizes known techniques.

A polypeptide of the present invention can be used to assay protein levels in a biological sample using antibody-based techniques. For example, protein expression in tissues can be studied with classical immunohistological methods. (Jalkanen, M., et al., J. Cell. Biol. 101:976-985 (1985); Jalkanen, M., et al., J. Cell . Biol. 105:3087-3096 (1987).) Other antibody-based methods useful for detecting protein gene expression include immunoassays, such as the enzyme linked immunosorbent assay (ELISA) and the radioimmunoassay (RIA). Suitable antibody assay labels are known in the art and include enzyme labels, such as, glucose oxidase, and radioisotopes, such as iodine (^{125}I , ^{121}I), carbon (^{14}C), sulfur (^{35}S), tritium (^3H), indium (^{112}In), and technetium ($^{99\text{m}}\text{Tc}$), and fluorescent labels, such as fluorescein and rhodamine, and biotin.

In addition to assaying secreted protein levels in a biological sample, proteins can also be detected in vivo by imaging. Antibody labels or markers for in vivo imaging of protein include those detectable by X-radiography, NMR or ESR. For X-radiography, suitable labels include radioisotopes such as barium or cesium, which emit detectable radiation but are not overtly harmful to the subject. Suitable markers for NMR and ESR include those with a detectable characteristic spin, such as deuterium, which may be incorporated into the antibody by labeling of nutrients for the relevant hybridoma.

A protein-specific antibody or antibody fragment which has been labeled with an appropriate detectable imaging moiety, such as a radioisotope (for example, ^{131}I , ^{112}In , $^{99\text{m}}\text{Tc}$), a radio-opaque substance, or a material detectable by nuclear magnetic resonance, is introduced (for example, parenterally, subcutaneously, or intraperitoneally) into the mammal. It will be understood in the art that the size of the subject and the imaging system used will determine the quantity of imaging moiety needed to produce diagnostic images. In the case of a radioisotope moiety, for a human subject, the quantity of radioactivity injected will normally range from about 5 to 20

millicuries of ^{99m}Tc . The labeled antibody or antibody fragment will then preferentially accumulate at the location of cells which contain the specific protein. In vivo tumor imaging is described in S.W. Burchiel et al., "Immunopharmacokinetics of Radiolabeled Antibodies and Their Fragments." (Chapter 13 in Tumor Imaging: The Radiochemical Detection of Cancer, S.W. Burchiel and B. A. Rhodes, eds., Masson Publishing Inc. (1982).)

Thus, the invention provides a diagnostic method of a disorder, which involves (a) assaying the expression of a polypeptide of the present invention in cells or body fluid of an individual; (b) comparing the level of gene expression with a standard gene expression level, whereby an increase or decrease in the assayed polypeptide gene expression level compared to the standard expression level is indicative of a disorder.

Moreover, polypeptides of the present invention can be used to treat disease. For example, patients can be administered a polypeptide of the present invention in an effort to replace absent or decreased levels of the polypeptide (e.g., insulin), to supplement absent or decreased levels of a different polypeptide (e.g., hemoglobin S for hemoglobin B), to inhibit the activity of a polypeptide (e.g., an oncogene), to activate the activity of a polypeptide (e.g., by binding to a receptor), to reduce the activity of a membrane bound receptor by competing with it for free ligand (e.g., soluble TNF receptors used in reducing inflammation), or to bring about a desired response (e.g., blood vessel growth).

Similarly, antibodies directed to a polypeptide of the present invention can also be used to treat disease. For example, administration of an antibody directed to a polypeptide of the present invention can bind and reduce overproduction of the polypeptide. Similarly, administration of an antibody can activate the polypeptide, such as by binding to a polypeptide bound to a membrane (receptor).

At the very least, the polypeptides of the present invention could be used as molecular weight markers on SDS-PAGE gels or on molecular sieve gel filtration columns using methods well known to those of skill in the art. Polypeptides can also be used to raise antibodies, which in turn are used to measure protein expression from a recombinant cell, as a way of assessing transformation of the host cell. Moreover, the polypeptides of the present invention can be used to test the following biological activities.

Biological Activities

The polynucleotides and polypeptides of the present invention can be used in assays to test for one or more biological activities. If these polynucleotides and polypeptides do exhibit activity in a particular assay, it is likely that these molecules

may be involved in the diseases associated with the biological activity. Thus, the polynucleotides and polypeptides could be used to treat the associated disease.

Immune Activity

5 A polypeptide or polynucleotide of the present invention may be useful in treating deficiencies or disorders of the immune system, by activating or inhibiting the proliferation, differentiation, or mobilization (chemotaxis) of immune cells. Immune cells develop through a process called hematopoiesis, producing myeloid (platelets, red blood cells, neutrophils, and macrophages) and lymphoid (B and T lymphocytes) cells
10 from pluripotent stem cells. The etiology of these immune deficiencies or disorders may be genetic, somatic, such as cancer or some autoimmune disorders, acquired (e.g., by chemotherapy or toxins), or infectious. Moreover, a polynucleotide or polypeptide of the present invention can be used as a marker or detector of a particular immune system disease or disorder.

15 A polynucleotide or polypeptide of the present invention may be useful in treating or detecting deficiencies or disorders of hematopoietic cells. A polypeptide or polynucleotide of the present invention could be used to increase differentiation and proliferation of hematopoietic cells, including the pluripotent stem cells, in an effort to treat those disorders associated with a decrease in certain (or many) types hematopoietic
20 cells. Examples of immunologic deficiency syndromes include, but are not limited to: blood protein disorders (e.g. agammaglobulinemia, dysgammaglobulinemia), ataxia telangiectasia, common variable immunodeficiency, Digeorge Syndrome, HIV infection, HTLV-BLV infection, leukocyte adhesion deficiency syndrome, lymphopenia, phagocyte bactericidal dysfunction, severe combined immunodeficiency
25 (SCIDs), Wiskott-Aldrich Disorder, anemia, thrombocytopenia, or hemoglobinuria.

Moreover, a polypeptide or polynucleotide of the present invention could also be used to modulate hemostatic (the stopping of bleeding) or thrombolytic activity (clot formation). For example, by increasing hemostatic or thrombolytic activity, a polynucleotide or polypeptide of the present invention could be used to treat blood
30 coagulation disorders (e.g., afibrinogenemia, factor deficiencies), blood platelet disorders (e.g. thrombocytopenia), or wounds resulting from trauma, surgery, or other causes. Alternatively, a polynucleotide or polypeptide of the present invention that can decrease hemostatic or thrombolytic activity could be used to inhibit or dissolve clotting. These molecules could be important in the treatment of heart attacks
35 (infarction), strokes, or scarring.

A polynucleotide or polypeptide of the present invention may also be useful in treating or detecting autoimmune disorders. Many autoimmune disorders result from

inappropriate recognition of self as foreign material by immune cells. This inappropriate recognition results in an immune response leading to the destruction of the host tissue. Therefore, the administration of a polypeptide or polynucleotide of the present invention that inhibits an immune response, particularly the proliferation, differentiation, or chemotaxis of T-cells, may be an effective therapy in preventing autoimmune disorders.

Examples of autoimmune disorders that can be treated or detected by the present invention include, but are not limited to: Addison's Disease, hemolytic anemia, antiphospholipid syndrome, rheumatoid arthritis, dermatitis, allergic encephalomyelitis, glomerulonephritis, Goodpasture's Syndrome, Graves' Disease, Multiple Sclerosis, Myasthenia Gravis, Neuritis, Ophthalmia, Bullous Pemphigoid, Pemphigus, Polyendocrinopathies, Purpura, Reiter's Disease, Stiff-Man Syndrome, Autoimmune Thyroiditis, Systemic Lupus Erythematosus, Autoimmune Pulmonary Inflammation, Guillain-Barre Syndrome, insulin dependent diabetes mellitus, and autoimmune inflammatory eye disease.

Similarly, allergic reactions and conditions, such as asthma (particularly allergic asthma) or other respiratory problems, may also be treated by a polypeptide or polynucleotide of the present invention. Moreover, these molecules can be used to treat anaphylaxis, hypersensitivity to an antigenic molecule, or blood group incompatibility.

A polynucleotide or polypeptide of the present invention may also be used to treat and/or prevent organ rejection or graft-versus-host disease (GVHD). Organ rejection occurs by host immune cell destruction of the transplanted tissue through an immune response. Similarly, an immune response is also involved in GVHD, but, in this case, the foreign transplanted immune cells destroy the host tissues. The administration of a polypeptide or polynucleotide of the present invention that inhibits an immune response, particularly the proliferation, differentiation, or chemotaxis of T-cells, may be an effective therapy in preventing organ rejection or GVHD.

Similarly, a polypeptide or polynucleotide of the present invention may also be used to modulate inflammation. For example, the polypeptide or polynucleotide may inhibit the proliferation and differentiation of cells involved in an inflammatory response. These molecules can be used to treat inflammatory conditions, both chronic and acute conditions, including inflammation associated with infection (e.g., septic shock, sepsis, or systemic inflammatory response syndrome (SIRS)), ischemia-reperfusion injury, endotoxin lethality, arthritis, complement-mediated hyperacute rejection, nephritis, cytokine or chemokine induced lung injury, inflammatory bowel disease, Crohn's disease, or resulting from over production of cytokines (e.g., TNF or IL-1.)

Hyperproliferative Disorders

A polypeptide or polynucleotide can be used to treat or detect hyperproliferative disorders, including neoplasms. A polypeptide or polynucleotide of the present invention may inhibit the proliferation of the disorder through direct or indirect interactions. Alternatively, a polypeptide or polynucleotide of the present invention may proliferate other cells which can inhibit the hyperproliferative disorder.

For example, by increasing an immune response, particularly increasing antigenic qualities of the hyperproliferative disorder or by proliferating, differentiating, or mobilizing T-cells, hyperproliferative disorders can be treated. This immune response may be increased by either enhancing an existing immune response, or by initiating a new immune response. Alternatively, decreasing an immune response may also be a method of treating hyperproliferative disorders, such as a chemotherapeutic agent.

Examples of hyperproliferative disorders that can be treated or detected by a polynucleotide or polypeptide of the present invention include, but are not limited to neoplasms located in the: abdomen, bone, breast, digestive system, liver, pancreas, peritoneum, endocrine glands (adrenal, parathyroid, pituitary, testicles, ovary, thymus, thyroid), eye, head and neck, nervous (central and peripheral), lymphatic system, pelvic, skin, soft tissue, spleen, thoracic, and urogenital.

Similarly, other hyperproliferative disorders can also be treated or detected by a polynucleotide or polypeptide of the present invention. Examples of such hyperproliferative disorders include, but are not limited to: hypergammaglobulinemia, lymphoproliferative disorders, paraproteinemias, purpura, sarcoidosis, Sezary Syndrome, Waldenström's Macroglobulinemia, Gaucher's Disease, histiocytosis, and any other hyperproliferative disease, besides neoplasia, located in an organ system listed above.

Infectious Disease

A polypeptide or polynucleotide of the present invention can be used to treat or detect infectious agents. For example, by increasing the immune response, particularly increasing the proliferation and differentiation of B and/or T cells, infectious diseases may be treated. The immune response may be increased by either enhancing an existing immune response, or by initiating a new immune response. Alternatively, the polypeptide or polynucleotide of the present invention may also directly inhibit the infectious agent, without necessarily eliciting an immune response.

Viruses are one example of an infectious agent that can cause disease or symptoms that can be treated or detected by a polynucleotide or polypeptide of the present invention. Examples of viruses, include, but are not limited to the following DNA and RNA viral families: Arbovirus, Adenoviridae, Arenaviridae, Arterivirus, Birnaviridae, Bunyaviridae, Caliciviridae, Circoviridae, Coronaviridae, Flaviviridae, Hepadnaviridae (Hepatitis), Herpesviridae (such as, Cytomegalovirus, Herpes Simplex, Herpes Zoster), Mononegavirus (e.g., Paramyxoviridae, Morbillivirus, Rhabdoviridae), Orthomyxoviridae (e.g., Influenza), Papovaviridae, Parvoviridae, Picornaviridae, Poxviridae (such as Smallpox or Vaccinia), Reoviridae (e.g., Rotavirus), Retroviridae (HTLV-I, HTLV-II, Lentivirus), and Togaviridae (e.g., Rubivirus). Viruses falling within these families can cause a variety of diseases or symptoms, including, but not limited to: arthritis, bronchiolitis, encephalitis, eye infections (e.g., conjunctivitis, keratitis), chronic fatigue syndrome, hepatitis (A, B, C, E, Chronic Active, Delta), meningitis, opportunistic infections (e.g., AIDS), pneumonia, Burkitt's Lymphoma, chickenpox, hemorrhagic fever, Measles, Mumps, Parainfluenza, Rabies, the common cold, Polio, leukemia, Rubella, sexually transmitted diseases, skin diseases (e.g., Kaposi's, warts), and viremia. A polypeptide or polynucleotide of the present invention can be used to treat or detect any of these symptoms or diseases.

Similarly, bacterial or fungal agents that can cause disease or symptoms and that can be treated or detected by a polynucleotide or polypeptide of the present invention include, but not limited to, the following Gram-Negative and Gram-positive bacterial families and fungi: Actinomycetales (e.g., Corynebacterium, Mycobacterium, Norcardia), Aspergillosis, Bacillaceae (e.g., Anthrax, Clostridium), Bacteroidaceae, Blastomycosis, Bordetella, Borrelia, Brucellosis, Candidiasis, Campylobacter, Coccidioidomycosis, Cryptococcosis, Dermatocycoses, Enterobacteriaceae (Klebsiella, Salmonella, Serratia, Yersinia), Erysipelothrix, Helicobacter, Legionellosis, Leptospirosis, Listeria, Mycoplasmatales, Neisseriaceae (e.g., Acinetobacter, Gonorrhea, Meningococcal), Pasteurellaceae Infections (e.g., Actinobacillus, Heamophilus, Pasteurella), Pseudomonas, Rickettsiaceae, Chlamydiaceae, Syphilis, and Staphylococcal. These bacterial or fungal families can cause the following diseases or symptoms, including, but not limited to: bacteremia, endocarditis, eye infections (conjunctivitis, tuberculosis, uveitis), gingivitis, opportunistic infections (e.g., AIDS related infections), paronychia, prosthesis-related infections, Reiter's Disease, respiratory tract infections, such as Whooping Cough or Empyema, sepsis, Lyme Disease, Cat-Scratch Disease, Dysentery, Paratyphoid Fever, food poisoning, Typhoid, pneumonia, Gonorrhea, meningitis, Chlamydia, Syphilis, Diphtheria,

Leprosy, Paratuberculosis, Tuberculosis, Lupus, Botulism, gangrene, tetanus, impetigo, Rheumatic Fever, Scarlet Fever, sexually transmitted diseases, skin diseases (e.g., cellulitis, dermatocycoses), toxemia, urinary tract infections, wound infections. A polypeptide or polynucleotide of the present invention can be used to treat or detect any of these symptoms or diseases.

Moreover, parasitic agents causing disease or symptoms that can be treated or detected by a polynucleotide or polypeptide of the present invention include, but not limited to, the following families: Amebiasis, Babesiosis, Coccidiosis, Cryptosporidiosis, Dientamoebiasis, Dourine, Ectoparasitic, Giardiasis, Helminthiasis, Leishmaniasis, Theileriasis, Toxoplasmosis, Trypanosomiasis, and Trichomonas. These parasites can cause a variety of diseases or symptoms, including, but not limited to: Scabies, Trombiculiasis, eye infections, intestinal disease (e.g., dysentery, giardiasis), liver disease, lung disease, opportunistic infections (e.g., AIDS related), Malaria, pregnancy complications, and toxoplasmosis. A polypeptide or polynucleotide of the present invention can be used to treat or detect any of these symptoms or diseases.

Preferably, treatment using a polypeptide or polynucleotide of the present invention could either be by administering an effective amount of a polypeptide to the patient, or by removing cells from the patient, supplying the cells with a polynucleotide of the present invention, and returning the engineered cells to the patient (ex vivo therapy). Moreover, the polypeptide or polynucleotide of the present invention can be used as an antigen in a vaccine to raise an immune response against infectious disease.

Regeneration

A polynucleotide or polypeptide of the present invention can be used to differentiate, proliferate, and attract cells, leading to the regeneration of tissues. (See, Science 276:59-87 (1997).) The regeneration of tissues could be used to repair, replace, or protect tissue damaged by congenital defects, trauma (wounds, burns, incisions, or ulcers), age, disease (e.g. osteoporosis, osteoarthritis, periodontal disease, liver failure), surgery, including cosmetic plastic surgery, fibrosis, reperfusion injury, or systemic cytokine damage.

Tissues that could be regenerated using the present invention include organs (e.g., pancreas, liver, intestine, kidney, skin, endothelium), muscle (smooth, skeletal or cardiac), vascular (including vascular endothelium), nervous, hematopoietic, and skeletal (bone, cartilage, tendon, and ligament) tissue. Preferably, regeneration occurs without or decreased scarring. Regeneration also may include angiogenesis.

Moreover, a polynucleotide or polypeptide of the present invention may increase regeneration of tissues difficult to heal. For example, increased tendon/ligament regeneration would quicken recovery time after damage. A polynucleotide or polypeptide of the present invention could also be used prophylactically in an effort to avoid damage. Specific diseases that could be treated include of tendinitis, carpal tunnel syndrome, and other tendon or ligament defects. A further example of tissue regeneration of non-healing wounds includes pressure ulcers, ulcers associated with vascular insufficiency, surgical, and traumatic wounds.

Similarly, nerve and brain tissue could also be regenerated by using a polynucleotide or polypeptide of the present invention to proliferate and differentiate nerve cells. Diseases that could be treated using this method include central and peripheral nervous system diseases, neuropathies, or mechanical and traumatic disorders (e.g., spinal cord disorders, head trauma, cerebrovascular disease, and stroke). Specifically, diseases associated with peripheral nerve injuries, peripheral neuropathy (e.g., resulting from chemotherapy or other medical therapies), localized neuropathies, and central nervous system diseases (e.g., Alzheimer's disease, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager syndrome), could all be treated using the polynucleotide or polypeptide of the present invention.

Chemotaxis

A polynucleotide or polypeptide of the present invention may have chemotaxis activity. A chemotactic molecule attracts or mobilizes cells (e.g., monocytes, fibroblasts, neutrophils, T-cells, mast cells, eosinophils, epithelial and/or endothelial cells) to a particular site in the body, such as inflammation, infection, or site of hyperproliferation. The mobilized cells can then fight off and/or heal the particular trauma or abnormality.

A polynucleotide or polypeptide of the present invention may increase chemotactic activity of particular cells. These chemotactic molecules can then be used to treat inflammation, infection, hyperproliferative disorders, or any immune system disorder by increasing the number of cells targeted to a particular location in the body. For example, chemotactic molecules can be used to treat wounds and other trauma to tissues by attracting immune cells to the injured location. Chemotactic molecules of the present invention can also attract fibroblasts, which can be used to treat wounds.

It is also contemplated that a polynucleotide or polypeptide of the present invention may inhibit chemotactic activity. These molecules could also be used to treat

disorders. Thus, a polynucleotide or polypeptide of the present invention could be used as an inhibitor of chemotaxis.

Binding Activity

5 A polypeptide of the present invention may be used to screen for molecules that bind to the polypeptide or for molecules to which the polypeptide binds. The binding of the polypeptide and the molecule may activate (agonist), increase, inhibit (antagonist), or decrease activity of the polypeptide or the molecule bound. Examples of such molecules include antibodies, oligonucleotides, proteins (e.g., receptors), or
10 small molecules.

Preferably, the molecule is closely related to the natural ligand of the polypeptide, e.g., a fragment of the ligand, or a natural substrate, a ligand, a structural or functional mimetic. (See, Coligan et al., Current Protocols in Immunology 1(2):Chapter 5 (1991).) Similarly, the molecule can be closely related to the natural
15 receptor to which the polypeptide binds, or at least, a fragment of the receptor capable of being bound by the polypeptide (e.g., active site). In either case, the molecule can be rationally designed using known techniques.

Preferably, the screening for these molecules involves producing appropriate cells which express the polypeptide, either as a secreted protein or on the cell
20 membrane. Preferred cells include cells from mammals, yeast, *Drosophila*, or *E. coli*. Cells expressing the polypeptide (or cell membrane containing the expressed polypeptide) are then preferably contacted with a test compound potentially containing the molecule to observe binding, stimulation, or inhibition of activity of either the polypeptide or the molecule.

25 The assay may simply test binding of a candidate compound to the polypeptide, wherein binding is detected by a label, or in an assay involving competition with a labeled competitor. Further, the assay may test whether the candidate compound results in a signal generated by binding to the polypeptide.

Alternatively, the assay can be carried out using cell-free preparations,
30 polypeptide/molecule affixed to a solid support, chemical libraries, or natural product mixtures. The assay may also simply comprise the steps of mixing a candidate compound with a solution containing a polypeptide, measuring polypeptide/molecule activity or binding, and comparing the polypeptide/molecule activity or binding to a standard.

35 Preferably, an ELISA assay can measure polypeptide level or activity in a sample (e.g., biological sample) using a monoclonal or polyclonal antibody. The

antibody can measure polypeptide level or activity by either binding, directly or indirectly, to the polypeptide or by competing with the polypeptide for a substrate.

All of these above assays can be used as diagnostic or prognostic markers. The molecules discovered using these assays can be used to treat disease or to bring about a particular result in a patient (e.g., blood vessel growth) by activating or inhibiting the polypeptide/molecule. Moreover, the assays can discover agents which may inhibit or enhance the production of the polypeptide from suitably manipulated cells or tissues.

Therefore, the invention includes a method of identifying compounds which bind to a polypeptide of the invention comprising the steps of: (a) incubating a candidate binding compound with a polypeptide of the invention; and (b) determining if binding has occurred. Moreover, the invention includes a method of identifying agonists/antagonists comprising the steps of: (a) incubating a candidate compound with a polypeptide of the invention, (b) assaying a biological activity, and (b) determining if a biological activity of the polypeptide has been altered.

Other Activities

A polypeptide or polynucleotide of the present invention may also increase or decrease the differentiation or proliferation of embryonic stem cells, besides, as discussed above, hematopoietic lineage.

A polypeptide or polynucleotide of the present invention may also be used to modulate mammalian characteristics, such as body height, weight, hair color, eye color, skin, percentage of adipose tissue, pigmentation, size, and shape (e.g., cosmetic surgery). Similarly, a polypeptide or polynucleotide of the present invention may be used to modulate mammalian metabolism affecting catabolism, anabolism, processing, utilization, and storage of energy.

A polypeptide or polynucleotide of the present invention may be used to change a mammal's mental state or physical state by influencing biorhythms, circadian rhythms, depression (including depressive disorders), tendency for violence, tolerance for pain, reproductive capabilities (preferably by Activin or Inhibin-like activity), hormonal or endocrine levels, appetite, libido, memory, stress, or other cognitive qualities.

A polypeptide or polynucleotide of the present invention may also be used as a food additive or preservative, such as to increase or decrease storage capabilities, fat content, lipid, protein, carbohydrate, vitamins, minerals, cofactors or other nutritional components.

Other Preferred Embodiments

Other preferred embodiments of the claimed invention include an isolated nucleic acid molecule comprising a nucleotide sequence which is at least 95% identical to a sequence of at least about 50 contiguous nucleotides in the nucleotide sequence of SEQ ID NO:X wherein X is any integer as defined in Table 1.

Also preferred is a nucleic acid molecule wherein said sequence of contiguous nucleotides is included in the nucleotide sequence of SEQ ID NO:X in the range of positions beginning with the nucleotide at about the position of the 5' Nucleotide of the Clone Sequence and ending with the nucleotide at about the position of the 3' Nucleotide of the Clone Sequence as defined for SEQ ID NO:X in Table 1.

Also preferred is a nucleic acid molecule wherein said sequence of contiguous nucleotides is included in the nucleotide sequence of SEQ ID NO:X in the range of positions beginning with the nucleotide at about the position of the 5' Nucleotide of the Start Codon and ending with the nucleotide at about the position of the 3' Nucleotide of the Clone Sequence as defined for SEQ ID NO:X in Table 1.

Similarly preferred is a nucleic acid molecule wherein said sequence of contiguous nucleotides is included in the nucleotide sequence of SEQ ID NO:X in the range of positions beginning with the nucleotide at about the position of the 5' Nucleotide of the First Amino Acid of the Signal Peptide and ending with the nucleotide at about the position of the 3' Nucleotide of the Clone Sequence as defined for SEQ ID NO:X in Table 1.

Also preferred is an isolated nucleic acid molecule comprising a nucleotide sequence which is at least 95% identical to a sequence of at least about 150 contiguous nucleotides in the nucleotide sequence of SEQ ID NO:X.

Further preferred is an isolated nucleic acid molecule comprising a nucleotide sequence which is at least 95% identical to a sequence of at least about 500 contiguous nucleotides in the nucleotide sequence of SEQ ID NO:X.

A further preferred embodiment is a nucleic acid molecule comprising a nucleotide sequence which is at least 95% identical to the nucleotide sequence of SEQ ID NO:X beginning with the nucleotide at about the position of the 5' Nucleotide of the First Amino Acid of the Signal Peptide and ending with the nucleotide at about the position of the 3' Nucleotide of the Clone Sequence as defined for SEQ ID NO:X in Table 1.

A further preferred embodiment is an isolated nucleic acid molecule comprising a nucleotide sequence which is at least 95% identical to the complete nucleotide sequence of SEQ ID NO:X.

Also preferred is an isolated nucleic acid molecule which hybridizes under stringent hybridization conditions to a nucleic acid molecule, wherein said nucleic acid molecule which hybridizes does not hybridize under stringent hybridization conditions to a nucleic acid molecule having a nucleotide sequence consisting of only A residues or of only T residues.

Also preferred is a composition of matter comprising a DNA molecule which comprises a human cDNA clone identified by a cDNA Clone Identifier in Table 1, which DNA molecule is contained in the material deposited with the American Type Culture Collection and given the ATCC Deposit Number shown in Table 1. for said cDNA Clone Identifier.

Also preferred is an isolated nucleic acid molecule comprising a nucleotide sequence which is at least 95% identical to a sequence of at least 50 contiguous nucleotides in the nucleotide sequence of a human cDNA clone identified by a cDNA Clone Identifier in Table 1, which DNA molecule is contained in the deposit given the ATCC Deposit Number shown in Table 1.

Also preferred is an isolated nucleic acid molecule, wherein said sequence of at least 50 contiguous nucleotides is included in the nucleotide sequence of the complete open reading frame sequence encoded by said human cDNA clone.

Also preferred is an isolated nucleic acid molecule comprising a nucleotide sequence which is at least 95% identical to sequence of at least 150 contiguous nucleotides in the nucleotide sequence encoded by said human cDNA clone.

A further preferred embodiment is an isolated nucleic acid molecule comprising a nucleotide sequence which is at least 95% identical to sequence of at least 500 contiguous nucleotides in the nucleotide sequence encoded by said human cDNA clone.

A further preferred embodiment is an isolated nucleic acid molecule comprising a nucleotide sequence which is at least 95% identical to the complete nucleotide sequence encoded by said human cDNA clone.

A further preferred embodiment is a method for detecting in a biological sample a nucleic acid molecule comprising a nucleotide sequence which is at least 95% identical to a sequence of at least 50 contiguous nucleotides in a sequence selected from the group consisting of: a nucleotide sequence of SEQ ID NO:X wherein X is any integer as defined in Table 1; and a nucleotide sequence encoded by a human cDNA clone identified by a cDNA Clone Identifier in Table 1 and contained in the deposit with the ATCC Deposit Number shown for said cDNA clone in Table 1; which method comprises a step of comparing a nucleotide sequence of at least one nucleic acid molecule in said sample with a sequence selected from said group and determining

whether the sequence of said nucleic acid molecule in said sample is at least 95% identical to said selected sequence.

Also preferred is the above method wherein said step of comparing sequences comprises determining the extent of nucleic acid hybridization between nucleic acid molecules in said sample and a nucleic acid molecule comprising said sequence selected from said group. Similarly, also preferred is the above method wherein said step of comparing sequences is performed by comparing the nucleotide sequence determined from a nucleic acid molecule in said sample with said sequence selected from said group. The nucleic acid molecules can comprise DNA molecules or RNA molecules.

A further preferred embodiment is a method for identifying the species, tissue or cell type of a biological sample which method comprises a step of detecting nucleic acid molecules in said sample, if any, comprising a nucleotide sequence that is at least 95% identical to a sequence of at least 50 contiguous nucleotides in a sequence selected from the group consisting of: a nucleotide sequence of SEQ ID NO:X wherein X is any integer as defined in Table 1; and a nucleotide sequence encoded by a human cDNA clone identified by a cDNA Clone Identifier in Table 1 and contained in the deposit with the ATCC Deposit Number shown for said cDNA clone in Table 1.

The method for identifying the species, tissue or cell type of a biological sample can comprise a step of detecting nucleic acid molecules comprising a nucleotide sequence in a panel of at least two nucleotide sequences, wherein at least one sequence in said panel is at least 95% identical to a sequence of at least 50 contiguous nucleotides in a sequence selected from said group.

Also preferred is a method for diagnosing in a subject a pathological condition associated with abnormal structure or expression of a gene encoding a secreted protein identified in Table 1, which method comprises a step of detecting in a biological sample obtained from said subject nucleic acid molecules, if any, comprising a nucleotide sequence that is at least 95% identical to a sequence of at least 50 contiguous nucleotides in a sequence selected from the group consisting of: a nucleotide sequence of SEQ ID NO:X wherein X is any integer as defined in Table 1; and a nucleotide sequence encoded by a human cDNA clone identified by a cDNA Clone Identifier in Table 1 and contained in the deposit with the ATCC Deposit Number shown for said cDNA clone in Table 1.

The method for diagnosing a pathological condition can comprise a step of detecting nucleic acid molecules comprising a nucleotide sequence in a panel of at least two nucleotide sequences, wherein at least one sequence in said panel is at least 95% identical to a sequence of at least 50 contiguous nucleotides in a sequence selected from said group.

Also preferred is a composition of matter comprising isolated nucleic acid molecules wherein the nucleotide sequences of said nucleic acid molecules comprise a panel of at least two nucleotide sequences, wherein at least one sequence in said panel is at least 95% identical to a sequence of at least 50 contiguous nucleotides in a sequence selected from the group consisting of: a nucleotide sequence of SEQ ID NO:X wherein X is any integer as defined in Table 1; and a nucleotide sequence encoded by a human cDNA clone identified by a cDNA Clone Identifier in Table 1 and contained in the deposit with the ATCC Deposit Number shown for said cDNA clone in Table 1. The nucleic acid molecules can comprise DNA molecules or RNA molecules.

Also preferred is an isolated polypeptide comprising an amino acid sequence at least 90% identical to a sequence of at least about 10 contiguous amino acids in the amino acid sequence of SEQ ID NO:Y wherein Y is any integer as defined in Table 1.

Also preferred is a polypeptide, wherein said sequence of contiguous amino acids is included in the amino acid sequence of SEQ ID NO:Y in the range of positions beginning with the residue at about the position of the First Amino Acid of the Secreted Portion and ending with the residue at about the Last Amino Acid of the Open Reading Frame as set forth for SEQ ID NO:Y in Table 1.

Also preferred is an isolated polypeptide comprising an amino acid sequence at least 95% identical to a sequence of at least about 30 contiguous amino acids in the amino acid sequence of SEQ ID NO:Y.

Further preferred is an isolated polypeptide comprising an amino acid sequence at least 95% identical to a sequence of at least about 100 contiguous amino acids in the amino acid sequence of SEQ ID NO:Y.

Further preferred is an isolated polypeptide comprising an amino acid sequence at least 95% identical to the complete amino acid sequence of SEQ ID NO:Y.

Further preferred is an isolated polypeptide comprising an amino acid sequence at least 90% identical to a sequence of at least about 10 contiguous amino acids in the complete amino acid sequence of a secreted protein encoded by a human cDNA clone identified by a cDNA Clone Identifier in Table 1 and contained in the deposit with the ATCC Deposit Number shown for said cDNA clone in Table 1.

Also preferred is a polypeptide wherein said sequence of contiguous amino acids is included in the amino acid sequence of a secreted portion of the secreted protein encoded by a human cDNA clone identified by a cDNA Clone Identifier in Table 1 and contained in the deposit with the ATCC Deposit Number shown for said cDNA clone in Table 1.

Also preferred is an isolated polypeptide comprising an amino acid sequence at least 95% identical to a sequence of at least about 30 contiguous amino acids in the

amino acid sequence of the secreted portion of the protein encoded by a human cDNA clone identified by a cDNA Clone Identifier in Table 1 and contained in the deposit with the ATCC Deposit Number shown for said cDNA clone in Table 1.

Also preferred is an isolated polypeptide comprising an amino acid sequence at
5 least 95% identical to a sequence of at least about 100 contiguous amino acids in the amino acid sequence of the secreted portion of the protein encoded by a human cDNA clone identified by a cDNA Clone Identifier in Table 1 and contained in the deposit with the ATCC Deposit Number shown for said cDNA clone in Table 1.

Also preferred is an isolated polypeptide comprising an amino acid sequence at
10 least 95% identical to the amino acid sequence of the secreted portion of the protein encoded by a human cDNA clone identified by a cDNA Clone Identifier in Table 1 and contained in the deposit with the ATCC Deposit Number shown for said cDNA clone in Table 1.

Further preferred is an isolated antibody which binds specifically to a
15 polypeptide comprising an amino acid sequence that is at least 90% identical to a sequence of at least 10 contiguous amino acids in a sequence selected from the group consisting of: an amino acid sequence of SEQ ID NO:Y wherein Y is any integer as defined in Table 1; and a complete amino acid sequence of a protein encoded by a human cDNA clone identified by a cDNA Clone Identifier in Table 1 and contained in
20 the deposit with the ATCC Deposit Number shown for said cDNA clone in Table 1.

Further preferred is a method for detecting in a biological sample a polypeptide comprising an amino acid sequence which is at least 90% identical to a sequence of at least 10 contiguous amino acids in a sequence selected from the group consisting of: an amino acid sequence of SEQ ID NO:Y wherein Y is any integer as defined in Table 1;
25 and a complete amino acid sequence of a protein encoded by a human cDNA clone identified by a cDNA Clone Identifier in Table 1 and contained in the deposit with the ATCC Deposit Number shown for said cDNA clone in Table 1; which method comprises a step of comparing an amino acid sequence of at least one polypeptide molecule in said sample with a sequence selected from said group and determining
30 whether the sequence of said polypeptide molecule in said sample is at least 90% identical to said sequence of at least 10 contiguous amino acids.

Also preferred is the above method wherein said step of comparing an amino acid sequence of at least one polypeptide molecule in said sample with a sequence selected from said group comprises determining the extent of specific binding of
35 polypeptides in said sample to an antibody which binds specifically to a polypeptide comprising an amino acid sequence that is at least 90% identical to a sequence of at least 10 contiguous amino acids in a sequence selected from the group consisting of: an

amino acid sequence of SEQ ID NO:Y wherein Y is any integer as defined in Table 1;
and a complete amino acid sequence of a protein encoded by a human cDNA clone
identified by a cDNA Clone Identifier in Table 1 and contained in the deposit with the
ATCC Deposit Number shown for said cDNA clone in Table 1.

5 Also preferred is the above method wherein said step of comparing sequences is
performed by comparing the amino acid sequence determined from a polypeptide
molecule in said sample with said sequence selected from said group.

Also preferred is a method for identifying the species, tissue or cell type of a
biological sample which method comprises a step of detecting polypeptide molecules in
10 said sample, if any, comprising an amino acid sequence that is at least 90% identical to
a sequence of at least 10 contiguous amino acids in a sequence selected from the group
consisting of: an amino acid sequence of SEQ ID NO:Y wherein Y is any integer as
defined in Table 1; and a complete amino acid sequence of a secreted protein encoded
by a human cDNA clone identified by a cDNA Clone Identifier in Table 1 and contained
15 in the deposit with the ATCC Deposit Number shown for said cDNA clone in Table 1.

Also preferred is the above method for identifying the species, tissue or cell type
of a biological sample, which method comprises a step of detecting polypeptide
molecules comprising an amino acid sequence in a panel of at least two amino acid
sequences, wherein at least one sequence in said panel is at least 90% identical to a
20 sequence of at least 10 contiguous amino acids in a sequence selected from the above
group.

Also preferred is a method for diagnosing in a subject a pathological condition
associated with abnormal structure or expression of a gene encoding a secreted protein
identified in Table 1, which method comprises a step of detecting in a biological sample
25 obtained from said subject polypeptide molecules comprising an amino acid sequence in
a panel of at least two amino acid sequences, wherein at least one sequence in said panel
is at least 90% identical to a sequence of at least 10 contiguous amino acids in a
sequence selected from the group consisting of: an amino acid sequence of SEQ ID
NO:Y wherein Y is any integer as defined in Table 1; and a complete amino acid
30 sequence of a secreted protein encoded by a human cDNA clone identified by a cDNA
Clone Identifier in Table 1 and contained in the deposit with the ATCC Deposit Number
shown for said cDNA clone in Table 1.

In any of these methods, the step of detecting said polypeptide molecules
includes using an antibody.

35 Also preferred is an isolated nucleic acid molecule comprising a nucleotide
sequence which is at least 95% identical to a nucleotide sequence encoding a
polypeptide wherein said polypeptide comprises an amino acid sequence that is at least

90% identical to a sequence of at least 10 contiguous amino acids in a sequence selected from the group consisting of: an amino acid sequence of SEQ ID NO:Y wherein Y is any integer as defined in Table 1; and a complete amino acid sequence of a secreted protein encoded by a human cDNA clone identified by a cDNA Clone Identifier in Table 1 and contained in the deposit with the ATCC Deposit Number shown for said cDNA clone in Table 1.

Also preferred is an isolated nucleic acid molecule, wherein said nucleotide sequence encoding a polypeptide has been optimized for expression of said polypeptide in a prokaryotic host.

Also preferred is an isolated nucleic acid molecule, wherein said polypeptide comprises an amino acid sequence selected from the group consisting of: an amino acid sequence of SEQ ID NO:Y wherein Y is any integer as defined in Table 1; and a complete amino acid sequence of a secreted protein encoded by a human cDNA clone identified by a cDNA Clone Identifier in Table 1 and contained in the deposit with the ATCC Deposit Number shown for said cDNA clone in Table 1.

Further preferred is a method of making a recombinant vector comprising inserting any of the above isolated nucleic acid molecule into a vector. Also preferred is the recombinant vector produced by this method. Also preferred is a method of making a recombinant host cell comprising introducing the vector into a host cell, as well as the recombinant host cell produced by this method.

Also preferred is a method of making an isolated polypeptide comprising culturing this recombinant host cell under conditions such that said polypeptide is expressed and recovering said polypeptide. Also preferred is this method of making an isolated polypeptide, wherein said recombinant host cell is a eukaryotic cell and said polypeptide is a secreted portion of a human secreted protein comprising an amino acid sequence selected from the group consisting of: an amino acid sequence of SEQ ID NO:Y beginning with the residue at the position of the First Amino Acid of the Secreted Portion of SEQ ID NO:Y wherein Y is an integer set forth in Table 1 and said position of the First Amino Acid of the Secreted Portion of SEQ ID NO:Y is defined in Table 1; and an amino acid sequence of a secreted portion of a protein encoded by a human cDNA clone identified by a cDNA Clone Identifier in Table 1 and contained in the deposit with the ATCC Deposit Number shown for said cDNA clone in Table 1. The isolated polypeptide produced by this method is also preferred.

Also preferred is a method of treatment of an individual in need of an increased level of a secreted protein activity, which method comprises administering to such an individual a pharmaceutical composition comprising an amount of an isolated

polypeptide, polynucleotide, or antibody of the claimed invention effective to increase the level of said protein activity in said individual.

Having generally described the invention, the same will be more readily understood by reference to the following examples, which are provided by way of illustration and are not intended as limiting.

Examples

Example 1: Isolation of a Selected cDNA Clone From the Deposited Sample

Each cDNA clone in a cited ATCC deposit is contained in a plasmid vector. Table 1 identifies the vectors used to construct the cDNA library from which each clone was isolated. In many cases, the vector used to construct the library is a phage vector from which a plasmid has been excised. The table immediately below correlates the related plasmid for each phage vector used in constructing the cDNA library. For example, where a particular clone is identified in Table 1 as being isolated in the vector "Lambda Zap," the corresponding deposited clone is in "pBluescript."

	<u>Vector Used to Construct Library</u>	<u>Corresponding Deposited Plasmid</u>
	Lambda Zap	pBluescript (pBS)
	Uni-Zap XR	pBluescript (pBS)
20	Zap Express	pBK
	lafmid BA	plafmid BA
	pSport1	pSport1
	pCMVSPORT 2.0	pCMVSPORT 2.0
	pCMVSPORT 3.0	pCMVSPORT 3.0
25	pCR [®] 2.1	pCR [®] 2.1

Vectors Lambda Zap (U.S. Patent Nos. 5,128,256 and 5,286,636), Uni-Zap XR (U.S. Patent Nos. 5,128, 256 and 5,286,636), Zap Express (U.S. Patent Nos. 5,128,256 and 5,286,636), pBluescript (pBS) (Short, J. M. et al., Nucleic Acids Res. 16:7583-7600 (1988); Alting-Mees, M. A. and Short, J. M., Nucleic Acids Res. 17:9494 (1989)) and pBK (Alting-Mees, M. A. et al., Strategies 5:58-61 (1992)) are commercially available from Stratagene Cloning Systems, Inc., 11011 N. Torrey Pines Road, La Jolla, CA, 92037. pBS contains an ampicillin resistance gene and pBK contains a neomycin resistance gene. Both can be transformed into E. coli strain XL-1 Blue, also available from Stratagene. pBS comes in 4 forms SK+, SK-, KS+ and KS. The S and K refers to the orientation of the polylinker to the T7 and T3 primer sequences which flank the polylinker region ("S" is for SacI and "K" is for KpnI which are the first sites on each respective end of the linker). "+" or "-" refer to the orientation

of the f1 origin of replication ("ori"), such that in one orientation, single stranded rescue initiated from the f1 ori generates sense strand DNA and in the other, antisense.

Vectors pSport1, pCMVSPORT 2.0 and pCMVSPORT 3.0, were obtained from Life Technologies, Inc., P. O. Box 6009, Gaithersburg, MD 20897. All Sport vectors
5 contain an ampicillin resistance gene and may be transformed into E. coli strain DH10B, also available from Life Technologies. (See, for instance, Gruber, C. E., et al., Focus 15:59 (1993).) Vector lafmid BA (Bento Soares, Columbia University, NY) contains an ampicillin resistance gene and can be transformed into E. coli strain XL-1 Blue. Vector pCR[®]2.1, which is available from Invitrogen, 1600 Faraday Avenue,
10 Carlsbad, CA 92008, contains an ampicillin resistance gene and may be transformed into E. coli strain DH10B, available from Life Technologies. (See, for instance, Clark, J. M., Nuc. Acids Res. 16:9677-9686 (1988) and Mead, D. et al., Bio/Technology 9: (1991).) Preferably, a polynucleotide of the present invention does not comprise the phage vector sequences identified for the particular clone in Table 1, as well as the
15 corresponding plasmid vector sequences designated above.

The deposited material in the sample assigned the ATCC Deposit Number cited in Table 1 for any given cDNA clone also may contain one or more additional plasmids, each comprising a cDNA clone different from that given clone. Thus, deposits sharing the same ATCC Deposit Number contain at least a plasmid for each cDNA clone
20 identified in Table 1. Typically, each ATCC deposit sample cited in Table 1 comprises a mixture of approximately equal amounts (by weight) of about 50 plasmid DNAs, each containing a different cDNA clone; but such a deposit sample may include plasmids for more or less than 50 cDNA clones, up to about 500 cDNA clones.

Two approaches can be used to isolate a particular clone from the deposited
25 sample of plasmid DNAs cited for that clone in Table 1. First, a plasmid is directly isolated by screening the clones using a polynucleotide probe corresponding to SEQ ID NO:X.

Particularly, a specific polynucleotide with 30-40 nucleotides is synthesized using an Applied Biosystems DNA synthesizer according to the sequence reported.
30 The oligonucleotide is labeled, for instance, with ³²P-γ-ATP using T4 polynucleotide kinase and purified according to routine methods. (E.g., Maniatis et al., Molecular Cloning: A Laboratory Manual, Cold Spring Harbor Press, Cold Spring, NY (1982).) The plasmid mixture is transformed into a suitable host, as indicated above (such as XL-1 Blue (Stratagene)) using techniques known to those of skill in the art, such as
35 those provided by the vector supplier or in related publications or patents cited above. The transformants are plated on 1.5% agar plates (containing the appropriate selection

agent, e.g., ampicillin) to a density of about 150 transformants (colonies) per plate. These plates are screened using Nylon membranes according to routine methods for bacterial colony screening (e.g., Sambrook et al., *Molecular Cloning: A Laboratory Manual*, 2nd Edit., (1989), Cold Spring Harbor Laboratory Press, pages 1.93 to 1.104), or other techniques known to those of skill in the art.

Alternatively, two primers of 17-20 nucleotides derived from both ends of the SEQ ID NO:X (i.e., within the region of SEQ ID NO:X bounded by the 5' NT and the 3' NT of the clone defined in Table 1) are synthesized and used to amplify the desired cDNA using the deposited cDNA plasmid as a template. The polymerase chain reaction is carried out under routine conditions, for instance, in 25 µl of reaction mixture with 0.5 ug of the above cDNA template. A convenient reaction mixture is 1.5-5 mM MgCl₂, 0.01% (w/v) gelatin, 20 µM each of dATP, dCTP, dGTP, dTTP, 25 pmol of each primer and 0.25 Unit of Taq polymerase. Thirty five cycles of PCR (denaturation at 94°C for 1 min; annealing at 55°C for 1 min; elongation at 72°C for 1 min) are performed with a Perkin-Elmer Cetus automated thermal cycler. The amplified product is analyzed by agarose gel electrophoresis and the DNA band with expected molecular weight is excised and purified. The PCR product is verified to be the selected sequence by subcloning and sequencing the DNA product.

Several methods are available for the identification of the 5' or 3' non-coding portions of a gene which may not be present in the deposited clone. These methods include but are not limited to, filter probing, clone enrichment using specific probes, and protocols similar or identical to 5' and 3' "RACE" protocols which are well known in the art. For instance, a method similar to 5' RACE is available for generating the missing 5' end of a desired full-length transcript. (Fromont-Racine et al., *Nucleic Acids Res.* 21(7):1683-1684 (1993).)

Briefly, a specific RNA oligonucleotide is ligated to the 5' ends of a population of RNA presumably containing full-length gene RNA transcripts. A primer set containing a primer specific to the ligated RNA oligonucleotide and a primer specific to a known sequence of the gene of interest is used to PCR amplify the 5' portion of the desired full-length gene. This amplified product may then be sequenced and used to generate the full length gene.

This above method starts with total RNA isolated from the desired source, although poly-A+ RNA can be used. The RNA preparation can then be treated with phosphatase if necessary to eliminate 5' phosphate groups on degraded or damaged RNA which may interfere with the later RNA ligase step. The phosphatase should then be inactivated and the RNA treated with tobacco acid pyrophosphatase in order to

remove the cap structure present at the 5' ends of messenger RNAs. This reaction leaves a 5' phosphate group at the 5' end of the cap cleaved RNA which can then be ligated to an RNA oligonucleotide using T4 RNA ligase.

This modified RNA preparation is used as a template for first strand cDNA synthesis using a gene specific oligonucleotide. The first strand synthesis reaction is used as a template for PCR amplification of the desired 5' end using a primer specific to the ligated RNA oligonucleotide and a primer specific to the known sequence of the gene of interest. The resultant product is then sequenced and analyzed to confirm that the 5' end sequence belongs to the desired gene.

Example 2: Isolation of Genomic Clones Corresponding to a Polynucleotide

A human genomic P1 library (Genomic Systems, Inc.) is screened by PCR using primers selected for the cDNA sequence corresponding to SEQ ID NO:X., according to the method described in Example 1. (See also, Sambrook.)

Example 3: Tissue Distribution of Polypeptide

Tissue distribution of mRNA expression of polynucleotides of the present invention is determined using protocols for Northern blot analysis, described by, among others, Sambrook et al. For example, a cDNA probe produced by the method described in Example 1 is labeled with P³² using the rediprime™ DNA labeling system (Amersham Life Science), according to manufacturer's instructions. After labeling, the probe is purified using CHROMA SPIN-100™ column (Clontech Laboratories, Inc.), according to manufacturer's protocol number PT1200-1. The purified labeled probe is then used to examine various human tissues for mRNA expression.

Multiple Tissue Northern (MTN) blots containing various human tissues (H) or human immune system tissues (IM) (Clontech) are examined with the labeled probe using ExpressHyb™ hybridization solution (Clontech) according to manufacturer's protocol number PT1190-1. Following hybridization and washing, the blots are mounted and exposed to film at -70°C overnight, and the films developed according to standard procedures.

Example 4: Chromosomal Mapping of the Polynucleotides

An oligonucleotide primer set is designed according to the sequence at the 5' end of SEQ ID NO:X. This primer preferably spans about 100 nucleotides. This primer set is then used in a polymerase chain reaction under the following set of

conditions : 30 seconds, 95°C; 1 minute, 56°C; 1 minute, 70°C. This cycle is repeated 32 times followed by one 5 minute cycle at 70°C. Human, mouse, and hamster DNA is used as template in addition to a somatic cell hybrid panel containing individual chromosomes or chromosome fragments (Bios, Inc). The reactions is analyzed on
5 either 8% polyacrylamide gels or 3.5 % agarose gels. Chromosome mapping is determined by the presence of an approximately 100 bp PCR fragment in the particular somatic cell hybrid.

Example 5: Bacterial Expression of a Polypeptide

10 A polynucleotide encoding a polypeptide of the present invention is amplified using PCR oligonucleotide primers corresponding to the 5' and 3' ends of the DNA sequence, as outlined in Example 1, to synthesize insertion fragments. The primers used to amplify the cDNA insert should preferably contain restriction sites, such as BamHI and XbaI, at the 5' end of the primers in order to clone the amplified product
15 into the expression vector. For example, BamHI and XbaI correspond to the restriction enzyme sites on the bacterial expression vector pQE-9. (Qiagen, Inc., Chatsworth, CA). This plasmid vector encodes antibiotic resistance (Amp^r), a bacterial origin of replication (ori), an IPTG-regulatable promoter/operator (P/O), a ribosome binding site (RBS), a 6-histidine tag (6-His), and restriction enzyme cloning sites.

20 The pQE-9 vector is digested with BamHI and XbaI and the amplified fragment is ligated into the pQE-9 vector maintaining the reading frame initiated at the bacterial RBS. The ligation mixture is then used to transform the E. coli strain M15/rep4 (Qiagen, Inc.) which contains multiple copies of the plasmid pREP4, which expresses the lacI repressor and also confers kanamycin resistance (Kan^r). Transformants are
25 identified by their ability to grow on LB plates and ampicillin/kanamycin resistant colonies are selected. Plasmid DNA is isolated and confirmed by restriction analysis.

Clones containing the desired constructs are grown overnight (O/N) in liquid culture in LB media supplemented with both Amp (100 ug/ml) and Kan (25 ug/ml). The O/N culture is used to inoculate a large culture at a ratio of 1:100 to 1:250. The
30 cells are grown to an optical density 600 (O.D.⁶⁰⁰) of between 0.4 and 0.6. IPTG (Isopropyl-B-D-thiogalacto pyranoside) is then added to a final concentration of 1 mM. IPTG induces by inactivating the lacI repressor, clearing the P/O leading to increased gene expression.

Cells are grown for an extra 3 to 4 hours. Cells are then harvested by
35 centrifugation (20 mins at 6000Xg). The cell pellet is solubilized in the chaotropic

agent 6 Molar Guanidine HCl by stirring for 3-4 hours at 4°C. The cell debris is removed by centrifugation, and the supernatant containing the polypeptide is loaded onto a nickel-nitrilo-tri-acetic acid ("Ni-NTA") affinity resin column (available from QIAGEN, Inc., *supra*). Proteins with a 6 x His tag bind to the Ni-NTA resin with high
5 affinity and can be purified in a simple one-step procedure (for details see: The QIAexpressionist (1995) QIAGEN, Inc., *supra*).

Briefly, the supernatant is loaded onto the column in 6 M guanidine-HCl, pH 8, the column is first washed with 10 volumes of 6 M guanidine-HCl, pH 8, then washed with 10 volumes of 6 M guanidine-HCl pH 6, and finally the polypeptide is eluted with
10 6 M guanidine-HCl, pH 5.

The purified protein is then renatured by dialyzing it against phosphate-buffered saline (PBS) or 50 mM Na-acetate, pH 6 buffer plus 200 mM NaCl. Alternatively, the protein can be successfully refolded while immobilized on the Ni-NTA column. The recommended conditions are as follows: renature using a linear 6M-1M urea gradient in
15 500 mM NaCl, 20% glycerol, 20 mM Tris/HCl pH 7.4, containing protease inhibitors. The renaturation should be performed over a period of 1.5 hours or more. After renaturation the proteins are eluted by the addition of 250 mM imidazole. Imidazole is removed by a final dialyzing step against PBS or 50 mM sodium acetate pH 6 buffer plus 200 mM NaCl. The purified protein is stored at 4°C or frozen at -80°C.

In addition to the above expression vector, the present invention further includes an expression vector comprising phage operator and promoter elements operatively linked to a polynucleotide of the present invention, called pHE4a. (ATCC Accession Number XXXXXX.) This vector contains: 1) a neomycinphosphotransferase gene as a selection marker, 2) an E. coli origin of replication, 3) a T5 phage promoter sequence,
25 4) two lac operator sequences, 5) a Shine-Delgarno sequence, and 6) the lactose operon repressor gene (*lacIq*). The origin of replication (*oriC*) is derived from pUC19 (LTI, Gaithersburg, MD). The promoter sequence and operator sequences are made synthetically.

DNA can be inserted into the pHEa by restricting the vector with NdeI and
30 XbaI, BamHI, XhoI, or Asp718, running the restricted product on a gel, and isolating the larger fragment (the stuffer fragment should be about 310 base pairs). The DNA insert is generated according to the PCR protocol described in Example 1, using PCR primers having restriction sites for NdeI (5' primer) and XbaI, BamHI, XhoI, or Asp718 (3' primer). The PCR insert is gel purified and restricted with compatible
35 enzymes. The insert and vector are ligated according to standard protocols.

The engineered vector could easily be substituted in the above protocol to express protein in a bacterial system.

Example 6: Purification of a Polypeptide from an Inclusion Body

- 5 The following alternative method can be used to purify a polypeptide expressed in *E. coli* when it is present in the form of inclusion bodies. Unless otherwise specified, all of the following steps are conducted at 4-10°C.

- Upon completion of the production phase of the *E. coli* fermentation, the cell culture is cooled to 4-10°C and the cells harvested by continuous centrifugation at
- 10 15,000 rpm (Heraeus Sepatech). On the basis of the expected yield of protein per unit weight of cell paste and the amount of purified protein required, an appropriate amount of cell paste, by weight, is suspended in a buffer solution containing 100 mM Tris, 50 mM EDTA, pH 7.4. The cells are dispersed to a homogeneous suspension using a high shear mixer.
- 15 The cells are then lysed by passing the solution through a microfluidizer (Microfluidics, Corp. or APV Gaulin, Inc.) twice at 4000-6000 psi. The homogenate is then mixed with NaCl solution to a final concentration of 0.5 M NaCl, followed by centrifugation at 7000 xg for 15 min. The resultant pellet is washed again using 0.5M NaCl, 100 mM Tris, 50 mM EDTA, pH 7.4.
- 20 The resulting washed inclusion bodies are solubilized with 1.5 M guanidine hydrochloride (GuHCl) for 2-4 hours. After 7000 xg centrifugation for 15 min., the pellet is discarded and the polypeptide containing supernatant is incubated at 4°C overnight to allow further GuHCl extraction.

- Following high speed centrifugation (30,000 xg) to remove insoluble particles,
- 25 the GuHCl solubilized protein is refolded by quickly mixing the GuHCl extract with 20 volumes of buffer containing 50 mM sodium, pH 4.5, 150 mM NaCl, 2 mM EDTA by vigorous stirring. The refolded diluted protein solution is kept at 4°C without mixing for 12 hours prior to further purification steps.

- To clarify the refolded polypeptide solution, a previously prepared tangential
- 30 filtration unit equipped with 0.16 µm membrane filter with appropriate surface area (e.g., Filtron), equilibrated with 40 mM sodium acetate, pH 6.0 is employed. The filtered sample is loaded onto a cation exchange resin (e.g., Poros HS-50, Perseptive Biosystems). The column is washed with 40 mM sodium acetate, pH 6.0 and eluted with 250 mM, 500 mM, 1000 mM, and 1500 mM NaCl in the same buffer, in a

stepwise manner. The absorbance at 280 nm of the effluent is continuously monitored. Fractions are collected and further analyzed by SDS-PAGE.

Fractions containing the polypeptide are then pooled and mixed with 4 volumes of water. The diluted sample is then loaded onto a previously prepared set of tandem
5 columns of strong anion (Poros HQ-50, Perseptive Biosystems) and weak anion (Poros CM-20, Perseptive Biosystems) exchange resins. The columns are equilibrated with 40 mM sodium acetate, pH 6.0. Both columns are washed with 40 mM sodium acetate, pH 6.0, 200 mM NaCl. The CM-20 column is then eluted using a 10 column
10 volume linear gradient ranging from 0.2 M NaCl, 50 mM sodium acetate, pH 6.0 to 1.0 M NaCl, 50 mM sodium acetate, pH 6.5. Fractions are collected under constant A_{280} monitoring of the effluent. Fractions containing the polypeptide (determined, for instance, by 16% SDS-PAGE) are then pooled.

The resultant polypeptide should exhibit greater than 95% purity after the above refolding and purification steps. No major contaminant bands should be observed from
15 Commassie blue stained 16% SDS-PAGE gel when 5 μ g of purified protein is loaded. The purified protein can also be tested for endotoxin/LPS contamination, and typically the LPS content is less than 0.1 ng/ml according to LAL assays.

Example 7: Cloning and Expression of a Polypeptide in a Baculovirus

20 Expression System

In this example, the plasmid shuttle vector pA2 is used to insert a polynucleotide into a baculovirus to express a polypeptide. This expression vector contains the strong polyhedrin promoter of the *Autographa californica* nuclear polyhedrosis virus (AcMNPV) followed by convenient restriction sites such as BamHI, Xba I and
25 Asp718. The polyadenylation site of the simian virus 40 ("SV40") is used for efficient polyadenylation. For easy selection of recombinant virus, the plasmid contains the beta-galactosidase gene from *E. coli* under control of a weak *Drosophila* promoter in the same orientation, followed by the polyadenylation signal of the polyhedrin gene. The inserted genes are flanked on both sides by viral sequences for cell-mediated
30 homologous recombination with wild-type viral DNA to generate a viable virus that express the cloned polynucleotide.

Many other baculovirus vectors can be used in place of the vector above, such as pAc373, pVL941, and pAcIM1, as one skilled in the art would readily appreciate, as long as the construct provides appropriately located signals for transcription,
35 translation, secretion and the like, including a signal peptide and an in-frame AUG as

required. Such vectors are described, for instance, in Luckow et al., *Virology* 170:31-39 (1989).

Specifically, the cDNA sequence contained in the deposited clone, including the AUG initiation codon and the naturally associated leader sequence identified in Table 1, is amplified using the PCR protocol described in Example 1. If the naturally occurring signal sequence is used to produce the secreted protein, the pA2 vector does not need a second signal peptide. Alternatively, the vector can be modified (pA2 GP) to include a baculovirus leader sequence, using the standard methods described in Summers et al., "A Manual of Methods for Baculovirus Vectors and Insect Cell Culture Procedures," Texas Agricultural Experimental Station Bulletin No. 1555 (1987).

The amplified fragment is isolated from a 1% agarose gel using a commercially available kit ("GeneClean," BIO 101 Inc., La Jolla, Ca.). The fragment then is digested with appropriate restriction enzymes and again purified on a 1% agarose gel.

The plasmid is digested with the corresponding restriction enzymes and optionally, can be dephosphorylated using calf intestinal phosphatase, using routine procedures known in the art. The DNA is then isolated from a 1% agarose gel using a commercially available kit ("GeneClean" BIO 101 Inc., La Jolla, Ca.).

The fragment and the dephosphorylated plasmid are ligated together with T4 DNA ligase. *E. coli* HB101 or other suitable *E. coli* hosts such as XL-1 Blue (Stratagene Cloning Systems, La Jolla, CA) cells are transformed with the ligation mixture and spread on culture plates. Bacteria containing the plasmid are identified by digesting DNA from individual colonies and analyzing the digestion product by gel electrophoresis. The sequence of the cloned fragment is confirmed by DNA sequencing.

Five μ g of a plasmid containing the polynucleotide is co-transfected with 1.0 μ g of a commercially available linearized baculovirus DNA ("BaculoGold™ baculovirus DNA", Pharmingen, San Diego, CA), using the lipofection method described by Felgner et al., *Proc. Natl. Acad. Sci. USA* 84:7413-7417 (1987). One μ g of BaculoGold™ virus DNA and 5 μ g of the plasmid are mixed in a sterile well of a microtiter plate containing 50 μ l of serum-free Grace's medium (Life Technologies Inc., Gaithersburg, MD). Afterwards, 10 μ l Lipofectin plus 90 μ l Grace's medium are added, mixed and incubated for 15 minutes at room temperature. Then the transfection mixture is added drop-wise to Sf9 insect cells (ATCC CRL 1711) seeded in a 35 mm tissue culture plate with 1 ml Grace's medium without serum. The plate is then incubated for 5 hours at 27° C. The transfection solution is then removed from the plate and 1 ml of Grace's insect medium supplemented with 10% fetal calf serum is added. Cultivation is then continued at 27° C for four days.

After four days the supernatant is collected and a plaque assay is performed, as described by Summers and Smith, *supra*. An agarose gel with "Blue Gal" (Life Technologies Inc., Gaithersburg) is used to allow easy identification and isolation of gal-expressing clones, which produce blue-stained plaques. (A detailed description of a
5 "plaque assay" of this type can also be found in the user's guide for insect cell culture and baculovirology distributed by Life Technologies Inc., Gaithersburg, page 9-10.) After appropriate incubation, blue stained plaques are picked with the tip of a micropipettor (e.g., Eppendorf). The agar containing the recombinant viruses is then resuspended in a microcentrifuge tube containing 200 µl of Grace's medium and the
10 suspension containing the recombinant baculovirus is used to infect Sf9 cells seeded in 35 mm dishes. Four days later the supernatants of these culture dishes are harvested and then they are stored at 4° C.

To verify the expression of the polypeptide, Sf9 cells are grown in Grace's medium supplemented with 10% heat-inactivated FBS. The cells are infected with the
15 recombinant baculovirus containing the polynucleotide at a multiplicity of infection ("MOI") of about 2. If radiolabeled proteins are desired, 6 hours later the medium is removed and is replaced with SF900 II medium minus methionine and cysteine (available from Life Technologies Inc., Rockville, MD). After 42 hours, 5 µCi of ³⁵S-methionine and 5 µCi ³⁵S-cysteine (available from Amersham) are added. The cells are
20 further incubated for 16 hours and then are harvested by centrifugation. The proteins in the supernatant as well as the intracellular proteins are analyzed by SDS-PAGE followed by autoradiography (if radiolabeled).

Microsequencing of the amino acid sequence of the amino terminus of purified protein may be used to determine the amino terminal sequence of the produced protein.

25 **Example 8: Expression of a Polypeptide in Mammalian Cells**

The polypeptide of the present invention can be expressed in a mammalian cell. A typical mammalian expression vector contains a promoter element, which mediates the initiation of transcription of mRNA, a protein coding sequence, and signals required for the termination of transcription and polyadenylation of the transcript. Additional
30 elements include enhancers, Kozak sequences and intervening sequences flanked by donor and acceptor sites for RNA splicing. Highly efficient transcription is achieved with the early and late promoters from SV40, the long terminal repeats (LTRs) from Retroviruses, e.g., RSV, HTLV, HIV and the early promoter of the cytomegalovirus (CMV). However, cellular elements can also be used (e.g., the human actin promoter).

35 Suitable expression vectors for use in practicing the present invention include, for example, vectors such as pSVL and pMSG (Pharmacia, Uppsala, Sweden),

pRSVcat (ATCC 37152), pSV2dhfr (ATCC 37146), pBC12MI (ATCC 67109), pCMVSPORT 2.0, and pCMVSPORT 3.0. Mammalian host cells that could be used include, human HeLa, 293, H9 and Jurkat cells, mouse NIH3T3 and C127 cells, Cos 1, Cos 7 and CV1, quail QC1-3 cells, mouse L cells and Chinese hamster ovary (CHO) cells.

Alternatively, the polypeptide can be expressed in stable cell lines containing the polynucleotide integrated into a chromosome. The co-transfection with a selectable marker such as dhfr, gpt, neomycin, hygromycin allows the identification and isolation of the transfected cells.

The transfected gene can also be amplified to express large amounts of the encoded protein. The DHFR (dihydrofolate reductase) marker is useful in developing cell lines that carry several hundred or even several thousand copies of the gene of interest. (See, e.g., Alt, F. W., et al., J. Biol. Chem. 253:1357-1370 (1978); Hamlin, J. L. and Ma, C., Biochem. et Biophys. Acta, 1097:107-143 (1990); Page, M. J. and Sydenham, M. A., Biotechnology 9:64-68 (1991).) Another useful selection marker is the enzyme glutamine synthase (GS) (Murphy et al., Biochem J. 227:277-279 (1991); Bebbington et al., Bio/Technology 10:169-175 (1992). Using these markers, the mammalian cells are grown in selective medium and the cells with the highest resistance are selected. These cell lines contain the amplified gene(s) integrated into a chromosome. Chinese hamster ovary (CHO) and NSO cells are often used for the production of proteins.

Derivatives of the plasmid pSV2-dhfr (ATCC Accession No. 37146), the expression vectors pC4 (ATCC Accession No. 209646) and pC6 (ATCC Accession No. 209647) contain the strong promoter (LTR) of the Rous Sarcoma Virus (Cullen et al., Molecular and Cellular Biology, 438-447 (March, 1985)) plus a fragment of the CMV-enhancer (Boshart et al., Cell 41:521-530 (1985).) Multiple cloning sites, e.g., with the restriction enzyme cleavage sites BamHI, XbaI and Asp718, facilitate the cloning of the gene of interest. The vectors also contain the 3' intron, the polyadenylation and termination signal of the rat preproinsulin gene, and the mouse DHFR gene under control of the SV40 early promoter.

Specifically, the plasmid pC6, for example, is digested with appropriate restriction enzymes and then dephosphorylated using calf intestinal phosphates by procedures known in the art. The vector is then isolated from a 1% agarose gel.

A polynucleotide of the present invention is amplified according to the protocol outlined in Example 1. If the naturally occurring signal sequence is used to produce the secreted protein, the vector does not need a second signal peptide. Alternatively, if the

naturally occurring signal sequence is not used, the vector can be modified to include a heterologous signal sequence. (See, e.g., WO 96/34891.)

5 The amplified fragment is isolated from a 1% agarose gel using a commercially available kit ("GeneClean," BIO 101 Inc., La Jolla, Ca.). The fragment then is digested with appropriate restriction enzymes and again purified on a 1% agarose gel.

The amplified fragment is then digested with the same restriction enzyme and purified on a 1% agarose gel. The isolated fragment and the dephosphorylated vector are then ligated with T4 DNA ligase. *E. coli* HB101 or XL-1 Blue cells are then transformed and bacteria are identified that contain the fragment inserted into plasmid pC6 using, for instance, restriction enzyme analysis.

Chinese hamster ovary cells lacking an active DHFR gene is used for transfection. Five μg of the expression plasmid pC6 is cotransfected with 0.5 μg of the plasmid pSVneo using lipofectin (Felgner et al., *supra*). The plasmid pSV2-neo contains a dominant selectable marker, the *neo* gene from Tn5 encoding an enzyme that confers resistance to a group of antibiotics including G418. The cells are seeded in alpha minus MEM supplemented with 1 mg/ml G418. After 2 days, the cells are trypsinized and seeded in hybridoma cloning plates (Greiner, Germany) in alpha minus MEM supplemented with 10, 25, or 50 ng/ml of methotrexate plus 1 mg/ml G418. After about 10-14 days single clones are trypsinized and then seeded in 6-well petri dishes or 10 ml flasks using different concentrations of methotrexate (50 nM, 100 nM, 200 nM, 400 nM, 800 nM). Clones growing at the highest concentrations of methotrexate are then transferred to new 6-well plates containing even higher concentrations of methotrexate (1 μM , 2 μM , 5 μM , 10 mM, 20 mM). The same procedure is repeated until clones are obtained which grow at a concentration of 100 - 200 μM . Expression of the desired gene product is analyzed, for instance, by SDS-PAGE and Western blot or by reversed phase HPLC analysis.

Example 9: Protein Fusions

The polypeptides of the present invention are preferably fused to other proteins. These fusion proteins can be used for a variety of applications. For example, fusion of the present polypeptides to His-tag, HA-tag, protein A, IgG domains, and maltose binding protein facilitates purification. (See Example 5; see also EP A 394,827; Traunecker, et al., Nature 331:84-86 (1988).) Similarly, fusion to IgG-1, IgG-3, and albumin increases the halflife time in vivo. Nuclear localization signals fused to the polypeptides of the present invention can target the protein to a specific subcellular localization, while covalent heterodimer or homodimers can increase or decrease the activity of a fusion protein. Fusion proteins can also create chimeric molecules having

more than one function. Finally, fusion proteins can increase solubility and/or stability of the fused protein compared to the non-fused protein. All of the types of fusion proteins described above can be made by modifying the following protocol, which outlines the fusion of a polypeptide to an IgG molecule, or the protocol described in Example 5.

Briefly, the human Fc portion of the IgG molecule can be PCR amplified, using primers that span the 5' and 3' ends of the sequence described below. These primers also should have convenient restriction enzyme sites that will facilitate cloning into an expression vector, preferably a mammalian expression vector.

For example, if pC4 (Accession No.209646) is used, the human Fc portion can be ligated into the BamHI cloning site. Note that the 3' BamHI site should be destroyed. Next, the vector containing the human Fc portion is re-restricted with BamHI, linearizing the vector, and a polynucleotide of the present invention, isolated by the PCR protocol described in Example 1, is ligated into this BamHI site. Note that the polynucleotide is cloned without a stop codon, otherwise a fusion protein will not be produced.

If the naturally occurring signal sequence is used to produce the secreted protein, pC4 does not need a second signal peptide. Alternatively, if the naturally occurring signal sequence is not used, the vector can be modified to include a heterologous signal sequence. (See, e.g., WO 96/34891.)

Human IgG Fc region:

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GGGATCCGGAGCCCAAATCTTCTGACAAACTCACACATGCCCACCGTGCC
CAGCACCTGAATTCGAGGGTGCACCGTCAGTCTTCCTCTTCCCCCAAAACC
25 CAAGGACACCCTCATGATCTCCCGGACTCCTGAGGTCACATGCGTGGTGGT
GGACGTAAGCCACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGACG
GCGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAAC
AGCACGTACCGTGTGGTCAGCGTCCTACCGTCCTGCACCAGGACTGGCTG
AATGGCAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAACCCCC
30 ATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAGGT
GTACACCCTGCCCCCATCCCGGGATGAGCTGACCAAGAACCAGGTGAGCCT
GACCTGCCTGGTCAAAGGCTTCTATCCAAGCGACATCGCCGTGGAGTGGGA
GAGCAATGGGCAGCCGGAGAACAACACTACAAGACCACGCCTCCCGTGCTGG
ACTCCGACGGCTCCTTCTTCTCTACAGCAAGCTCACCGTGGACAAGAGCA
35 GGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGAGGCTCTGC
ACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAATGAGTGC
GACGGCCGCGACTCTAGAGGAT (SEQ ID NO:1)
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Example 10: Production of an Antibody from a Polypeptide

The antibodies of the present invention can be prepared by a variety of methods. (See, Current Protocols, Chapter 2.) For example, cells expressing a polypeptide of the present invention is administered to an animal to induce the production of sera containing polyclonal antibodies. In a preferred method, a preparation of the secreted protein is prepared and purified to render it substantially free of natural contaminants. Such a preparation is then introduced into an animal in order to produce polyclonal antisera of greater specific activity.

In the most preferred method, the antibodies of the present invention are monoclonal antibodies (or protein binding fragments thereof). Such monoclonal antibodies can be prepared using hybridoma technology. (Köhler et al., Nature 256:495 (1975); Köhler et al., Eur. J. Immunol. 6:511 (1976); Köhler et al., Eur. J. Immunol. 6:292 (1976); Hammerling et al., in: Monoclonal Antibodies and T-Cell Hybridomas, Elsevier, N.Y., pp. 563-681 (1981).) In general, such procedures involve immunizing an animal (preferably a mouse) with polypeptide or, more preferably, with a secreted polypeptide-expressing cell. Such cells may be cultured in any suitable tissue culture medium; however, it is preferable to culture cells in Earle's modified Eagle's medium supplemented with 10% fetal bovine serum (inactivated at about 56°C), and supplemented with about 10 g/l of nonessential amino acids, about 1,000 U/ml of penicillin, and about 100 µg/ml of streptomycin.

The splenocytes of such mice are extracted and fused with a suitable myeloma cell line. Any suitable myeloma cell line may be employed in accordance with the present invention; however, it is preferable to employ the parent myeloma cell line (SP2O), available from the ATCC. After fusion, the resulting hybridoma cells are selectively maintained in HAT medium, and then cloned by limiting dilution as described by Wands et al. (Gastroenterology 80:225-232 (1981).) The hybridoma cells obtained through such a selection are then assayed to identify clones which secrete antibodies capable of binding the polypeptide.

Alternatively, additional antibodies capable of binding to the polypeptide can be produced in a two-step procedure using anti-idiotypic antibodies. Such a method makes use of the fact that antibodies are themselves antigens, and therefore, it is possible to obtain an antibody which binds to a second antibody. In accordance with this method, protein specific antibodies are used to immunize an animal, preferably a mouse. The splenocytes of such an animal are then used to produce hybridoma cells, and the hybridoma cells are screened to identify clones which produce an antibody

whose ability to bind to the protein-specific antibody can be blocked by the polypeptide. Such antibodies comprise anti-idiotypic antibodies to the protein-specific antibody and can be used to immunize an animal to induce formation of further protein-specific antibodies.

5 It will be appreciated that Fab and F(ab')₂ and other fragments of the antibodies of the present invention may be used according to the methods disclosed herein. Such fragments are typically produced by proteolytic cleavage, using enzymes such as papain (to produce Fab fragments) or pepsin (to produce F(ab')₂ fragments). Alternatively, secreted protein-binding fragments can be produced through the application of
10 recombinant DNA technology or through synthetic chemistry.

For in vivo use of antibodies in humans, it may be preferable to use "humanized" chimeric monoclonal antibodies. Such antibodies can be produced using genetic constructs derived from hybridoma cells producing the monoclonal antibodies described above. Methods for producing chimeric antibodies are known in the art.
15 (See, for review, Morrison, Science 229:1202 (1985); Oi et al., BioTechniques 4:214 (1986); Cabilly et al., U.S. Patent No. 4,816,567; Taniguchi et al., EP 171496; Morrison et al., EP 173494; Neuberger et al., WO 8601533; Robinson et al., WO 8702671; Boulianne et al., Nature 312:643 (1984); Neuberger et al., Nature 314:268 (1985).)

20

Example 11: Production Of Secreted Protein For High-Throughput Screening Assays

The following protocol produces a supernatant containing a polypeptide to be tested. This supernatant can then be used in the Screening Assays described in
25 Examples 13-20.

First, dilute Poly-D-Lysine (644 587 Boehringer-Mannheim) stock solution (1mg/ml in PBS) 1:20 in PBS (w/o calcium or magnesium 17-516F Biowhittaker) for a working solution of 50ug/ml. Add 200 ul of this solution to each well (24 well plates) and incubate at RT for 20 minutes. Be sure to distribute the solution over each well
30 (note: a 12-channel pipetter may be used with tips on every other channel). Aspirate off the Poly-D-Lysine solution and rinse with 1ml PBS (Phosphate Buffered Saline). The PBS should remain in the well until just prior to plating the cells and plates may be poly-lysine coated in advance for up to two weeks.

Plate 293T cells (do not carry cells past P+20) at 2×10^5 cells/well in .5ml
35 DMEM(Dulbecco's Modified Eagle Medium)(with 4.5 G/L glucose and L-glutamine (12-604F Biowhittaker))/10% heat inactivated FBS(14-503F Biowhittaker)/1x Penstrep(17-602E Biowhittaker). Let the cells grow overnight.

The next day, mix together in a sterile solution basin: 300 ul Lipofectamine (18324-012 Gibco/BRL) and 5ml Optimem I (31985070 Gibco/BRL)/96-well plate. With a small volume multi-channel pipetter, aliquot approximately 2ug of an expression vector containing a polynucleotide insert, produced by the methods described in Examples 8 or 9, into an appropriately labeled 96-well round bottom plate. With a multi-channel pipetter, add 50ul of the Lipofectamine/Optimem I mixture to each well. Pipette up and down gently to mix. Incubate at RT 15-45 minutes. After about 20 minutes, use a multi-channel pipetter to add 150ul Optimem I to each well. As a control, one plate of vector DNA lacking an insert should be transfected with each set of transfections.

Preferably, the transfection should be performed by tag-teaming the following tasks. By tag-teaming, hands on time is cut in half, and the cells do not spend too much time on PBS. First, person A aspirates off the media from four 24-well plates of cells, and then person B rinses each well with .5-1ml PBS. Person A then aspirates off PBS rinse, and person B, using a 12-channel pipetter with tips on every other channel, adds the 200ul of DNA/Lipofectamine/Optimem I complex to the odd wells first, then to the even wells, to each row on the 24-well plates. Incubate at 37°C for 6 hours.

While cells are incubating, prepare appropriate media, either 1%BSA in DMEM with 1x penstrep, or CHO-5 media (see below) with 2mm glutamine and 1x penstrep. (BSA (81-068-3 Bayer) 100gm dissolved in 1L DMEM for a 10% BSA stock solution). Filter the media and collect 50 ul for endotoxin assay in 15ml polystyrene conical.

The transfection reaction is terminated, preferably by tag-teaming, at the end of the incubation period. Person A aspirates off the transfection media, while person B adds 1.5ml appropriate media to each well. Incubate at 37°C for 45 or 72 hours depending on the media used: 1%BSA for 45 hours or CHO-5 for 72 hours.

On day four, using a 300ul multichannel pipetter, aliquot 600ul in one 1ml deep well plate and the remaining supernatant into a 2ml deep well. The supernatants from each well can then be used in the assays described in Examples 13-20.

It is specifically understood that when activity is obtained in any of the assays described below using a supernatant, the activity originates from either the polypeptide directly (e.g., as a secreted protein) or by the polypeptide inducing expression of other proteins, which are then secreted into the supernatant. Thus, the invention further provides a method of identifying the protein in the supernatant characterized by an activity in a particular assay.

HGS-CHO-5 medium formulation:**Inorganic Salts**

CaCl ₂ (anhyd)	116.6 mg/L
CuSO ₄ ·5H ₂ O	0.00130
Fe(NO ₃) ₃ ·9H ₂ O	0.050
FeSO ₄ ·7H ₂ O	0.417
KCl	311.80
MgCl ₂	28.64
MgSO ₄	48.84
NaCl	6995.50
NaHCO ₃	2400.0
NaH ₂ PO ₄ ·H ₂ O	62.50
Na ₂ HPO ₄	71.02
ZnSO ₄ ·7H ₂ O	.4320

5 Lipids

Arachidonic Acid	.002 mg/L
Cholesterol	1.022
DL-alpha-Tocopherol-Acetate	.070
Linoleic Acid	0.0520
Linolenic Acid	0.010
Myristic Acid	0.010
Oleic Acid	0.010
Palmitric Acid	0.010
Palmitic Acid	0.010
Pluronic F-68	100
Stearic Acid	0.010
Tween 80	2.20

Carbon Source

D-Glucose	4551 mg/L
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Amino Acids

L- Alanine	130.85 mg/ml
L-Arginine-HCL	147.50
L-Asparagine-H ₂ O	7.50
L-Aspartic Acid	6.65
L-Cystine-2HCL-H ₂ O	29.56
L-Cystine-2HCL	31.29
L-Glutamic Acid	7.35
L-Glutamine	365.0
Glycine	18.75
L-Histidine-HCL-	52.48

H ₂ O	
L-Isoleucine	106.97
L-Leucine	111.45
L-Lysine HCL	163.75
L-Methionine	32.34
L-Phenylalanine	68.48
L-Proline	40.0
L-Serine	26.25
L-Threonine	101.05
L-Tryptophan	19.22
L-Tyrosine-2Na-2H ₂ O	91.79
L-Valine	99.65

Vitamins

Biotin	0.0035 mg/L
D-Ca Pantothenate	3.24
Choline Chloride	11.78
Folic Acid	4.65
i-Inositol	15.60
Niacinamide	3.02
Pyridoxal HCL	3.00
Pyridoxine HCL	0.031
Riboflavin	0.319
Thiamine HCL	3.17
Thymidine	0.365
Vitamin B ₁₂	0.680

Other Components

HEPES Buffer	25 mM
Na Hypoxanthine	2.39 mg/L
Lipoic Acid	0.105
Sodium Putrescine-2HCL	0.081
Sodium Pyruvate	55.0
Sodium Selenite	0.0067
Ethanolamine	20uM
Ferric Citrate	0.122
Methyl-B-Cyclodextrin complexed with Linoleic Acid	41.70
Methyl-B-Cyclodextrin complexed with Oleic Acid	33.33
Methyl-B-Cyclodextrin complexed with Retinal Acetate	10

5

Adjust osmolarity to 327 mOsm

Example 12: Construction of GAS Reporter Construct

One signal transduction pathway involved in the differentiation and proliferation of cells is called the Jaks-STATs pathway. Activated proteins in the Jaks-STATs pathway bind to gamma activation site "GAS" elements or interferon-sensitive responsive element ("ISRE"), located in the promoter of many genes. The binding of a protein to these elements alter the expression of the associated gene.

GAS and ISRE elements are recognized by a class of transcription factors called Signal Transducers and Activators of Transcription, or "STATs." There are six members of the STATs family. Stat1 and Stat3 are present in many cell types, as is Stat2 (as response to IFN-alpha is widespread). Stat4 is more restricted and is not in many cell types though it has been found in T helper class I, cells after treatment with IL-12. Stat5 was originally called mammary growth factor, but has been found at higher concentrations in other cells including myeloid cells. It can be activated in tissue culture cells by many cytokines.

The STATs are activated to translocate from the cytoplasm to the nucleus upon tyrosine phosphorylation by a set of kinases known as the Janus Kinase ("Jaks") family. Jaks represent a distinct family of soluble tyrosine kinases and include Tyk2, Jak1, Jak2, and Jak3. These kinases display significant sequence similarity and are generally catalytically inactive in resting cells.

The Jaks are activated by a wide range of receptors summarized in the Table below. (Adapted from review by Schidler and Darnell, Ann. Rev. Biochem. 64:621-51 (1995).) A cytokine receptor family, capable of activating Jaks, is divided into two groups: (a) Class 1 includes receptors for IL-2, IL-3, IL-4, IL-6, IL-7, IL-9, IL-11, IL-12, IL-15, Epo, PRL, GH, G-CSF, GM-CSF, LIF, CNTF, and thrombopoietin; and (b) Class 2 includes IFN-a, IFN-g, and IL-10. The Class 1 receptors share a conserved cysteine motif (a set of four conserved cysteines and one tryptophan) and a WSXWS motif (a membrane proximal region encoding Trp-Ser-Xxx-Trp-Ser (SEQ ID NO:2)).

Thus, on binding of a ligand to a receptor, Jaks are activated, which in turn activate STATs, which then translocate and bind to GAS elements. This entire process is encompassed in the Jaks-STATs signal transduction pathway.

Therefore, activation of the Jaks-STATs pathway, reflected by the binding of the GAS or the ISRE element, can be used to indicate proteins involved in the proliferation and differentiation of cells. For example, growth factors and cytokines are known to activate the Jaks-STATs pathway. (See Table below.) Thus, by using GAS elements linked to reporter molecules, activators of the Jaks-STATs pathway can be identified.

	<u>ISRE</u> <u>Ligand</u>	<u>JAKs</u>				<u>STATS</u>	<u>GAS(elements) or</u>
		<u>tyk2</u>	<u>Jak1</u>	<u>Jak2</u>	<u>Jak3</u>		
5	<u>IFN family</u>						
	IFN-a/B	+	+	-	-	1,2,3	ISRE
	IFN-g (IRF1>Lys6>IFP)		+	+	-	1	GAS
	Il-10	+	?	?	-	1,3	
10	<u>gp130 family</u>						
	IL-6 (Pleiotrohic) (IRF1>Lys6>IFP)	+	+	+	?	1,3	GAS
	Il-11(Pleiotrohic)	?	+	?	?	1,3	
15	OnM(Pleiotrohic)	?	+	+	?	1,3	
	LIF(Pleiotrohic)	?	+	+	?	1,3	
	CNTF(Pleiotrohic)	-/+	+	+	?	1,3	
	G-CSF(Pleiotrohic)	?	+	?	?	1,3	
	IL-12(Pleiotrohic)	+	-	+	+	1,3	
20	<u>g-C family</u>						
	IL-2 (lymphocytes)	-	+	-	+	1,3,5	GAS
	IL-4 (lymph/myeloid) >>Ly6)(IgH)	-	+	-	+	6	GAS (IRF1 = IFP)
25	IL-7 (lymphocytes)	-	+	-	+	5	GAS
	IL-9 (lymphocytes)	-	+	-	+	5	GAS
	IL-13 (lymphocyte)	-	+	?	?	6	GAS
	IL-15	?	+	?	+	5	GAS
30	<u>gp140 family</u>						
	IL-3 (myeloid) (IRF1>IFP>>Ly6)	-	-	+	-	5	GAS
	IL-5 (myeloid)	-	-	+	-	5	GAS
	GM-CSF (myeloid)	-	-	+	-	5	GAS
35	<u>Growth hormone family</u>						
	GH	?	-	+	-	5	
	PRL	?	+/-	+	-	1,3,5	
	EPO	?	-	+	-	5	
40	CAS>IRF1=IFP>>Ly6)						GAS(B-
	<u>Receptor Tyrosine Kinases</u>						
	EGF	?	+	+	-	1,3	GAS (IRF1)
45	PDGF	?	+	+	-	1,3	
	CSF-1	?	+	+	-	1,3	GAS (not IRF1)

To construct a synthetic GAS containing promoter element, which is used in the Biological Assays described in Examples 13-14, a PCR based strategy is employed to generate a GAS-SV40 promoter sequence. The 5' primer contains four tandem copies of the GAS binding site found in the IRF1 promoter and previously demonstrated to
 5 bind STATs upon induction with a range of cytokines (Rothman et al., Immunity 1:457-468 (1994).), although other GAS or ISRE elements can be used instead. The 5' primer also contains 18bp of sequence complementary to the SV40 early promoter sequence and is flanked with an XhoI site. The sequence of the 5' primer is:
 5':GCGCCTCGAGATTTCCCGAAATCTAGATTTCCCGAAATGATTTCCCGG
 10 AAATGATTTCCCGAAATATCTGCCATCTCAATTAG:3' (SEQ ID NO:3)

The downstream primer is complementary to the SV40 promoter and is flanked with a Hind III site: 5':GCGGCAAGCTTTTTGCAAAGCCTAGGC:3' (SEQ ID NO:4)

PCR amplification is performed using the SV40 promoter template present in
 15 the B-gal:promoter plasmid obtained from Clontech. The resulting PCR fragment is digested with XhoI/Hind III and subcloned into BLSK2-. (Stratagene.) Sequencing with forward and reverse primers confirms that the insert contains the following sequence:
 5':CTCGAGATTTCCCGAAATCTAGATTTCCCGAAATGATTTCCCGAAATG
 20 ATTTCCCGAAATATCTGCCATCTCAATTAGTCAGCAACCATAGTCCCGCCC
 CTAATCCGCCCATCCCGCCCCTAACTCCGCCCAGTTCGCCCATTCTCCGC
 CCCATGGCTGACTAATTTTTTTTATTTATGCAGAGGCCGAGGCCGCCTCGGC
 CTCTGAGCTATTCCAGAAGTAGTGAGGAGGCTTTTTTGGAGGCCTAGGCTTT
 TGCAAAAAGCTT:3' (SEQ ID NO:5)

25 With this GAS promoter element linked to the SV40 promoter, a GAS:SEAP2 reporter construct is next engineered. Here, the reporter molecule is a secreted alkaline phosphatase, or "SEAP." Clearly, however, any reporter molecule can be instead of SEAP, in this or in any of the other Examples. Well known reporter molecules that can
 30 be used instead of SEAP include chloramphenicol acetyltransferase (CAT), luciferase, alkaline phosphatase, B-galactosidase, green fluorescent protein (GFP), or any protein detectable by an antibody.

The above sequence confirmed synthetic GAS-SV40 promoter element is subcloned into the pSEAP-Promoter vector obtained from Clontech using HindIII and
 35 XhoI, effectively replacing the SV40 promoter with the amplified GAS:SV40 promoter element, to create the GAS-SEAP vector. However, this vector does not contain a

neomycin resistance gene, and therefore, is not preferred for mammalian expression systems.

Thus, in order to generate mammalian stable cell lines expressing the GAS-SEAP reporter, the GAS-SEAP cassette is removed from the GAS-SEAP vector using
5 Sall and NotI, and inserted into a backbone vector containing the neomycin resistance gene, such as pGFP-1 (Clontech), using these restriction sites in the multiple cloning site, to create the GAS-SEAP/Neo vector. Once this vector is transfected into mammalian cells, this vector can then be used as a reporter molecule for GAS binding as described in Examples 13-14.

10 Other constructs can be made using the above description and replacing GAS with a different promoter sequence. For example, construction of reporter molecules containing NFK-B and EGR promoter sequences are described in Examples 15 and 16. However, many other promoters can be substituted using the protocols described in these Examples. For instance, SRE, IL-2, NFAT, or Osteocalcin promoters can be
15 substituted, alone or in combination (e.g., GAS/NF-KB/EGR, GAS/NF-KB, IL-2/NFAT, or NF-KB/GAS). Similarly, other cell lines can be used to test reporter construct activity, such as HELA (epithelial), HUVEC (endothelial), Reh (B-cell), Saos-2 (osteoblast), HUVAC (aortic), or Cardiomyocyte.

20 **Example 13: High-Throughput Screening Assay for T-cell Activity.**

The following protocol is used to assess T-cell activity by identifying factors, such as growth factors and cytokines, that may proliferate or differentiate T-cells. T-cell activity is assessed using the GAS/SEAP/Neo construct produced in Example 12. Thus, factors that increase SEAP activity indicate the ability to activate the Jaks-STATS
25 signal transduction pathway. The T-cell used in this assay is Jurkat T-cells (ATCC Accession No. TIB-152), although Molt-3 cells (ATCC Accession No. CRL-1552) and Molt-4 cells (ATCC Accession No. CRL-1582) cells can also be used.

Jurkat T-cells are lymphoblastic CD4+ Th1 helper cells. In order to generate stable cell lines, approximately 2 million Jurkat cells are transfected with the GAS-
30 SEAP/neo vector using DMRIE-C (Life Technologies)(transfection procedure described below). The transfected cells are seeded to a density of approximately 20,000 cells per well and transfectants resistant to 1 mg/ml gentamicin selected. Resistant colonies are expanded and then tested for their response to increasing concentrations of interferon gamma. The dose response of a selected clone is demonstrated.

35 Specifically, the following protocol will yield sufficient cells for 75 wells containing 200 ul of cells. Thus, it is either scaled up, or performed in multiple to generate sufficient cells for multiple 96 well plates. Jurkat cells are maintained in RPMI

+ 10% serum with 1% Pen-Strep. Combine 2.5 mls of OPTI-MEM (Life Technologies) with 10 ug of plasmid DNA in a T25 flask. Add 2.5 ml OPTI-MEM containing 50 ul of DMRIE-C and incubate at room temperature for 15-45 mins.

5 During the incubation period, count cell concentration, spin down the required number of cells (10^7 per transfection), and resuspend in OPTI-MEM to a final concentration of 10^7 cells/ml. Then add 1ml of 1×10^7 cells in OPTI-MEM to T25 flask and incubate at 37°C for 6 hrs. After the incubation, add 10 ml of RPMI + 15% serum.

10 The Jurkat:GAS-SEAP stable reporter lines are maintained in RPMI + 10% serum, 1 mg/ml Gentamicin, and 1% Pen-Strep. These cells are treated with supernatants containing a polypeptide as produced by the protocol described in Example 11.

On the day of treatment with the supernatant, the cells should be washed and resuspended in fresh RPMI + 10% serum to a density of 500,000 cells per ml. The exact number of cells required will depend on the number of supernatants being screened. For one 96 well plate, approximately 10 million cells (for 10 plates, 100 million cells) are required.

Transfer the cells to a triangular reservoir boat, in order to dispense the cells into a 96 well dish, using a 12 channel pipette. Using a 12 channel pipette, transfer 200 ul of cells into each well (therefore adding 100, 000 cells per well).

20 After all the plates have been seeded, 50 ul of the supernatants are transferred directly from the 96 well plate containing the supernatants into each well using a 12 channel pipette. In addition, a dose of exogenous interferon gamma (0.1, 1.0, 10 ng) is added to wells H9, H10, and H11 to serve as additional positive controls for the assay.

25 The 96 well dishes containing Jurkat cells treated with supernatants are placed in an incubator for 48 hrs (note: this time is variable between 48-72 hrs). 35 ul samples from each well are then transferred to an opaque 96 well plate using a 12 channel pipette. The opaque plates should be covered (using sellophane covers) and stored at -20°C until SEAP assays are performed according to Example 17. The plates containing the remaining treated cells are placed at 4°C and serve as a source of material for repeating the assay on a specific well if desired.

30 As a positive control, 100 Unit/ml interferon gamma can be used which is known to activate Jurkat T cells. Over 30 fold induction is typically observed in the positive control wells.

Example 14: High-Throughput Screening Assay Identifying Myeloid Activity

The following protocol is used to assess myeloid activity by identifying factors, such as growth factors and cytokines, that may proliferate or differentiate myeloid cells.

- 5 Myeloid cell activity is assessed using the GAS/SEAP/Neo construct produced in Example 12. Thus, factors that increase SEAP activity indicate the ability to activate the Jaks-STATS signal transduction pathway. The myeloid cell used in this assay is U937, a pre-monocyte cell line, although TF-1, HL60, or KG1 can be used.

- 10 To transiently transfect U937 cells with the GAS/SEAP/Neo construct produced in Example 12, a DEAE-Dextran method (Kharbanda et. al., 1994, Cell Growth & Differentiation, 5:259-265) is used. First, harvest 2×10^7 U937 cells and wash with PBS. The U937 cells are usually grown in RPMI 1640 medium containing 10% heat-inactivated fetal bovine serum (FBS) supplemented with 100 units/ml penicillin and 100 mg/ml streptomycin.

- 15 Next, suspend the cells in 1 ml of 20 mM Tris-HCl (pH 7.4) buffer containing 0.5 mg/ml DEAE-Dextran, 8 ug GAS-SEAP2 plasmid DNA, 140 mM NaCl, 5 mM KCl, 375 uM $\text{Na}_2\text{HPO}_4 \cdot 7\text{H}_2\text{O}$, 1 mM MgCl_2 , and 675 uM CaCl_2 . Incubate at 37°C for 45 min.

- 20 Wash the cells with RPMI 1640 medium containing 10% FBS and then resuspend in 10 ml complete medium and incubate at 37°C for 36 hr.

The GAS-SEAP/U937 stable cells are obtained by growing the cells in 400 ug/ml G418. The G418-free medium is used for routine growth but every one to two months, the cells should be re-grown in 400 ug/ml G418 for couple of passages.

- 25 These cells are tested by harvesting 1×10^8 cells (this is enough for ten 96-well plates assay) and wash with PBS. Suspend the cells in 200 ml above described growth medium, with a final density of 5×10^5 cells/ml. Plate 200 ul cells per well in the 96-well plate (or 1×10^5 cells/well).

- 30 Add 50 ul of the supernatant prepared by the protocol described in Example 11. Incubate at 37°C for 48 to 72 hr. As a positive control, 100 Unit/ml interferon gamma can be used which is known to activate U937 cells. Over 30 fold induction is typically observed in the positive control wells. SEAP assay the supernatant according to the protocol described in Example 17.

Example 15: High-Throughput Screening Assay Identifying Neuronal Activity.

When cells undergo differentiation and proliferation, a group of genes are activated through many different signal transduction pathways. One of these genes,
5 EGR1 (early growth response gene 1), is induced in various tissues and cell types upon activation. The promoter of EGR1 is responsible for such induction. Using the EGR1 promoter linked to reporter molecules, activation of cells can be assessed.

Particularly, the following protocol is used to assess neuronal activity in PC12 cell lines. PC12 cells (rat phenochromocytoma cells) are known to proliferate and/or
10 differentiate by activation with a number of mitogens, such as TPA (tetradecanoyl phorbol acetate), NGF (nerve growth factor), and EGF (epidermal growth factor). The EGR1 gene expression is activated during this treatment. Thus, by stably transfecting PC12 cells with a construct containing an EGR promoter linked to SEAP reporter, activation of PC12 cells can be assessed.

15 The EGR/SEAP reporter construct can be assembled by the following protocol. The EGR-1 promoter sequence (-633 to +1)(Sakamoto K et al., Oncogene 6:867-871 (1991)) can be PCR amplified from human genomic DNA using the following primers:

20 5' GCGCTCGAGGGATGACAGCGATAGAACCCCGG -3' (SEQ ID NO:6)
5' GCGAAGCTTCGCGACTCCCCGGATCCGCCTC-3' (SEQ ID NO:7)

Using the GAS:SEAP/Neo vector produced in Example 12, EGR1 amplified product can then be inserted into this vector. Linearize the GAS:SEAP/Neo vector using restriction enzymes XhoI/HindIII, removing the GAS/SV40 stuffer. Restrict the
25 EGR1 amplified product with these same enzymes. Ligate the vector and the EGR1 promoter.

To prepare 96 well-plates for cell culture, two mls of a coating solution (1:30 dilution of collagen type I (Upstate Biotech Inc. Cat#08-115) in 30% ethanol (filter sterilized)) is added per one 10 cm plate or 50 ml per well of the 96-well plate, and
30 allowed to air dry for 2 hr.

PC12 cells are routinely grown in RPMI-1640 medium (Bio Whittaker) containing 10% horse serum (JRH BIOSCIENCES, Cat. # 12449-78P), 5% heat-inactivated fetal bovine serum (FBS) supplemented with 100 units/ml penicillin and 100 ug/ml streptomycin on a precoated 10 cm tissue culture dish. One to four split is done
35 every three to four days. Cells are removed from the plates by scraping and resuspended with pipetting up and down for more than 15 times.

Transfect the EGR/SEAP/Neo construct into PC12 using the Lipofectamine protocol described in Example 11. EGR-SEAP/PC12 stable cells are obtained by growing the cells in 300 ug/ml G418. The G418-free medium is used for routine growth but every one to two months, the cells should be re-grown in 300 ug/ml G418 for couple of passages.

To assay for neuronal activity, a 10 cm plate with cells around 70 to 80% confluent is screened by removing the old medium. Wash the cells once with PBS (Phosphate buffered saline). Then starve the cells in low serum medium (RPMI-1640 containing 1% horse serum and 0.5% FBS with antibiotics) overnight.

The next morning, remove the medium and wash the cells with PBS. Scrape off the cells from the plate, suspend the cells well in 2 ml low serum medium. Count the cell number and add more low serum medium to reach final cell density as 5×10^5 cells/ml.

Add 200 ul of the cell suspension to each well of 96-well plate (equivalent to 1×10^5 cells/well). Add 50 ul supernatant produced by Example 11, 37°C for 48 to 72 hr. As a positive control, a growth factor known to activate PC12 cells through EGR can be used, such as 50 ng/ul of Neuronal Growth Factor (NGF). Over fifty-fold induction of SEAP is typically seen in the positive control wells. SEAP assay the supernatant according to Example 17.

Example 16: High-Throughput Screening Assay for T-cell Activity

NF- κ B (Nuclear Factor κ B) is a transcription factor activated by a wide variety of agents including the inflammatory cytokines IL-1 and TNF, CD30 and CD40, lymphotoxin-alpha and lymphotoxin-beta, by exposure to LPS or thrombin, and by expression of certain viral gene products. As a transcription factor, NF- κ B regulates the expression of genes involved in immune cell activation, control of apoptosis (NF- κ B appears to shield cells from apoptosis), B and T-cell development, anti-viral and antimicrobial responses, and multiple stress responses.

In non-stimulated conditions, NF- κ B is retained in the cytoplasm with I- κ B (Inhibitor κ B). However, upon stimulation, I- κ B is phosphorylated and degraded, causing NF- κ B to shuttle to the nucleus, thereby activating transcription of target genes. Target genes activated by NF- κ B include IL-2, IL-6, GM-CSF, ICAM-1 and class I MHC.

Due to its central role and ability to respond to a range of stimuli, reporter constructs utilizing the NF- κ B promoter element are used to screen the supernatants produced in Example 11. Activators or inhibitors of NF- κ B would be useful in treating diseases. For example, inhibitors of NF- κ B could be used to treat those diseases
5 related to the acute or chronic activation of NF- κ B, such as rheumatoid arthritis.

To construct a vector containing the NF- κ B promoter element, a PCR based strategy is employed. The upstream primer contains four tandem copies of the NF- κ B binding site (GGGGACTTTCCC) (SEQ ID NO:8), 18 bp of sequence complementary to the 5' end of the SV40 early promoter sequence, and is flanked with an XhoI site:
10 5':GCGGCCTCGAGGGGACTTTCCCGGGGACTTTCCGGGGACTTTCCGGGGAC
TTTCCATCCTGCCATCTCAATTAG:3' (SEQ ID NO:9)

The downstream primer is complementary to the 3' end of the SV40 promoter and is flanked with a Hind III site:

5':GCGGCAAGCTTTTTGCAAAGCCTAGGC:3' (SEQ ID NO:4)

15 PCR amplification is performed using the SV40 promoter template present in the pB-gal:promoter plasmid obtained from Clontech. The resulting PCR fragment is digested with XhoI and Hind III and subcloned into BLSK2-. (Stratagene)
Sequencing with the T7 and T3 primers confirms the insert contains the following sequence:

20 5':CTCGAGGGGACTTTCCCGGGGACTTTCCGGGGACTTTCCGGGGACTTTCC
ATCTGCCATCTCAATTAGTCAGCAACCATAGTCCCGCCCCTAACTCCGCCCCA
TCCCGCCCCTAACTCCGCCCAGTTCCGCCCATTCTCCGCCCCATGGCTGACT
AATTTTTTTTTATTTATGCAGAGGCCGAGGCCGCTCGGCCTCTGAGCTATTC
CAGAAGTAGTGAGGAGGCTTTTTTGGAGGCCTAGGCTTTTGCAAAAAGCTT:
25 3' (SEQ ID NO:10)

Next, replace the SV40 minimal promoter element present in the pSEAP2- promoter plasmid (Clontech) with this NF- κ B/SV40 fragment using XhoI and HindIII. However, this vector does not contain a neomycin resistance gene, and therefore, is not
30 preferred for mammalian expression systems.

In order to generate stable mammalian cell lines, the NF- κ B/SV40/SEAP cassette is removed from the above NF- κ B/SEAP vector using restriction enzymes SalI and NotI, and inserted into a vector containing neomycin resistance. Particularly, the

NF- κ B/SV40/SEAP cassette was inserted into pGFP-1 (Clontech), replacing the GFP gene, after restricting pGFP-1 with SalI and NotI.

- Once NF- κ B/SV40/SEAP/Neo vector is created, stable Jurkat T-cells are created and maintained according to the protocol described in Example 13. Similarly, the method for assaying supernatants with these stable Jurkat T-cells is also described in Example 13. As a positive control, exogenous TNF alpha (0.1, 1, 10 ng) is added to wells H9, H10, and H11, with a 5-10 fold activation typically observed.

Example 17: Assay for SEAP Activity

- As a reporter molecule for the assays described in Examples 13-16, SEAP activity is assayed using the Tropix Phospho-light Kit (Cat. BP-400) according to the following general procedure. The Tropix Phospho-light Kit supplies the Dilution, Assay, and Reaction Buffers used below.

- Prime a dispenser with the 2.5x Dilution Buffer and dispense 15 μ l of 2.5x dilution buffer into Optiplates containing 35 μ l of a supernatant. Seal the plates with a plastic sealer and incubate at 65°C for 30 min. Separate the Optiplates to avoid uneven heating.

- Cool the samples to room temperature for 15 minutes. Empty the dispenser and prime with the Assay Buffer. Add 50 μ l Assay Buffer and incubate at room temperature 5 min. Empty the dispenser and prime with the Reaction Buffer (see the table below). Add 50 μ l Reaction Buffer and incubate at room temperature for 20 minutes. Since the intensity of the chemiluminescent signal is time dependent, and it takes about 10 minutes to read 5 plates on luminometer, one should treat 5 plates at each time and start the second set 10 minutes later.

- Read the relative light unit in the luminometer. Set H12 as blank, and print the results. An increase in chemiluminescence indicates reporter activity.

Reaction Buffer Formulation:

# of plates	Rxn buffer diluent (ml)	CSPD (ml)
10	60	3
11	65	3.25
12	70	3.5
13	75	3.75
14	80	4

15	85	4.25
16	90	4.5
17	95	4.75
18	100	5
19	105	5.25
20	110	5.5
21	115	5.75
22	120	6
23	125	6.25
24	130	6.5
25	135	6.75
26	140	7
27	145	7.25
28	150	7.5
29	155	7.75
30	160	8
31	165	8.25
32	170	8.5
33	175	8.75
34	180	9
35	185	9.25
36	190	9.5
37	195	9.75
38	200	10
39	205	10.25
40	210	10.5
41	215	10.75
42	220	11
43	225	11.25
44	230	11.5
45	235	11.75
46	240	12
47	245	12.25
48	250	12.5
49	255	12.75
50	260	13

Example 18: High-Throughput Screening Assay Identifying Changes in Small Molecule Concentration and Membrane Permeability

Binding of a ligand to a receptor is known to alter intracellular levels of small molecules, such as calcium, potassium, sodium, and pH, as well as alter membrane potential. These alterations can be measured in an assay to identify supernatants which bind to receptors of a particular cell. Although the following protocol describes an assay for calcium, this protocol can easily be modified to detect changes in potassium, sodium, pH, membrane potential, or any other small molecule which is detectable by a fluorescent probe.

The following assay uses Fluorometric Imaging Plate Reader ("FLIPR") to measure changes in fluorescent molecules (Molecular Probes) that bind small molecules. Clearly, any fluorescent molecule detecting a small molecule can be used instead of the calcium fluorescent molecule, fluo-3, used here.

For adherent cells, seed the cells at 10,000 -20,000 cells/well in a Co-star black 96-well plate with clear bottom. The plate is incubated in a CO₂ incubator for 20 hours. The adherent cells are washed two times in Biotek washer with 200 ul of HBSS (Hank's Balanced Salt Solution) leaving 100 ul of buffer after the final wash.

A stock solution of 1 mg/ml fluo-3 is made in 10% pluronic acid DMSO. To load the cells with fluo-3, 50 ul of 12 ug/ml fluo-3 is added to each well. The plate is incubated at 37°C in a CO₂ incubator for 60 min. The plate is washed four times in the Biotek washer with HBSS leaving 100 ul of buffer.

For non-adherent cells, the cells are spun down from culture media. Cells are re-suspended to 2-5x10⁶ cells/ml with HBSS in a 50-ml conical tube. 4 ul of 1 mg/ml fluo-3 solution in 10% pluronic acid DMSO is added to each ml of cell suspension. The tube is then placed in a 37°C water bath for 30-60 min. The cells are washed twice with HBSS, resuspended to 1x10⁶ cells/ml, and dispensed into a microplate, 100 ul/well. The plate is centrifuged at 1000 rpm for 5 min. The plate is then washed once in Denley CellWash with 200 ul, followed by an aspiration step to 100 ul final volume.

For a non-cell based assay, each well contains a fluorescent molecule, such as fluo-3. The supernatant is added to the well, and a change in fluorescence is detected.

To measure the fluorescence of intracellular calcium, the FLIPR is set for the following parameters: (1) System gain is 300-800 mW; (2) Exposure time is 0.4 second; (3) Camera F/stop is F/2; (4) Excitation is 488 nm; (5) Emission is 530 nm; and (6) Sample addition is 50 ul. Increased emission at 530 nm indicates an extracellular

signaling even which has resulted in an increase in the intracellular Ca^{++} concentration.

Example 19: High-Throughput Screening Assay Identifying Tyrosine

5 Kinase Activity

The Protein Tyrosine Kinases (PTK) represent a diverse group of transmembrane and cytoplasmic kinases. Within the Receptor Protein Tyrosine Kinase (RPTK) group are receptors for a range of mitogenic and metabolic growth factors including the PDGF, FGF, EGF, NGF, HGF and Insulin receptor subfamilies. In addition there are a large family of RPTKs for which the corresponding ligand is unknown. Ligands for RPTKs include mainly secreted small proteins, but also membrane-bound and extracellular matrix proteins.

Activation of RPTK by ligands involves ligand-mediated receptor dimerization, resulting in transphosphorylation of the receptor subunits and activation of the cytoplasmic tyrosine kinases. The cytoplasmic tyrosine kinases include receptor associated tyrosine kinases of the src-family (e.g., src, yes, lck, lyn, fyn) and non-receptor linked and cytosolic protein tyrosine kinases, such as the Jak family, members of which mediate signal transduction triggered by the cytokine superfamily of receptors (e.g., the Interleukins, Interferons, GM-CSF, and Leptin).

Because of the wide range of known factors capable of stimulating tyrosine kinase activity, the identification of novel human secreted proteins capable of activating tyrosine kinase signal transduction pathways are of interest. Therefore, the following protocol is designed to identify those novel human secreted proteins capable of activating the tyrosine kinase signal transduction pathways.

Seed target cells (e.g., primary keratinocytes) at a density of approximately 25,000 cells per well in a 96 well Loprodyne Silent Screen Plates purchased from Nalge Nunc (Naperville, IL). The plates are sterilized with two 30 minute rinses with 100% ethanol, rinsed with water and dried overnight. Some plates are coated for 2 hr with 100 ml of cell culture grade type I collagen (50 mg/ml), gelatin (2%) or polylysine (50 mg/ml), all of which can be purchased from Sigma Chemicals (St. Louis, MO) or 10% Matrigel purchased from Becton Dickinson (Bedford, MA), or calf serum, rinsed with PBS and stored at 4°C. Cell growth on these plates is assayed by seeding 5,000 cells/well in growth medium and indirect quantitation of cell number through use of alamarBlue as described by the manufacturer Alamar Biosciences, Inc. (Sacramento, CA) after 48 hr. Falcon plate covers #3071 from Becton Dickinson (Bedford, MA) are

used to cover the Loprodyne Silent Screen Plates. Falcon Microtest III cell culture plates can also be used in some proliferation experiments.

To prepare extracts, A431 cells are seeded onto the nylon membranes of Loprodyne plates (20,000/200ml/well) and cultured overnight in complete medium.

- 5 Cells are quiesced by incubation in serum-free basal medium for 24 hr. After 5-20 minutes treatment with EGF (60ng/ml) or 50 ul of the supernatant produced in Example 11, the medium was removed and 100 ml of extraction buffer ((20 mM HEPES pH 7.5, 0.15 M NaCl, 1% Triton X-100, 0.1% SDS, 2 mM Na₃VO₄, 2 mM Na₄P₂O₇ and a cocktail of protease inhibitors (# 1836170) obtained from Boehringer Mannheim
- 10 (Indianapolis, IN) is added to each well and the plate is shaken on a rotating shaker for 5 minutes at 4°C. The plate is then placed in a vacuum transfer manifold and the extract filtered through the 0.45 mm membrane bottoms of each well using house vacuum. Extracts are collected in a 96-well catch/assay plate in the bottom of the vacuum manifold and immediately placed on ice. To obtain extracts clarified by centrifugation,
- 15 the content of each well, after detergent solubilization for 5 minutes, is removed and centrifuged for 15 minutes at 4°C at 16,000 x g.

Test the filtered extracts for levels of tyrosine kinase activity. Although many methods of detecting tyrosine kinase activity are known, one method is described here.

- Generally, the tyrosine kinase activity of a supernatant is evaluated by
- 20 determining its ability to phosphorylate a tyrosine residue on a specific substrate (a biotinylated peptide). Biotinylated peptides that can be used for this purpose include PSK1 (corresponding to amino acids 6-20 of the cell division kinase cdc2-p34) and PSK2 (corresponding to amino acids 1-17 of gastrin). Both peptides are substrates for a range of tyrosine kinases and are available from Boehringer Mannheim.

- 25 The tyrosine kinase reaction is set up by adding the following components in order. First, add 10ul of 5uM Biotinylated Peptide, then 10ul ATP/Mg₂⁺ (5mM ATP/50mM MgCl₂), then 10ul of 5x Assay Buffer (40mM imidazole hydrochloride, pH7.3, 40 mM beta-glycerophosphate, 1mM EGTA, 100mM MgCl₂, 5 mM MnCl₂, 0.5 mg/ml BSA), then 5ul of Sodium Vanadate(1mM), and then 5ul of water. Mix the
- 30 components gently and preincubate the reaction mix at 30°C for 2 min. Initiate the reaction by adding 10ul of the control enzyme or the filtered supernatant.

The tyrosine kinase assay reaction is then terminated by adding 10 ul of 120mM EDTA and place the reactions on ice.

- Tyrosine kinase activity is determined by transferring 50 ul aliquot of reaction
- 35 mixture to a microtiter plate (MTP) module and incubating at 37°C for 20 min. This

allows the streptavidin coated 96 well plate to associate with the biotinylated peptide. Wash the MTP module with 300ul/well of PBS four times. Next add 75 ul of anti-phosphotyrosine antibody conjugated to horse radish peroxidase(anti-P-Tyr-POD(0.5u/ml)) to each well and incubate at 37°C for one hour. Wash the well as
5 above.

Next add 100ul of peroxidase substrate solution (Boehringer Mannheim) and incubate at room temperature for at least 5 mins (up to 30 min). Measure the absorbance of the sample at 405 nm by using ELISA reader. The level of bound peroxidase activity is quantitated using an ELISA reader and reflects the level of
10 tyrosine kinase activity.

Example 20: High-Throughput Screening Assay Identifying Phosphorylation Activity

As a potential alternative and/or complement to the assay of protein tyrosine
15 kinase activity described in Example 19, an assay which detects activation (phosphorylation) of major intracellular signal transduction intermediates can also be used. For example, as described below one particular assay can detect tyrosine phosphorylation of the Erk-1 and Erk-2 kinases. However, phosphorylation of other molecules, such as Raf, JNK, p38 MAP, Map kinase kinase (MEK), MEK kinase,
20 Src, Muscle specific kinase (MuSK), IRAK, Tec, and Janus, as well as any other phosphoserine, phosphotyrosine, or phosphothreonine molecule, can be detected by substituting these molecules for Erk-1 or Erk-2 in the following assay.

Specifically, assay plates are made by coating the wells of a 96-well ELISA plate with 0.1ml of protein G (1ug/ml) for 2 hr at room temp, (RT). The plates are then
25 rinsed with PBS and blocked with 3% BSA/PBS for 1 hr at RT. The protein G plates are then treated with 2 commercial monoclonal antibodies (100ng/well) against Erk-1 and Erk-2 (1 hr at RT) (Santa Cruz Biotechnology). (To detect other molecules, this step can easily be modified by substituting a monoclonal antibody detecting any of the above described molecules.) After 3-5 rinses with PBS, the plates are stored at 4°C
30 until use.

A431 cells are seeded at 20,000/well in a 96-well Loprodyne filterplate and cultured overnight in growth medium. The cells are then starved for 48 hr in basal medium (DMEM) and then treated with EGF (6ng/well) or 50 ul of the supernatants obtained in Example 11 for 5-20 minutes. The cells are then solubilized and extracts
35 filtered directly into the assay plate.

After incubation with the extract for 1 hr at RT, the wells are again rinsed. As a positive control, a commercial preparation of MAP kinase (10ng/well) is used in place of A431 extract. Plates are then treated with a commercial polyclonal (rabbit) antibody (1ug/ml) which specifically recognizes the phosphorylated epitope of the Erk-1 and Erk-2 kinases (1 hr at RT). This antibody is biotinylated by standard procedures. The bound polyclonal antibody is then quantitated by successive incubations with Europium-streptavidin and Europium fluorescence enhancing reagent in the Wallac DELFIA instrument (time-resolved fluorescence). An increased fluorescent signal over background indicates a phosphorylation.

Example 21: Method of Determining Alterations in a Gene Corresponding to a Polynucleotide

RNA isolated from entire families or individual patients presenting with a phenotype of interest (such as a disease) is be isolated. cDNA is then generated from these RNA samples using protocols known in the art. (See, Sambrook.) The cDNA is then used as a template for PCR, employing primers surrounding regions of interest in SEQ ID NO:X. Suggested PCR conditions consist of 35 cycles at 95°C for 30 seconds; 60-120 seconds at 52-58°C; and 60-120 seconds at 70°C, using buffer solutions described in Sidransky, D., et al., Science 252:706 (1991).

PCR products is then sequenced using primers labeled at their 5' end with T4 polynucleotide kinase, employing SequiTherm Polymerase. (Epicentre Technologies). The intron-exon borders of selected exons is also determined and genomic PCR products analyzed to confirm the results. PCR products harboring suspected mutations is then cloned and sequenced to validate the results of the direct sequencing.

PCR products is cloned into T-tailed vectors as described in Holton, T.A. and Graham, M.W., Nucleic Acids Research, 19:1156 (1991) and sequenced with T7 polymerase (United States Biochemical). Affected individuals is identified by mutations not present in unaffected individuals.

Genomic rearrangements are also observed as a method of determining alterations in a gene corresponding to a polynucleotide. Genomic clones isolated according to Example 2 are nick-translated with digoxigenindeoxy-uridine 5'-triphosphate (Boehringer Mannheim), and FISH performed as described in Johnson, Cg. et al., Methods Cell Biol. 35:73-99 (1991). Hybridization with the labeled probe is carried out using a vast excess of human cot-1 DNA for specific hybridization to the corresponding genomic locus.

Chromosomes are counterstained with 4,6-diamino-2-phenylidole and propidium iodide, producing a combination of C- and R-bands. Aligned images for precise mapping are obtained using a triple-band filter set (Chroma Technology, Brattleboro, VT) in combination with a cooled charge-coupled device camera
5 (Photometrics, Tucson, AZ) and variable excitation wavelength filters. (Johnson, Cv. et al., Genet. Anal. Tech. Appl., 8:75 (1991).) Image collection, analysis and chromosomal fractional length measurements are performed using the ISee Graphical Program System. (Inovision Corporation, Durham, NC.) Chromosome alterations of the genomic region hybridized by the probe are identified as insertions, deletions, and
10 translocations. These alterations are used as a diagnostic marker for an associated disease.

Example 22: Method of Detecting Abnormal Levels of a Polypeptide in a Biological Sample

15 A polypeptide of the present invention can be detected in a biological sample, and if an increased or decreased level of the polypeptide is detected, this polypeptide is a marker for a particular phenotype. Methods of detection are numerous, and thus, it is understood that one skilled in the art can modify the following assay to fit their particular needs.

20 For example, antibody-sandwich ELISAs are used to detect soluble polypeptides in a sample, preferably a biological sample. Wells of a microtiter plate are coated with specific antibodies, at a final concentration of 0.2 to 10 ug/ml. The antibodies are either monoclonal or polyclonal and are produced by the method described in Example 10. The wells are blocked so that non-specific binding of the
25 polypeptide to the well is reduced.

The coated wells are then incubated for > 2 hours at RT with a sample containing the polypeptide. Preferably, serial dilutions of the sample should be used to validate results. The plates are then washed three times with deionized or distilled water to remove unbounded polypeptide.

30 Next, 50 ul of specific antibody-alkaline phosphatase conjugate, at a concentration of 25-400 ng, is added and incubated for 2 hours at room temperature. The plates are again washed three times with deionized or distilled water to remove unbounded conjugate.

35 Add 75 ul of 4-methylumbelliferyl phosphate (MUP) or p-nitrophenyl phosphate (NPP) substrate solution to each well and incubate 1 hour at room temperature. Measure the reaction by a microtiter plate reader. Prepare a standard curve, using serial dilutions of a control sample, and plot polypeptide concentration on

the X-axis (log scale) and fluorescence or absorbance of the Y-axis (linear scale).
Interpolate the concentration of the polypeptide in the sample using the standard curve.

Example 23: Formulating a Polypeptide

5 The secreted polypeptide composition will be formulated and dosed in a fashion consistent with good medical practice, taking into account the clinical condition of the individual patient (especially the side effects of treatment with the secreted polypeptide alone), the site of delivery, the method of administration, the scheduling of administration, and other factors known to practitioners. The "effective amount" for
10 purposes herein is thus determined by such considerations.

 As a general proposition, the total pharmaceutically effective amount of secreted polypeptide administered parenterally per dose will be in the range of about 1 µg/kg/day to 10 mg/kg/day of patient body weight, although, as noted above, this will be subject to therapeutic discretion. More preferably, this dose is at least 0.01 mg/kg/day, and
15 most preferably for humans between about 0.01 and 1 mg/kg/day for the hormone. If given continuously, the secreted polypeptide is typically administered at a dose rate of about 1 µg/kg/hour to about 50 µg/kg/hour, either by 1-4 injections per day or by continuous subcutaneous infusions, for example, using a mini-pump. An intravenous bag solution may also be employed. The length of treatment needed to observe changes
20 and the interval following treatment for responses to occur appears to vary depending on the desired effect.

 Pharmaceutical compositions containing the secreted protein of the invention are administered orally, rectally, parenterally, intracisternally, intravaginally, intraperitoneally, topically (as by powders, ointments, gels, drops or transdermal
25 patch), buccally, or as an oral or nasal spray. "Pharmaceutically acceptable carrier" refers to a non-toxic solid, semisolid or liquid filler, diluent, encapsulating material or formulation auxiliary of any type. The term "parenteral" as used herein refers to modes of administration which include intravenous, intramuscular, intraperitoneal, intrasternal, subcutaneous and intraarticular injection and infusion.

30 The secreted polypeptide is also suitably administered by sustained-release systems. Suitable examples of sustained-release compositions include semi-permeable polymer matrices in the form of shaped articles, e.g., films, or microcapsules. Sustained-release matrices include polylactides (U.S. Pat. No. 3,773,919, EP 58,481), copolymers of L-glutamic acid and gamma-ethyl-L-glutamate (Sidman, U. et al.,
35 Biopolymers 22:547-556 (1983)), poly (2- hydroxyethyl methacrylate) (R. Langer et al., J. Biomed. Mater. Res. 15:167-277 (1981), and R. Langer, Chem. Tech. 12:98-105 (1982)), ethylene vinyl acetate (R. Langer et al.) or poly-D- (-)-3-hydroxybutyric

acid (EP 133,988). Sustained-release compositions also include liposomally entrapped polypeptides. Liposomes containing the secreted polypeptide are prepared by methods known per se: DE 3,218,121; Epstein et al., Proc. Natl. Acad. Sci. USA 82:3688-3692 (1985); Hwang et al., Proc. Natl. Acad. Sci. USA 77:4030-4034 (1980); EP 52,322; EP 36,676; EP 88,046; EP 143,949; EP 142,641; Japanese Pat. Appl. 83-118008; U.S. Pat. Nos. 4,485,045 and 4,544,545; and EP 102,324. Ordinarily, the liposomes are of the small (about 200-800 Angstroms) unilamellar type in which the lipid content is greater than about 30 mol. percent cholesterol, the selected proportion being adjusted for the optimal secreted polypeptide therapy.

For parenteral administration, in one embodiment, the secreted polypeptide is formulated generally by mixing it at the desired degree of purity, in a unit dosage injectable form (solution, suspension, or emulsion), with a pharmaceutically acceptable carrier, i.e., one that is non-toxic to recipients at the dosages and concentrations employed and is compatible with other ingredients of the formulation. For example, the formulation preferably does not include oxidizing agents and other compounds that are known to be deleterious to polypeptides.

Generally, the formulations are prepared by contacting the polypeptide uniformly and intimately with liquid carriers or finely divided solid carriers or both. Then, if necessary, the product is shaped into the desired formulation. Preferably the carrier is a parenteral carrier, more preferably a solution that is isotonic with the blood of the recipient. Examples of such carrier vehicles include water, saline, Ringer's solution, and dextrose solution. Non-aqueous vehicles such as fixed oils and ethyl oleate are also useful herein, as well as liposomes.

The carrier suitably contains minor amounts of additives such as substances that enhance isotonicity and chemical stability. Such materials are non-toxic to recipients at the dosages and concentrations employed, and include buffers such as phosphate, citrate, succinate, acetic acid, and other organic acids or their salts; antioxidants such as ascorbic acid; low molecular weight (less than about ten residues) polypeptides, e.g., polyarginine or tripeptides; proteins, such as serum albumin, gelatin, or immunoglobulins; hydrophilic polymers such as polyvinylpyrrolidone; amino acids, such as glycine, glutamic acid, aspartic acid, or arginine; monosaccharides, disaccharides, and other carbohydrates including cellulose or its derivatives, glucose, manose, or dextrans; chelating agents such as EDTA; sugar alcohols such as mannitol or sorbitol; counterions such as sodium; and/or nonionic surfactants such as polysorbates, poloxamers, or PEG.

The secreted polypeptide is typically formulated in such vehicles at a concentration of about 0.1 mg/ml to 100 mg/ml, preferably 1-10 mg/ml, at a pH of

about 3 to 8. It will be understood that the use of certain of the foregoing excipients, carriers, or stabilizers will result in the formation of polypeptide salts.

Any polypeptide to be used for therapeutic administration can be sterile.

5 Sterility is readily accomplished by filtration through sterile filtration membranes (e.g., 0.2 micron membranes). Therapeutic polypeptide compositions generally are placed into a container having a sterile access port, for example, an intravenous solution bag or vial having a stopper pierceable by a hypodermic injection needle.

Polypeptides ordinarily will be stored in unit or multi-dose containers, for example, sealed ampoules or vials, as an aqueous solution or as a lyophilized
10 formulation for reconstitution. As an example of a lyophilized formulation, 10-ml vials are filled with 5 ml of sterile-filtered 1% (w/v) aqueous polypeptide solution, and the resulting mixture is lyophilized. The infusion solution is prepared by reconstituting the lyophilized polypeptide using bacteriostatic Water-for-Injection.

The invention also provides a pharmaceutical pack or kit comprising one or
15 more containers filled with one or more of the ingredients of the pharmaceutical compositions of the invention. Associated with such container(s) can be a notice in the form prescribed by a governmental agency regulating the manufacture, use or sale of pharmaceuticals or biological products, which notice reflects approval by the agency of manufacture, use or sale for human administration. In addition, the polypeptides of the
20 present invention may be employed in conjunction with other therapeutic compounds.

Example 24: Method of Treating Decreased Levels of the Polypeptide

It will be appreciated that conditions caused by a decrease in the standard or normal expression level of a secreted protein in an individual can be treated by
25 administering the polypeptide of the present invention, preferably in the secreted form. Thus, the invention also provides a method of treatment of an individual in need of an increased level of the polypeptide comprising administering to such an individual a pharmaceutical composition comprising an amount of the polypeptide to increase the activity level of the polypeptide in such an individual.

30 For example, a patient with decreased levels of a polypeptide receives a daily dose 0.1-100 ug/kg of the polypeptide for six consecutive days. Preferably, the polypeptide is in the secreted form. The exact details of the dosing scheme, based on administration and formulation, are provided in Example 23.

Example 25: Method of Treating Increased Levels of the Polypeptide

Antisense technology is used to inhibit production of a polypeptide of the present invention. This technology is one example of a method of decreasing levels of a polypeptide, preferably a secreted form, due to a variety of etiologies, such as cancer.

5 For example, a patient diagnosed with abnormally increased levels of a polypeptide is administered intravenously antisense polynucleotides at 0.5, 1.0, 1.5, 2.0 and 3.0 mg/kg day for 21 days. This treatment is repeated after a 7-day rest period if the treatment was well tolerated. The formulation of the antisense polynucleotide is provided in Example 23.

Example 26: Method of Treatment Using Gene Therapy

One method of gene therapy transplants fibroblasts, which are capable of expressing a polypeptide, onto a patient. Generally, fibroblasts are obtained from a subject by skin biopsy. The resulting tissue is placed in tissue-culture medium and
15 separated into small pieces. Small chunks of the tissue are placed on a wet surface of a tissue culture flask, approximately ten pieces are placed in each flask. The flask is turned upside down, closed tight and left at room temperature over night. After 24 hours at room temperature, the flask is inverted and the chunks of tissue remain fixed to the bottom of the flask and fresh media (e.g., Ham's F12 media, with 10% FBS,
20 penicillin and streptomycin, is added. The flasks are then incubated at 37°C for approximately one week.

At this time, fresh media is added and subsequently changed every several days. After an additional two weeks in culture, a monolayer of fibroblasts emerge. The monolayer is trypsinized and scaled into larger flasks.

25 pMV-7 (Kirschmeier, P.T. et al., DNA, 7:219-25 (1988)), flanked by the long terminal repeats of the Moloney murine sarcoma virus, is digested with EcoRI and HindIII and subsequently treated with calf intestinal phosphatase. The linear vector is fractionated on agarose gel and purified, using glass beads.

The cDNA encoding a polypeptide of the present invention can be amplified
30 using PCR primers which correspond to the 5' and 3' end sequences respectively as set forth in Example 1. Preferably, the 5' primer contains an EcoRI site and the 3' primer includes a HindIII site. Equal quantities of the Moloney murine sarcoma virus linear backbone and the amplified EcoRI and HindIII fragment are added together, in the presence of T4 DNA ligase. The resulting mixture is maintained under conditions
35 appropriate for ligation of the two fragments. The ligation mixture is then used to

transform bacteria HB101, which are then plated onto agar containing kanamycin for the purpose of confirming that the vector has the gene of interest properly inserted.

5 The amphotropic pA317 or GP+am12 packaging cells are grown in tissue culture to confluent density in Dulbecco's Modified Eagles Medium (DMEM) with 10% calf serum (CS), penicillin and streptomycin. The MSV vector containing the gene is then added to the media and the packaging cells transduced with the vector. The packaging cells now produce infectious viral particles containing the gene (the packaging cells are now referred to as producer cells).

10 Fresh media is added to the transduced producer cells, and subsequently, the media is harvested from a 10 cm plate of confluent producer cells. The spent media, containing the infectious viral particles, is filtered through a millipore filter to remove detached producer cells and this media is then used to infect fibroblast cells. Media is removed from a sub-confluent plate of fibroblasts and quickly replaced with the media from the producer cells. This media is removed and replaced with fresh media. If the
15 titer of virus is high, then virtually all fibroblasts will be infected and no selection is required. If the titer is very low, then it is necessary to use a retroviral vector that has a selectable marker, such as neo or his. Once the fibroblasts have been efficiently infected, the fibroblasts are analyzed to determine whether protein is being produced.

20 The engineered fibroblasts are then transplanted onto the host, either alone or after having been grown to confluence on cytodex 3 microcarrier beads.

It will be clear that the invention may be practiced otherwise than as particularly described in the foregoing description and examples. Numerous modifications and variations of the present invention are possible in light of the above teachings and, therefore, are within the scope of the appended claims.

25 The entire disclosure of each document cited (including patents, patent applications, journal articles, abstracts, laboratory manuals, books, or other disclosures) in the Background of the Invention, Detailed Description, and Examples is hereby incorporated herein by reference.

(1) GENERAL INFORMATION:

5 (i) APPLICANT: Human Genome Sciences, Inc. et al.

(ii) TITLE OF INVENTION: 186 Human Secreted Proteins

10 (iii) NUMBER OF SEQUENCES: 644

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Human Genome Sciences, Inc.

15 (B) STREET: 9410 Key West Avenue

(C) CITY: Rockville

20 (D) STATE: Maryland

(E) COUNTRY: USA

(F) ZIP: 20850

25

(v) COMPUTER READABLE FORM:

30 (A) MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage

(B) COMPUTER: HP Vectra 486/33

(C) OPERATING SYSTEM: MSDOS version 6.2

35 (D) SOFTWARE: ASCII Text

40 (vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER:

(B) FILING DATE: March 6, 1998

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50 (vii) PRIOR APPLICATION DATA:

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55

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: A. Anders Brookes, Esq.

(B) REGISTRATION NUMBER: 36,373

(C) REFERENCE/DOCKET NUMBER: PS002.PCT

(vi) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: (301) 309-8504

(B) TELEFAX: (301) 309-8439

(2) INFORMATION FOR SEQ ID NO: 1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 733 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

30 GGGATCCGGA GCCCAAATCT TCTGACAAAA CTCACACATG CCCACCGTGC CCAGCACCTG 60
AATTCGAGGG TGCACCGTCA GTC'TTCCTCT' TCCCCCAAA ACCCAAGGAC ACCCTCATGA 120
35 TCTCCCGGAC TCCTGAGGTC ACATGCGTGG TGGTGGACGT AAGCCACGAA GACCCTGAGG 180
TCAAGTTCAA CTGGTACGTG GACGGCGTGG AGGTGCATAA TGCCAAGACA AAGCCGCGGG 240
AGGAGCAGTA CAACAGCACG TACCGTGTGG TCAGCGTCCT CACCGTCCTG CACCAGGACT 300
40 GGCTGAATGG CAAGGAGTAC AAGTGCAAGG TCTCCAACAA AGCCCTCCCA ACCCCCATCG 360
AGAAAACCAT CTCCAAAGCC AAAGGCGAGC CCCGAGAACC ACAGGTGTAC ACCCTGCCCC 420
45 CATCCCGGGA TGAGCTGACC AAGAACCAGG TCAGCCIGAC CTGCCTGGTC AAAGGCTTCT 480
ATCCAAGCGA CATCGCCGTG GAGTGGGAGA GCAATGGGCA GCCGAGAAC AACTACAAGA 540
CCACGCCTCC CGTGCTGGAC TCCGACGGCT CCTTCTTCCT CTACAGCAAG CTCACCGTGG 600
50 ACAAGAGCAG GTGGCAGCAG GGAACGTCT TCTCATGCTC CGTGATGCAT GAGGCTCTGC 660
ACAACCACTA CACGAGAAG AGCCTCTCCC TGTCCTCGGG TAAATGAGTG CGACGGCCGC 720
55 GACTCTAGAG GAT 733

(2) INFORMATION FOR SEQ ID NO: 2:

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 5 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

10

Trp Ser Xaa Trp Ser
1 5

15

(2) INFORMATION FOR SEQ ID NO: 3:

(i) SEQUENCE CHARACTERISTICS:

- 20 (A) LENGTH: 86 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

GCGCCTCGAG ATTTCCCCGA AATCTAGATT TCCCCGAAAT GATTTCCTCG AAATGATTTC 60

CCCGAAATAT CTGCCATCTC AATTAG 86

30

(2) INFORMATION FOR SEQ ID NO: 4:

35

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
40 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

GCGGCAAGCT TTTTGCAAAG CCTAGGC 27

45

(2) INFORMATION FOR SEQ ID NO: 5:

50

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 271 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
55 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

CTCGAGATTT CCCCGAAATC TAGATTTCCC CGAAATGATT TCCCCGAAAT GATTTCCTCG 60

60

AAATATCTGC CATCTCAATT AGTCAGCAAC CATAGTCCCG CCCCTAACTC CGCCCATCCC 120
GCCCCCTAACT CCGCCCAAGTT CGGCCCATTC TCCGCCCCAT GGCTGACTAA TTTTITTTTAT 180
5 TTATGCAGAG GCCGAGGCCG CCTCGGCCTC TGAGCTATTC CAGAAGTAGT GAGGAGGCTT 240
TTTGGAGGC CTAGGCTTTT GCAAAAAGCT T 271

10

(2) INFORMATION FOR SEQ ID NO: 6:

(i) SEQUENCE CHARACTERISTICS:
15 (A) LENGTH: 32 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

GCGCTCGAGG GATGACAGCG ATAGAACCCC GG 32

25

(2) INFORMATION FOR SEQ ID NO: 7:

(i) SEQUENCE CHARACTERISTICS:
30 (A) LENGTH: 31 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

GCGAAGCTTC GCGACTCCCC GGATCCGCCT C 31

40

(2) INFORMATION FOR SEQ ID NO: 8:

(i) SEQUENCE CHARACTERISTICS:
45 (A) LENGTH: 12 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:

GGGGACTTTC CC 12

55

(2) INFORMATION FOR SEQ ID NO: 9:

60 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 73 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:

GCAGCCTCGA GGGGACTTTC CCGGGGACTT TCCGGGGACT TTCCGGGACT TTCCATCCTG 60
10 CCATCTCAAT TAG 73

15 (2) INFORMATION FOR SEQ ID NO: 10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 256 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:

25 CTCGAGGGGA CTTTCCCGGG GACTTTCCGG GGACTTTCCG GGACTTTCCA TCTGCCATCT 60
CAATTAGTCA GCAACCATAG TCCCGCCCTT AACTCCGCCC ATCCCGCCCC TAACTCCGCC 120
CAGTTCGGCC CATCTCCGC CCCATGGCTG ACTAATTTT TTTATTTATG CAGAGGCCGA 180
30 GGCCGCCTCG GCCTCTGAGC TATTCAGAA GTAGTGAGGA GGCTTTTTTG GAGGCCTAGG 240
CTTTTGCAA AAGCTT 256

35

(2) INFORMATION FOR SEQ ID NO: 11:

40 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 582 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:

GGCACGAGGT AATTCTTACC AGAAATTTCC AGAGCATTAT GTAGGTAGAA AAAAAATGCAA 60
50 GCAAGCTGTT AAAGATCTTG GATCCCATTA TATAGTATGT ATAGCTGAAA TCTGTAATTC 120
AATCACTTTT TCTCTTTTAT CCTCTAACCA AAAAATGTT TAATTTTGCA TCCCAAATGT 180
TTTTAATCTT TGTATATTTT TTAAAAATCC TTTTCTCCTC ATCATTCCTT TTTTGTGGT 240
55 TGTAATAGA CTTACTTGCA CTTGAAGAT GAGTTACTCC TTGTCATCTT ACAAATATGT 300
GATATGGTAA TTTTCATAAC AGATGTCAGT TTTGAACCAA GAATGGTGA TTTGTTTATA 360
60 AGAAAAAAC TGGCTTCATT TCTGTGAAAT TGCTCTTTGA AAATTTCTTT TTACACGTGT 420

AAGCCAAC TG AGATACCG TG ATGGTGTTGA TTCTCTTCAA TGATGCTTAC CATCTATTTT 480
 5 AGCCACTGAG CCTTTTATTA TTGTCTATT TGTAAGTTT ATTTGTCTTA ACTCATTTAA 540
 TAAATATACT GTTTATCTGT TTCTGAAAAA AAAAAAAAAA AA 582

10

(2) INFORMATION FOR SEQ ID NO: 12:

(i) SEQUENCE CHARACTERISTICS:

15

- (A) LENGTH: 465 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:

20

GTTTGGGGGT GAGGCCGAGC TGCTGCGGGG CTTCTGTCGCC GGCCAGGACA CAGCTACTCG 60
 CACGGCGGCG GCGCCTGGCT ATGATGTTCC TCACCCAGGG CGGGCTCTG CCCTCTACTC 120
 25 GTGCCAGGCC CACTTGCCAG GCAGGAGCCC TCCCCAAGCC TTCAGGGCTG CTCGGAGTCA 180
 CCTGTGGAA TGGACTAAAA GGACCCCTGT GTGGGAACAG GTGCTCCCCA AACACCCCTGC 240
 TGCTGGCTGC CAGGCAGGCC CTCTGGAAGG GAAGGGGCAG GACTCATCAG GACCTCCCTG 300
 30 GACCCCTGCA GGGCAGGCAG CTTGGGCCCC AGCCCAAGCA TTTGGCTCTG CTGCCCCCAA 360
 GGGGACAGGA AGCCTCTTGG GCCTCTTCCC TTCCTGGACA AGGCCCCCTG CCTTTGCCTC 420
 35 ACATAAACTG TACAGTATTT TCATTAAAAG CCTCTTTCAT AAAAA 465

40

(2) INFORMATION FOR SEQ ID NO: 13:

(i) SEQUENCE CHARACTERISTICS:

45

- (A) LENGTH: 474 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13:

50 ATGCAATCC TGCTCACAGC CTTCTGTTG GTGCCACTTC TGGCTCTTTG TGATGTCCCC 60
 ATATCCCTAG GCTTCTCCCC CTCTAGAAG GGCTTCTTGA TAGATTAGAA AATAAGAATG 120
 AGTGACATTT CCTATGTGCA TATAAGAAGG AGCCACAAGA CATGTCTTTT AAATAAAAGG 180
 55 ACAGTGTCCA TCCTTTTAGC TGCCGAATAG AACCTTGGTC TCATCCTCCT GGAGCTAGGC 240
 CTTTAAACA GCTTCTGTGT TTCTCATTTG TCTCAGTGT TTGCCAGGGT TTTATCGGAA 300
 60 AGATAATGTT CCGTTTAAAA TATTTCTTAA TGAGGCCGGG CCGGTGGCT CACCCCTGTA 360

	ACCCTAGCAM TTGGGGGCTG AGCGGGTGGA TCACGAGGTC AGGAGATCGA GACCATCCTG	420
5	GSTAACATGG TGAAACCCCG TCTCTACTAA AAATACAAAA AAAAAAAAAA AAAA	474
10	(2) INFORMATION FOR SEQ ID NO: 14:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 314 base pairs	
	(B) TYPE: nucleic acid	
15	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 14:	
20	TTATGTTGGG GAGCAAGACC TGATAGCCAG CCTTTACATG GGAGTATAAT TCTGTCCTCC	60
	ATCTCATAAG CCCCACTACC TGAGCCAGAA TGATTATAAC CAACCACACT GTCTCTTTAT	120
	CATGGATGGC TTAGCAGTA GGTATTATTTC ATCATGCGCA TTGTAGCTC TACAGTGGTT	180
25	TATAGTAATT TCATCTCTT TAAGTCTCTC CCTCAGTGCC TGTGTGTATC AAACATCATG	240
	CTCTCTCANG CAGTTGAGCT CTGCATCTC CCYTATGGGG GAGAGCTGTG TTGGAGAGAG	300
30	AGAATATNAC TTCC	314
35	(2) INFORMATION FOR SEQ ID NO: 15:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 613 base pairs	
	(B) TYPE: nucleic acid	
40	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 15:	
45	CTCATATTGC CGTCTGGCTA AAAGTGAACA TGCCATTGAT CAATCTGCTT TTATTATATT	60
	ATGTTCTTAA TGGTGGCAAG CAAGACAAGA AGTAGAAAGA AAGATGGTGT AAGCTCAAGA	120
	ACCCACTAAA TCTATCCTAT GGCCTGGGTT CACCCAGCCT GCCTTGTGGA TTTTGTCTCA	180
50	CTATAACAGA GCTCCAAGG AGACTGCAGA GTCAGCTCCC TTAAGCACTG TAACTAAAGC	240
	CTAACTCTTC CGTTCACCC AACAATGTTC CCAGCTCATC CTCTTTCCCR AAGTCCCTT	300
55	TCTGCCCCAG ATGCGAATTG CATTTAACTA ATCCTCAAGT GAAATGTCCA CACAGRATTC	360
	CATTTTAATT AGCATACCAT AGTTTTTGTG CAAATTTGCT TTCAGARGAC TCCCATTGCA	420
	GCTGCTCAGA GACGCTAAWG GCAGGGCCTC TTGAWGCTTT CCCGATAGCT TTCAGCTGCA	480
60	ATAGCTCTTA GGCAGAATGC CATGAGCGTC CTGCCCAACT GTATTACTGG GGAACACCTG	540

ATTGGCTAGA AGTTGATCCT CCTGTAACCTT TTCTGAGTTC TTTACATTTA CTCGTGAAAC 600
CCAAATATGC CAC 613

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10 (2) INFORMATION FOR SEQ ID NO: 16:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 356 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 16:

20 CCCCCCAT TGAACCTGG GCTGTGAAAG TTTTGCCTG TGTGGTCTG TCTGTGTGGC 60
GCCTGGTGTG TGGKTCCCAA CTCCTGTTCG AAAGTGGCAG CAGCCAATCA TGAAGCGCCC 120
TTATTTTGTAG TTGCAGATGA CCAGGTCTCC CCCCCACAGC CTCGTGTCTGG TCCCTCATTG 180
25 GTGAGTGGTC TGCCTGCCCA AGGAGCCTGA TTGGTGGGAA ATGGCATCAT CTAATATGAT 240
GGGAAGGCAT TTGGTCTCGG TTATGTTTAT TACAACATCA TTGCACTCTG GGACTCCAGT 300
CCCTGAAAAC GTAATTTGTG GTGTTACCAA AGGACCACAG GGGAAAAAAA AAAAAA 356

30

35 (2) INFORMATION FOR SEQ ID NO: 17:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 414 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 17:

45 GAAACTANAT CCCGGGGCTT TTAACNGGTA CTGGGAAAT AAGTATTGGG TAATCACTAA 60
GNGGACATTG ACTGCACCAA ACCAAAGCTA TAGAAAGAAA TGATTGACTT TTTAAAATAT 120
ATTCACATTA ACTGTCCTAG GATACTTCTC TTGAGGCTTT GGAAAACTTC TTCCTTGAAA 180
50 TTTGCATATC CACTCCAGTT CTGTCACCAA AGATTTTAAT CTTCAGATCG CAATTTCTTC 240
TCTCCAGAA AAAAGTACTA CAACAGGCTC AAGGGATATG CTTTGGTGGT CAAGGGATTA 300
CACTATGGTT TTCCTTCTGT TCACAATGGT ATTTACAGGA GACCTTGTCA TCAGAGGACG 360
55 TACTGAACTA TCTTTATGAC TTTGGATTGT ATCAGAGGTT TAAAAAAA AAAA 414

60

(2) INFORMATION FOR SEQ ID NO: 18:

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 469 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 18:

10 AATCACCATT GCAATACAAA TGATCTGCCT GGTGAATGYT GAGCTGTACC CCACATTCGT 60
CAGGAACYTC GGAGTGATGG TGTGTTCCCTC CCTGTGTGAC ATAGGTGGGA TAATCACCCC 120
15 CTTTCATAGTC TTCAGGCTGA GGGAGGTCTG GCAAGCCTTG CCCCTCATTT TGTTCGCGGT 180
GTTGGGCGCTG CTGCGCGGG GAGTGACGCT ACTTCTTCCA GAGACCAAGG GGGTCGCTTT 240
GCCAGAGACC ATGAAGGACG CCGAGAACCT TGGGAGAAAA GCAAAGCCCA AAGAAAACAC 300
20 GATTTACCTT AAGGTCCAAA CCTCAGAACCT CTCGGGCACC TGAGAGAGAT GTTTTCGGGC 360
GATGTCGTGT TGGAGGGATG AAGATGGAGT TATCCTCTGC AGAAATTCCT AGACGCCTTC 420
25 ACTTCTCTGT ATTCTCTCTC ATACTTGCTT ACCCCCAAAT TAATATCAG 469

30 (2) INFORMATION FOR SEQ ID NO: 19:

(i) SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH: 550 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 19:

40 CCCCCCCCC CCCCACACT TTCAGGAGTC ACCCCCCAGC ATTTGGGGTT GGGTTGGCCC 60
TACTCCAGCC TGGAGCTCCC TGAGGGAGCC TGCCTCCCT GCTCCCAATC CCCGCTACTG 120
GTGCAGGGAT GCAGCCTGGA GCTGGCGTCC TTGTTCTGGG CCGCTGCTG CCGCCACCCC 180
45 AGAGCCCCAG CCTGTCTGA ATTGACATCA GTGCTTCCCT GAACTGCCTC CCCCACCCCT 240
GGGCATTATC CCAGGAACT TTATGTTTTC TAGAAGCTAA GCAGCTGCTG GGACTCAGGG 300
50 ACTGGTGCAG GTAGGCTGAG TGGCAGCTCA GTCCTAGAAG GTCTCTGAAG ATCTGGACTG 360
AGGACCTTGC TACTCCCCAA GCCAGAGCCC ATCAGCCAGG CCGCTGTGA GCCACCTGCC 420
TGTGGAGTGC TGAGCTCAAC CAAAGGCTGG CAAGCTCTGG GCCTCATTTA AGGGATTCTG 480
55 ATGAGCCGAT GGGCCCTGGA GGCAGCCCAT TAAAGCATCT GGCTCGTTTT TGGAAAAAAA 540
AAAAAAAAA 550

60

(2) INFORMATION FOR SEQ ID NO: 20:

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(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 741 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 20:

TCTTGAAGAG TGTACAGTAC AGGATTATTA TAATGAAAGT TTATATCAAC AGGGTTTCGT	60
15 TGGCTCTGCA TATATTATAA GCAAAAGAGA TTGGTAAAGT GCCACAGTAT TCCAGATAAC	120
TTTTCAGTTG CGGCCTTTCT TCTCGTTCTT TAATTTGAAA CCTAGATACA TGCAGTAAAA	180
ACTAGGAGAA TGACTTTTAC CCTTGGGGAC AGCCAAGTTT TGTTGATAAA CCTATTTCTT	240
20 AGCATGCCCT CAGGAAGTTG TGCCAGACCC TAGATTGTGA AGGACCCACT GTTCTTCTGT	300
TGTACGAGCT CCCTGAACCA TTGTTTCAGAG GACCAATGTC ACATCGCTTC ATGGGCATGG	360
25 NCCATGGGAG CATCTGGGTG ATAYCTGTCT ACAGTATTGG CTCTTCTGCG AGGCTGATAC	420
ACAAGGCCTC TCTTCCACAT GATCATTTGC AAACCTCCCC CAGCCCCTAC CATCCAATGT	480
GGAAGGAAAA CAAGAACTGC CTGAAGAAGA GTCCAAGCTA CAGATACACA GCGTGTGCAT	540
30 TCGCGCTGTC ACCTTCTCTC TCCCACTTCT GTATCCTCAG AGATGCTGCG TGGATGTTTC	600
CTTAACCTCA GCTGACTTCC CTGTGAATGT CTAATGCTAG TTCAGGGCCT CCAGGCATTG	660
35 ATTTGTACAG TGGTAACTCC CAATGAGGCT TCTGTTATCA TTTGGTGTGC TTTTCTGTGC	720
ATTAAAAGAA ATGATTTTCC C	741

40

(2) INFORMATION FOR SEQ ID NO: 21:

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(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 991 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 21:

GGCACGAGTC TCCCTGGGG AAGTTTTTCT TTTTCAGGAG GGAGGAGGGC TTTCCAGGT	60
55 AATGTGTCTA GAGTGTGGG CAGAAAATCT GGGACCACAC CACACCAGTT CTCTCCTTAA	120
TCCACGTCAT TTGCCTTCTA TCCAGCTAT GTTTCAGTG TCCTCTGGGT GTTCCAAGA	180
GCAACAAGAA ATGAATAAAT CTCTGGTGAG TTGTTTATTT GTTCTTCACT TTGTTTACA	240
60 CTGTATTTTC TGAGTTTATG GGTGTCTGTG AATTAAAAAG GAAAAGTAGA AATAAGTAAA	300

ACTCAGGTTG AAGGAAATAT ACATAAATAA GATAAAGCTG ACCTGTAGAT ATAGCAGGTT 360
 ATAAAGCTTA GAGTTGTCTA AGTTGAGTGC AAATTTTCCT CTGATCTTTC TGATGCCGAA 420
 5 CAAAAAGCA GTCATGTTTG TTAATGTGATT GGAATGGAAC CCGAGAAGAG AGCATGCTGT 480
 GTTCTTGTGG GACAGGAAAG CTTGCGTGCA CCAAGTCTGA ACCACCACCT TCATGGTGAC 540
 10 ATAGATTATG TGCTGGAACA TATTTCACAC CGGCCTGGCA GTAAACACTT GTAGTGTGTG 600
 GCAGTGAAA CGGTCATCTT CCGCTAAAGC ACGGCGTGTG GTGCAGCGGA AATGGTCATC 660
 15 TGCTGCTAAA ACACAGCTTC CATCGTAATG TATGCTCCTT ACTCAAAGAG TGTGGTCCCA 720
 AACAGCCCTT GGGAGGTCCT CCTTGATTCA TGGATGAAAC CTGGAACATC TTGAGGACTG 780
 AGTTAACCAT AGGTCCTTAA ATAACTCTCC ACACGTTTTT CTTAGTTTAT CTCTACATGC 840
 20 AGGGTGTGCA GCAGCCTGTT CAAAGTCATA TTTTCTGGGA AATATTTCCA GTGTTTATTT 900
 GCACTTTAGC CCACTCTGTG TAGCCTTATT TCTCTAAAC TCACCATTAA TCTGAATAAT 960
 25 AGTCAAATTT AGGGGGACTG TATTTGCCTT A 991

30 (2) INFORMATION FOR SEQ ID NO: 22:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 653 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 35 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 22:

CCACGCGTCC GGAATTCCTCC TGAGGATCTT GGGCTATCTT TGACAGGGGA TTCTTGCAAG 60
 40 TTGATGCTTT CTACAAGTGA ATATAGTCAG TCCCAAAGA TGGAGAGCTT GAGTTCTCAC 120
 AGAATTGATG AAGATGGAGA AAACACACAG ATTGAGGATA CGGAACCCAT GTCTCCAGTT 180
 45 CTCAATTCTA AATTGTGTTCC TGCTGAAAT GATAGTATCC TGATGAATCC AGCACAGGAT 240
 GGTGAAGTAC AACTGAGTCA GAATGATGAC AAAACAAAGG GAGATGATAC AGACACCAGG 300
 50 GATGACATTA GTATTTTAGC CACTGGTTGC AAGGCAGAG AAGAAACGGT AGCAGAAGAA 360
 GTTTGTATG ATCTCACTTG TGATTGCGGG AGTCAGGCAG TTCCGTCACC AGCTACTCGA 420
 TCTGAGGCAC TTTCTAGTGT GTTAGATCAG GAGGAAGCTA TGGAATTAA AGAACACCAT 480
 55 CCAGAGGAGG GGTCTTCAGG GTCTGAGGTG GAAGAAATCC CTGAGACACC TTGTGAAAGT 540
 CAAGGAGAGG AACTCAAAGA AGAAATATG GAGAGTGTTC CGTTGCACCT TTCTCTGACT 600
 60 GAAACTCAGT CCCAAGGGTT GTGTCTCGG AGGCATCCAA AAAAAAAAAA AAA 653

(2) INFORMATION FOR SEQ ID NO: 23:

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(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1486 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

10

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 23:

15	GGCAGGCTGA CGACCTGCAA GCCACAGTGG CTGCCCTGTG CGTGCTGCGA GGTGGGGGAC	60
	CCTGGGCAGG AAGCTGGCTG AGCCCCAAGA CCCCAGGGGC CATGGGCGGG GATCTGGTGC	120
	TTGGCCTGGG GGCCTTGAGA CGCCGAAAGC GCTTGCTGGA GCAGGAGAAG TCTCTRGCCG	180
20	GCTGGGCACT GGTGCTGGCA SGARCTGGCA TTGGACTCAT GGTGCTGCAT GCAGAGATGC	240
	TGTGGTTCGG GGGGTGCTCG GCTGTCAATG CCACTGGGCA CCTTTCAGAC ACACTTTGGC	300
	TGATCCCCAT CACATTCTCTG ACCATCGGCT ATGGTGACGT GGTGCCGGGC ACCATGTGGG	360
25	GCAAGATCGT YTGCTGTGC ACTGGAGTCA TGGGTGTCTG CTGCACAGCC CTGCTGGTGG	420
	CCGTGGTGGC CCGGAAGCTG GAGTTTAACA AGGCAGAGAA GCACGTGCAC AACTTCATGA	480
30	TGGATATCCA GTATACAAA GAGATGAAGG AGTCCGCTGC CCGAGTGCTA CAAGAAGCCT	540
	GGATGTTCTA CAAACATACT CGCAGGAAGG AGTCTCATGC TGCCCGCANG CATCAGCGCA	600
35	ANCTGCTGGC CGCCATCAAC GCGTTCGGCC AGGTGCGGCT GAAACACCGG AAGCTCCGGG	660
	AACAAGTGAA CTCCATGGTG GACATCTCCA AGATGCACAT GATCCTGTAT GACCTGCAGC	720
	AGAATCTGAG CAGCTCACAC CGGGCCCTGG AGAAACAGAT TGACACGCTG GCGGGGAAGC	780
40	TGGATGCCCT GACTGAGCTG CTTAGCACTG CCCTGGGGCC GAGGCAGCTT CCAGAACCCA	840
	GCCAGCAGTC CAAGTAGCTG GACCCACGAG GAGGAACCAG GCTACTTTCC CCAGTACTGA	900
45	GGTGGTGGAC ATCGTCTCTG CCACTCCTGA CCCAGCCCTG AACAAAGCAC CTCAAGTGCA	960
	AGGACCAAAG GGGGCCCTGG CTTGGAGTGG GTTGGCTTGC TGATGGCTGC TGGAGGGGAC	1020
	GCTGGCTAAA GTGGGKAGGC CTTGGCCAC CTGAGGCCCC AGGTGGGAAC ATGGTCACCC	1080
50	CCACTCTGCA TACCTCATC AAAAACAATC TCACTATGCT GCTATGGACG ACCTCCAGCT	1140
	CTCAGTTACA AGTGCAGGCG ACTGGAGGCA GGAATCCTGG GTCCCTGGGA AAGAGGGTAC	1200
55	TAGGGGCCCC GATCCAGGAT TCTGGGAGGC TTCAGTTACC GCTGGCCGAG CTGAAGAACT	1260
	GGGTATGAGG CTGGGGCGGG GCTGGAGGTG GCGCCCCCTG GTGGGACAAC AAAGAGGACA	1320
	CCATTTTTC AGAGCTGCAG AGAGCACCTG GTGGGGAGGA AGAAGTGTA CTCACCAGCC	1380
60	TCTGCTCTTA TCTTTGTAAT AAATGTTAAA GCCAGAAAAA AATAAAAAAA AAAAAAAAAA	1440

AACTCGAGGG GGGCCCRKAC CCAATCWCCC TATAGTAKAC GTANNN

1486

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(2) INFORMATION FOR SEQ ID NO: 24:

(i) SEQUENCE CHARACTERISTICS:

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(A) LENGTH: 2323 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 24:

CTTCGCCGTT	TCTCCTGCCA	GGGAGGTCC	CGGCTTCCCG	TGGAGGCTCC	GGACCAAGCC	60
CCTTCAGCTT	CTCCCTCCGG	ATCGATGTGC	TGCCGCCGCC	GCCGCCGCCG	TCCCGCGTCC	120
TTCGGTCTCT	GCTCCCGGGA	CCCGGCTCCG	CGCAGCCAGC	CAGCATGTGC	GGGATCAAGA	180
AGCAAAAGAC	GGAGAACCAG	CAGAAATCCA	CCAATGTAGT	CTATCAGGCC	CACCATGTGA	240
GCAGGAATAA	GAGAGGGCAA	GTGGTTGGAA	CAAGGGGTGG	GTTCCGAGGA	TGTACCGTGT	300
GGCTAACAGG	TCTCTCTGGT	GCTGGGAAAA	ACAACGATAA	GTTTGGCCCT	GGAGGAGTAC	360
TTGTCTCCCA	TGCCATCCCT	GTTAATTCCCT	GGATGGGGAC	AATGTCCGTC	ATGGCCTTAA	420
CAGAAATCCC	CAGATGGCTT	CATGGCCCCC	AAAGCATGGA	AGGTCCCTGAC	AGATTATTAC	480
AGGTCCCTGC	AGAAGAACTA	AGCCTTTGGT	CCAGAGTTTC	TTTCTGAAGT	GCTCTTTGAT	540
TACCTTTTCT	ATTTTTATGA	TTAGATGCTT	TGTATTAAAT	TGCTTCTCAA	TGATGCATTT	600
TAATCTTTTA	TAATGAAGTA	AAAGTTGTGT	CTATAATTAA	AAAAATATAT	ATATATATAC	660
ACACACACAT	ATACATACAA	AGTCAAACCTG	AAGACCAAAT	CTTAGCAGGT	AAAAGCAATA	720
TTCTTATACA	TTTCATAATA	AAATTAGCTC	TATGTATTTT	CTACTGCACC	TGAGCAGGCA	780
GGTCCAGAT	TTCTTAAGGC	TTTGTTTGAC	CATGTGTCTA	GTTACTTGCT	GAAAAGTGAA	840
TATATTTTCC	AGCATGTCTT	GACAACCTGT	ACTCTTCCAA	TGTCATTTAT	CAGTTGTAAA	900
ATATATCAGA	TGTGTCTCTT	TCTGTACAAT	TGACAAAAAA	AAAAATTTTT	TTTTCTCACT	960
CTAAAAGAGG	TGTGGCTCAC	ATCAAGATTC	TTCTTGATAT	TTTACCTCAT	GCTGTACAAA	1020
GCCTTAATGT	TGTAATCATA	TCTTACGTGT	TGAAGACCTG	ACTGGAGAAA	CAAAATGTGC	1080
AATAACGTGA	ATTTTATCTT	AGAGATCTGT	GCAGCCTATT	TCTGTCACAA	AAGTTATATT	1140
GTCTAATAAG	AGAAGTCTTA	ATGGCCTCTG	TGAATAATGT	AACTCCAGTT	ACACGGTGAC	1200
TTTTAATAGC	ATACAGTGAT	TTGATGAAAG	GACGTCAAAC	AATGTGGCGA	TGTCGTGGAA	1260
AGTTATCTTT	CCCCTCTTTT	GCTGTGGTCA	TTGTGTCTTG	CAGAAAGGAT	GGCCCTGATG	1320

60

	CAGCAGCAGC GCCAGCTGTA ATAAAAAATA ATTCACACTA TCAGACTAGC AAGGCACTAG	1380
	AACTGGAAAA GACCACAGAA AACAAAGAAT CCAACCCCTTT CATCTTACAG GTGAACAAAC	1440
5	TGTGATGATG CACATGTATG TGTMTTGTA GCTGTGAGCA CCGTAACAAA ATGTAAATTT	1500
	GCCATTATTA GGAAGTGCTG GTGGCAGTGA AGAAGCACCC AGGCCACTTG ACTCCCACTC	1560
10	TGGTGCCCTG TCTACACCAG ACAACACAGG AGCTGGGTCA GATTCCCTTC AGCTGCTTAA	1620
	CAAAGTTCTT CGAACAGAAA GTGCTTACAA AGCTGCCTTC TCGGATACTG AAAGGTCGAG	1680
	TTTTCTGAAC TGCACGTATT TTATTGCAGT TGAAAAAATA AAAAAGCTAT TCCAAAGATT	1740
15	TCAAGCTGTT CTGAGACATC TTCTGATGGC TTTACTTCCT GAGAGGCAAT GTTTTACTT	1800
	TATGCATAAT TCATTGTTGC CAAGGAATAA AGTGAAGAAA CAGCACCTTT TAATATATAG	1860
20	GTCTCTCTGG AAGAGACCTA AATTAGAAAG AGAAACTGT GACAATTTTC ATATTCTCAT	1920
	TCITAAAAAA CACTAATCTT AACTAACAAA AGTTCCTTTG AGAATAAGTT ACACACAATG	1980
	GCCACAGCAG TTTGTCTTTA ATAGTATAGT GCCTATACTC ATGTAATCGG TTACTCACTA	2040
25	CTGCCTTTAA AAAAAAAAC CAGCATATTT ATTGAAAACA TGAGACAGGA TTATAGTGCC	2100
	TTAACCGATA TATTTTGTGA CTAAAAAAT ACATTTAAAA CTGCTCTTCT GCTCTAGTAC	2160
30	CATGCTTAGT GCAAATGATT ATTTCTATGT ACAACTGATG CTTGTCTTTA TTTTAATAAA	2220
	TTTATCAGAG TGAAAAAATA AAAAAAATA AAAAAAATA AAAAAAATA AAAAAAATA	2280
	AAAAAATA AAAAAAATA AAAAAAATA AAAAAAATA AAA	2323
35		

(2) INFORMATION FOR SEQ ID NO: 25:

- 40 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 683 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear
- 45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 25:

	GGCAGCAGCC TGTGTGGTCA TGTTCTCGT GGTGCAGTAC CTGACATGAG CCAGCCACGC	60
50	TCAGTGGCTG AACAGCATTC CCACAGCCTG CAAGTGTGTG TGTGTGTGAA AGAGAGAGGG	120
	GGGCCCAGAG CCGCCTTTTG AAATGTTTGC CTGTCTGAAC TGTGAAGACA CTTGGGAGTG	180
55	ATTGTGGTCT AATTTCACAC CTGCTCTGTT TTCTGTGACA TCTTGGAGGG GAGCTAGTGC	240
	CACACCATGC GCGGTGCTTA GAAATGAAA AGTCCCGGGT CTGTCTCTCT CACTCTCGCT	300
	CTCATGGGGG AGGGAAGAA TGGCTTTGGT GGCTTTGTTT ACACAGCTGA TGCGTGCTGG	360
60	GAAGGTGTCC ACAGTGAGCC TGTGTGCAGG ACTGTCCACA CGGTTCACAC TTGTCACCAT	420

CAGGCCTTTC TGGTCCTGAT AGGGTGGAGC AAAAGTGGAA AGGAAAGGAA AGAGGCTTTT 480
 CTCACAGCCA TTATATTAAA TAGTAGGTCG ATTCACATCT CGTGCTCCTG GCCACCTTCC 540
 CCTGTGCCCTC AGTGACATGT AGATGACTGA CTGCCAATAC TTGTCAACCAT TCCCTGGAAG 600
 CAGCTACCTA GGGGAAACAA GATGTAGTGC TATTGCCGAT AACAAGTAAG ATTTTCCACA 660
 CTAAAAAAAA AAAAAAAAAA AAA 683

(2) INFORMATION FOR SEQ ID NO: 26:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2036 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 26:

CTGAGAAAGG AAAGCATTCG GATCTGCTGC AAAAACACAT ATATCCATAA AGACTCATGT 60
 TATTCAGAAA ACAGATTGTG AACACAATCA CATTGCGATG AATCCTTTAA AAGGAAGAAG 120
 ACCTTAAAGT ATCTGCAAAT CTGAATTTCT ATTTATTCCT TCACTGAATA TAGAAACAAT 180
 GGTATCTGA TTATTAGAGA TATTATTTTG GATATGTTAC TTATTAACCTT GCTATGGCTG 240
 GTAACCATGA TAAAGTCTGT TATTAATAAC AACATAATTC TTTTTTTAAA GAAGAAAAGC 300
 TTATTTTTCA TTGACAGTGT ATAGATTAT CTACTTAGTT GTGTTTTGCT ATTAGTGTTC 360
 TAATTTTTTT TTTAAGTTGA GTGTTTGATA AATTTTAAGA CCCTGTCCCC ACCTTGTTTT 420
 GAGTCTGTG TTGACTACAG GTATATAGCY CAWTTTAAAA ATCCTAAAGC AAAAGAATTT 480
 TATTTATAAA AGAATCMAMC MGTGCGATGC ATGAGGCTGT GAAGTCAGAT ATTTAGTAAT 540
 AAAAGCAGCA GTGCCTTTTT TTGTATTAC CCATGACCC CCACCAAATG CAACTGTTTT 600
 ATATTAAGAA AATAGTAACA ATTTTAAAT CTCAGAGTAA AATCTATTTC ACTACATGCT 660
 TTTCCCCCTT TGTTCGATT TAAGCAGTGT GTACTTGGCA TCTCTACATT GTCCTAGGGA 720
 CAGTGGTGTT CTACAATATT ATCATGTATG ATGTTTTATT GTTGCTTTTT ATTCATAGTG 780
 GCTTCTTACC AGAAACAGTA GGAAGAAACA CATGAACTGT GTACAAGACA TGAAACATG 840
 CTGCTGATAT GTTGTTTTTT CACATGCTTT TGAGTTTTCA CTTTTTAAAC GAGAGCCAGC 900
 AAGCAAATA GATGTGGCTG GGTCTGCCTG TCCGGGCGGC TYTTTGCAAC GAGCTCTCAA 960
 ATCTGTGTA TTGAGGGTTC CTTTTGGTA CTCAGGATTG GAGCTACAGC TGGGCCCCC 1020
 TCTCTCCCAT TCGTTTGAAG AGACACTGAG GGAAACAAGG GTTCTTTTTG AGGTGTCCTT 1080

	GGCTGCCTTT TACGGGATGG GAGCCTTCTC CGGATCTTTT GTTCTTCTGC ACCTCTTGTA	1140
	GCTACTGCCG GTGCAAGGTT GTAGATGTTA TTCCCCAGGA GCCTGGGCTK GGGGGCTGAG	1200
5	CTGGGCTGAA TGCAAAAGCA TGCAACCAGA AGGCGGGCAA GGGGAGGAAA AGCAGGCCTG	1260
	GCCTCATTTGG TCCCCTGGAG ATGTCTGTAG CAGTCAGCTC CAGCTTGGGC CTGGGGAAGC	1320
10	AGCCTGACCA AGGCGCTCAG GTGTGCCTGT TACAAGAAGA ACCTGCAGAA GGATAATTTG	1380
	CACATGGAGC TGTGATAACA CTAATGTTGA TTTT'TTTTT TTTTACAAGT CATCAGRGAT	1440
	GT'TTGCAAAG TGAGTTT'TAT TTTT'TGTAA TTCCTT'TATC TTTACTTAAA GGTGAATGTG	1500
15	TATTCCTCTG GGAGGAATAG GAAGAAAACA GGAATGTTAA TAATGTCGAA CAGAAAAC'TT	1560
	CCTCCCTAT TAATATATAA TCYTCATGTA TTTATGCCNT AATGTAAGCT GACTTTTAAA	1620
20	AAGCTT'TCTT TTGTGTCATG CCCTGTGCAG GCATCTGTAT TGTACATGCA TGCCTTTCGT	1680
	CCTGTTT'TCC TGTATAAAGT TAGTGAACAA AGAAATATTT TTGCCCTAGT TCATGTTGCC	1740
	AAGCAATGCA TATTTTTTAA ATTTGTCATA TATGGAAAGA GCATGTTTGT TACATGTAAA	1800
25	AGCTTTACTG ATATACAGAT ATACTAATGT TTGAAGATGC TGTTCTTTGC AAGTGTACAG	1860
	TTTTCAAATG TTGTTACCAG TGAACACCC TTGTGGTTTA AACTTGCTAC AATGTATTTA	1920
30	TTATTCATTT CCTCCCATGT AACTAAGAAT CATGGCTATA TTTCATATCA ACGTTATATT	1980
	GAAAGTGAAG GGAATGATT AATACAAGGT TTTGTAACAA AAAAAANAA ANNA'A	2036

35

(2) INFORMATION FOR SEQ ID NO: 27:

(i) SEQUENCE CHARACTERISTICS:

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- (A) LENGTH: 717 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 27:

45

	GGCACGAGAT AACATAGGCA CAATAATACT GTATGTCTAC TTCTAGGATT ATAAGGAATT	60
	AACATTGAGA TGACATTTCC ATTTGAGAAG AAAATAGTTG CT'TTCAGTGC CT'TTATTTG	120
50	ATTCTTGAG AGAGCAGACT CGCACCAACA TTCAACCCCA GCGCTGATAT GACAGTAATC	180
	CTCAGAGGCA GAGCCAGCA CAAAACAGCA ATGCTAGAAA GTTACAATTG GAAAGTTTCC	240
55	TGCCAGCTTC GGGAAATGACA CTGCAAAGCT GATGCCAGAA ACTGCCAGAG TAATTCTCCT	300
	CATTACTGCT CTACCCACCC ACTTTCAGCT CCCCAAATTA ACTAGTGCAG TTGACTAATC	360
	CTCTTTACCT TTATCATTTA GGTGAGGCAT TGCACAAAA CTCTCGACTT TGCCATATAA	420
60	GGGCTGTGGT TCTCTGTGGT CCTGGATAAG AGGCATCACC ATTATCTGGA AACATGCAGT	480

5 AAATGCAGAT TCTTCATCTT CTCCCAGAC CTCCTGAGTT AGAAATTCAC AAGTTCCTCA 540
 GGTGATCTCA TACATGCTAA AGTTTGAGAA CCATGAGTA AAGTTAATGC ATTAAGAAGA 600
 GATTAGATAG GGATGGTGGC GTATCTTCCT ACAGTTTCCC TGTTAACAAG AAAGTCAGAG 660
 10 GTCAGTTGAT CAGACATTAG ATTATTTATT GCTAAACTA AAAAAAATTA AAAAAA 717

(2) INFORMATION FOR SEQ ID NO: 28:

15 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 495 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 20 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 28:

GAATTCGGCA CGAGCAGCAT CCTAATTTTA GTTTGGAGAT GCATTCTAAA GGATCTTCTC 60
 25 TATTGCTTTT TCTCCACAA TTAATCTTGA TTCTGCCTGT CTGTGCACAT TTGCATGAGG 120
 AACTGAACTG TTGTTTTCAT AGGTAAATGA GAGACTGAGT TTTTTCATTT CTGAAGAGAA 180
 AGGGCATTTG CTCCTACAAG CTGAAAGGCA CCCCTGGGTG GCTGGGGCCC TCGTGGGAGT 240
 30 TTCTGGGGGA TTGACCCTTA CAACATGCAG TGGCCCTACA GAAAAACCTG CAACTAAAAA 300
 TTATTTTTTA AAAAGGCTCC TCCAGGAAAT GCATATAAGG GCTAATCACC CAGTATTTTG 360
 35 ARGCTTCGAA GARGTAATAR AMCCCTGGAG AGAGAACTG AGACATGTAA GAGGGTGGGA 420
 ATGACTCAGT GGTGGCACAC TATGGAGTCC TGCCCAACAAG TAGCACACAT CAACCCACTA 480
 40 CACAGAAATC CTAGG 495

(2) INFORMATION FOR SEQ ID NO: 29:

45 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 556 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 50 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 29:

AGCTTAACGT CATGATTCAT TAGGGGAATG CAAGCAAAA CCATGATGAG AATGCCCTTA 60
 55 GACACCTCTT AGAAGAGCTG CTAGAAAGGC AGACAGCACC AAGCGCTTAA ATGAGATGGG 120
 GGCAGTGGTG CTTCTTCTGT GCCTACTGGT AGGGGTGCAG CAGAGTGGTT CAGTCTGGGA 180
 60 CAGTTAGCTG GACATCACGT GGACCAACA CACGCATTTC CTGGGTACT TACCAAGGAG 240

AATAGAAAGC AGGCAGATCT TTACAGCAGC TCTTACCTGW TTGCAAAACA ATGGAAATGC 300
 5 CCACATGTCC ACAACAAGT KTGTGGTCTG CCTGTGCCAT GAAGCACAGT GTGGCTGAGC 360
 GTCAAGAGTC CCCACACTCA AAGGAGGCAG CAGATACAGG GCTGCACACT GTGTGATTCC 420
 ACACATGTGA CATCTCGGAC ACGGACATGC TGGATGGCAA AACGAGCATC GGGCTGAGAG 480
 10 GACTGCTGAG AAGGGGAACG GGGCTGCTGG GATGTGGGTT GATTGTAGCA GTAGCTCATG 540
 GAGATGTGAC CTCAAA 556

15

(2) INFORMATION FOR SEQ ID NO: 30:

20 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 434 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 30:

CTAAATGGTG ACTGTGGCTT TGTCGAGACA GGCCCCAAAT GGTAGGTGTG AACACAACAT 60
 GCACAGAATG AGGAGACATG CAGAGTGCTG AAATACTGTC CTGGACAGAT GTGTTACATG 120
 30 ACTTTCCTTT CAGCTTATTT CTGTGGCCTG CCTTTGAAGA TAGAGCTTTG TTGATATTTA 180
 CATTAAACCA AATGTATATA YATGTTCCTA TTCTGACATG TTATTTAGCA AARGAAAAAR 240
 35 GAGTAATTCT ACATCAGCAT CTTTAGTGCA TGCTAAAAGA TTAAAAATGT CTTTGGGGGA 300
 ACATGTTTTG TATACATAAA TGTTTAGATA GAAATATTTA TAGAATNCTC TATGTGAGTA 360
 TTATCTCCC TATGTATATT TATATCTAGA TGTGTCAATC TTTGTATTGA TATGAAATGC 420
 40 TATGAATAGT GAGA 434

45

(2) INFORMATION FOR SEQ ID NO: 31:

50 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 715 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 31:

CCACGCGTCC GATCTCACAG CTCCGACACT ATTGCGAGCC ATACACAACC TGGTGTGAGG 60
 AAACGTACTC CCAAACTAAG CCAAGATGC AAAGTTTGGT TCAATGGGGG TTAGACAGCT 120
 60 ATGACTATCT CCAAAATGCA CCTCCTGGAT TTTTCCGAG ACTTGGTGTT ATTGGTTTTG 180

CTGGCCTTAT TGGACTCCTT TTGGCTAGAG GTTCAAAAAT AAAGAAGCTA GTGTATCCGC 240
 CTGGTTTCAT GGGATTAGCT GCCTCCCTCT ATTATCCACA ACAAGCCATC GTGTTTGCCC 300
 5 AGGTCAGTGG GGAGAGATTA TATGACTGGG GTTTACGAGG ATATATAGTC ATAGAAGATT 360
 TGTGGAAGGA GAACTTTCAA AAGCCAGGAA ATGTGAAGAA TTCACCTGGA ACTAAGTAGA 420
 10 AAATCCATG CTCTGCCATC TTAATCAGTT ATAGGTAAAC ATTGGAAGTC CATAGAATAA 480
 ATCAGTATTT CTACAGAAAA ATGGCATAGA AGTCAGTATT GAATGTATTA AATTGGCTTT 540
 15 CTTCTTCAGG AAAAAGTAGA CCAGACCTCT GTTATCTTCT GTGAAATCAT CCTACAAGCA 600
 AACTAACCTG GAATCCCTTC ACCTAGAGAT AATGTACAAG CCTTAGAACT CCTCATTCTC 660
 ATGTTGCTAT TTATGTACCT AATTAAAACC CAAGTTAAAA AAAAAAAAAA AAAAA 715
 20

(2) INFORMATION FOR SEQ ID NO: 32:

25 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 486 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 30 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 32:

GAGCCAGTGC CGGCGAAAGG GGACCTTCCT CTACTTCCTG CCACAGACCC TGTCCCCACA 60
 35 CACTTCCTGC CCCTGCTCTG CTGGGAGGCC ACTTCCTCCC CCAGTGCTGG ATTCCACCCC 120
 CAGCTACCCC TCAAACATGG CCCCCTCTCT CCTCTGCTT GCCCTCTCT GCTCCCTGGA 180
 40 GGCTGTTCTG TCCTCCCTC TTGAAAAGCA ATGCCAGCTT CTTGGGATCT TCTGCCAACT 240
 CCAGCTACCA TGCCCTTTGC TCCTGTCAGC TCAGCTCCTC AAGGGAATTG TCTAMCCTCG 300
 GTGTCCTGCT TCCTCCCTC AACCTCCTCA CCTGCTCCA AGCTGGCATC TGCCCTCCA 360
 45 CTGCACAGAA CGNTCCCCC ACCACCTGCC TTTACAGGGA GGAAGCAGCA ACATGGAAGA 420
 ANCGAACTAT AGGGGCTACA ANGATGCTCA GCTCTGATCC CGAAGGCAAA AAGNATCTTT 480
 50 GGGCAC 486

(2) INFORMATION FOR SEQ ID NO: 33:

55 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 725 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 60 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 33:

5	GTCCTCTGG TAATAATTAG GTTATCCCA GAAGCACAGT GTCATTCTTT AAATAAAAGC	60
	TTTCCTGTTT AAAGCTTTTC AAAGGAGCAG ACCACCTTGA AGATTCCCC TAGGGTIGAT	120
	ATGTGCTAA TTCATTTTAT AAAAATTATT CTGTCTTCA TTTTAAAGCT TTGGCTATAT	180
10	AGTCAGAAAT GTCCTAAATA ACAAACTATT TTGTATTTAA TTTAGGGAAG ACTAAAGGGA	240
	AGAAAAATGA AAATCAGTC TTTATGTAAG CTCCAAGGAT ATTAGGGCTT AAAGGGCTTT	300
15	TCTAGTTTTA TGAGAATTG TACTACTGAT TTTATATAT TCCTGTTTTT GATGAACAGA	360
	TCTCTGGGA AATTGTTGAG TTACAATGGC ATTTCACTGT GATCCCTCTC AAGCTCAGAT	420
	CAGTCTATA ACCCAATGAC AACCTGTCTC TTTGGTTTAC TGTCTGTGA AATGTCAGCT	480
20	CAAGTTTCCC AGAAGTCGTG TGTATATGAT GAGTCAGAGT GCTTTTCCTC GGTGGGACAG	540
	TTGTGGCCC TCTAATTTT GGTGTATGTG CTTCCAAGTA TCTAAACCTC CAGTCTGATC	600
	TGTATATGCT ATCCTAACTG TTAATTGTAT TATTGATTAT GTTGATTATC TTGCTTGAAG	660
25	GTTCATACTT TTCAATTGA TAGAAATAAA GTTTTTTCT GCTTATAAAA AAAAAAAAAA	720
	AAAAA	725

30

(2) INFORMATION FOR SEQ ID NO: 34:

35	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 437 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
40	(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 34:

	CACACAGCAT GTCGCCCTCA GACGTGTCCA TCCTGTACCA CATGAAAACG CTGCTGCTCC	60
45	TGCAAGATAC TGAGAGATTG AAGCATGCTC TGGAAATGTT CCCAGAACAT TGCACGATGC	120
	CTCTGCTTT TATTGGCTCT TGTGAAATC AAATTGGAAG ATCTTCAGTC CCAGCTGCAC	180
50	CCAACGTGGA AAAGTATTCC AGGTCCATCC CCAAGGAACC AACACCGATG ACATGGACTC	240
	AGGAATCTTA TAACCTACGT GGACTCTTTC CATCCGTACA TTGTCGTGCA CATGCCACTC	300
	ATCACCTGGC GTGCCAGAT CCTCGCARGG CAACACCCTG TGATAATTCC AGGTGATTCT	360
55	CTACATCTGC AGCTTGAGGT TAGCCTCATA TCACATTACA TTCTCACTAN AAACNAAAAA	420
	AAAAAAAAA AACTCNA	437

60

(2) INFORMATION FOR SEQ ID NO: 35:

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 943 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 35:

GGCAGGAGCT GGAACAGAGA CTAAATCCCA CGAAACTGAC ATTGTTAAAC AACTAAAAC 60
AGAAGTACTT ACCTCTTGAA GATTTAATAT ATAATGGTTG ACATGATACA TGTACATGAT 120
15 GAATGACCAG ATGCTTATGG TCTACATTTT CCTTTATCCT GTTAGTATTA CCTTCCTTAA 180
TCTTTGTTC ATAACATGCT AATTCCTCTT CAGTGTTTAT TTTCTAGTGA CAGAAATGCTA 240
20 ACATTTCTTA CACCCTGGCA GAAGGGAGAG AAATGTGTTT TGGGGTGGGT AACTAAATTT 300
TTGAGTGAAA TATCATAAGA TGANAATGGA AANAAGGAGA CACAAANAGT TATNACAAAA 360
AAACAATGGT TTTTTTAGCC ATTTGACTGG CTCTTTAAAT AGTCTACAAG ACATTCACGT 420
25 TTAACATCAC TTTTAGTGAA ATAAAATGTG CCATACTAGT ATGTGCTTCA AAAGGGCAAA 480
TGTGCTTTAG TGCCCTAAGG CTAAATTTTG GTCATTTGAC ATCAGAGATG TTGTAAGTAT 540
30 TGCACTTAAT ACGCACCTAT TTNTCAATAG TGTATTTTTT TGGNTAGCAT TTTTTTTACC 600
ACTATNTTGT TGATAGCTTT TTGTTCTNIN AGGTTGNAAN ATGACAGTGC TNATNTCAA 660
CAGATTACCC ATNTGCAGAA CTAAGGGAAG CNATTTATGT ATGAAAGNAA TTNTTGAATT 720
35 NGTCATTNTC AACCNPTGNA TTAAAGCTTA GACTAAATAG TAATATATNG TGGGNAGGAT 780
TTTGTTTTTG TGATATTTNT GTGNATTAAG GNATAGATGT TAACCNITAT TTTGTAGNAA 840
40 AGTGANTTGT ATGTGGTTAA TTATAAATAA AACTGGTACC AGGNAAAAAA AAAAAAAAN 900
NAAAAAAAA AAAAAAAAA AAAAAAAAA AAAAAAAAA AAA 943

45

(2) INFORMATION FOR SEQ ID NO: 36:

(i) SEQUENCE CHARACTERISTICS:

- 50 (A) LENGTH: 604 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 36:

GGCAGGAGAA ATCTTCATGC TGTAAGTCACT CCAGACCATG GAGTGGCTTT CCAGCTGAAT 60
GAATCCTATG TCTCGCGTGC AGGTGGTTGG TTTTCAATGT TCTTGCTAAT TTTTTTCTA 120
60

TTGGATCTTG GGAGTTTCTT TTGTTTGCTC CTGTGTTTGC CCAGCTTTAA TAAAACCAGG 180
 CGCAAACAAA AACCATAGCA TTCTGAACAA TAGGGGGCCC ACATTGGACC CAGTATGTCA 240
 5 CTTTAATGGA CTTCAAGAAA AAATCTGAAT GGGAAAAATG AACTAGGAA TGTATACTCC 300
 ACACATTTTA TGCCATATAA TGGTGTGTTT TCTTAATTTT GTTCTTGTG GCGAAATGTG 360
 10 GCTTTCAAAT TAAAATGACC TTTTCTTCTT TGAAACTTTT TGTTTIGACT TGTATAATTA 420
 AGGGTTTGA AAGATTGATA ATTCTGAGAG AGGTTTGCAA CCAGGAGATA CAAAGAAGTC 480
 TCAGTAGTAA TCTGTTCAT GTGCTTTTAC AGCCAGCTAC ATTTAAGGAT GTATTAGTTA 540
 15 CAGAAATTAT ATGTCTGTGT ATGTGTCTCT ACTCAATAAA GTACATGCCT CCACAAAAAA 600
 AAAA 604

20

(2) INFORMATION FOR SEQ ID NO: 37:

25 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 349 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 37:

GTGAGTGCCC GGGAGCCCCG AGGCCCTGCC CCTAAGAAGG ATATCTYTRA CCGCTCCCTT 60
 GTCCACACCC TAACCCCCCA GCTGCTCAGG CAGTGGGCAC ATGGCAGGGG CCTCACTGGG 120
 35 GGCACATAGA GCATTTGGGG GACTGCGAGT GCTCACCTTT GACTTCCTGC AGGTCGGGGG 180
 AAAACCAGAT CATGATGACC AAAGTYTACA TATCTTGAT CTTTCATGGTG CTGATCCTGC 240
 40 CCTCCCTGGG TCTCACCAGG TATATGCCAC CACYTCTGY TCTAAATCA GAATAAGAGT 300
 CACATCAGGA GAGCACTGTC CCCAGGANAA TGCAAACGGG TTGGCAGCA 349

45

(2) INFORMATION FOR SEQ ID NO: 38:

50 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 672 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 38:

GTAGTCGTTG CGGTTGCCGG GATGGCGAAG ATCTCGCCGT TTGAAGTCGT AAAACGCACC 60
 TCGGTACCGG TGCTTGTTGG TTTGGTGATT GTWATCGTTG CTACAGAGCT GATGGTGCCA 120
 60

GGAACGGCAG CAGCGGTCAC AGGCAAGTAA ATAGTAATGC CGGAGCAAGT TTCCTCCGGC 180
 TTTATCATGT CACCCACTGT GGTATATGCG TTGTGGTCTG CCAACTTTGC CGTGAACAAT 240
 5 TTCAGCAATA ATCAGATGGC GGCTGGCGCA ATATTCAAGA TAACGCCCTGG CAGTGGTGGC 300
 GCTGATGGTT CAGTGCCTGC GSCACCGTTT YTGCCGTATG TTGCACACCA GGNTCITTAA 360
 ACAGTTTTCG SACCCGCTTT AGCGTCAAGG GTTCAATGCC GGTCCGTAGC TCGTCCTTAG 420
 10 GTTCACCGCG AGCATAAGCA TTAAACATCT CATCAATTG CTTCTGGCTG GCGCTATCAA 480
 TACTTTCCAG CATATGTTTA CGCTGGCGGA AACGGGTTAG CGTTTGCCCC ARCMGWTCAT 540
 15 AGGCAATGGG CTTAATGAGA TAATCAAATA CACCACAACG TACGGCTTCA GACACCGTTT 600
 CCATATCGCT GGCTGCAGTG GTAAACACCA CGTCGCCGGG ATAATGCGCC TGCACCAGTT 660
 CATGCAGTAA AT 672
 20

25 (2) INFORMATION FOR SEQ ID NO: 39:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1908 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 30 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 39:

35 AGAGTTGATA TTTTATAGAA CAGTAATTTT ACTTTTAAGG AAATGGGCTA GCTCTTTGAC 60
 TNAGAGCTG TAGGAAGCTC AACATTTCCT TGTAGAGAAC GTTGCTTTT TTGGATTGTA 120
 CAGGTATAAA AACATTGCTT TTGTTGAATT GTATAGGTGT AAAAAGGGAA TAACTGTATG 180
 40 CAGGTTTGAA AAGGAAATGT GCTTTAGGCA TGAGTCATAA GATGCCATTG TACTTGTAGG 240
 CATTTTATTT TCCTTTAGAA ATGGACATCA GCTCTTCTCT TCTGACTGGT AACACATAGC 300
 45 CCCAAAGCAT GAGATTATTT TTCATTGGGT TTTTATTGTT GTTTAGTTTT GGTTTGTTAC 360
 GCCAGCCCAG TCTGTCTGCG GAACACTGAC TCTGCTCTCT AATGAGAACA AAGTTAGAAA 420
 TCTGCCGATA ACCTAAAATA ATTTAGAAAT GAATTAAAAA TGTGAAATCG GGTAAAGTG 480
 50 ATGATGATAA AATAGCATGC AAGAAACAAG CTCCTTCCAT CAGACTTGGC TACTGTTTTT 540
 TTCTGGTACG ATTTGGTTTG GAAGAGCCTC TTGTTTCCTT CTCPTTGGGG TATGTCCTCG 600
 TTCTTAATA TGTTTGTAAC ATTATGAGA TATAATTCAC ATACCTTACA ATTCACTTAT 660
 55 TTTAAGGGTA CAATTTAGTG GTTTTAGTG TATTCACAAA GTTGTGTAAC CGTGACCACA 720
 GTCAATTTTA GAACATTTTC TTACCCCAA AAGAAACCTT GTACCTTGA GCAGTCACCT 780
 60 CTCATTTTCT CCCAGTGCCC ACCCATCCC CGAGCCCKG GAACCACTAA TCTATTTCTC 840

	TCTCTGTAGA TTTGCTTATT CTGGTCATTT CATATAAATG GAATTCCTACA ATATTCGGTC	900
5	TTTTGGGACT GGCTTCCCAA ATATGATTTT CTATATGGAG TGAGAAAATT CTTCTCATCT	960
	TGAGAACTCT TATTGCTGTG AAAGGGAGTG GTTGGTAAAA TCAATAGATT TCAGGCAAGA	1020
	GGGCCAGATA CCTAACAGGT TTTTCTCCGT GAATCTTATG CTGAGTAGTT TTTCTCATA	1080
10	ACCAAGCATT TATGATATAT TACTACTTAT AATACTGTGG CTAGTCTCTA GAATGGATGT	1140
	TGAAATCTTT GCCTCCTCAG TCGGGAAGAG TCCTGCTAAA AATCAGGCTA AAAATCAGGC	1200
15	CAAAAATCAG GCCAAATGAC TTGGCAAATA ATTGACAAAG TGGTTTTCAC GTGTGTCTAT	1260
	CTTTGCTAGC AGCTTGTATA CCTCAGGCCA GGTGAGCTCC CCAAATTTCT TTTTTCATTT	1320
	ACTCCAGTGA GTTCTGCTG TCTTTTTCAA GTATGTACCA TAGGACTPAA AGGTGATTTG	1380
20	GATGCGTTGT AACACTGCTA AATATGCTAA GTACAGAATT TTATCTACAG TACTGTGAGA	1440
	CAGTCAATTA TTGCCTAGGG TAGTTCAAAA ATATGATGTG AGCTAGTTAA GCCTTTGCTT	1500
25	GACTGATTTT AGTGATATTC AGAAGTGTGT ACCAATCAAG GCTCTTTAAA ATACGGAACG	1560
	ACTCACTTAA TAACCAGGGA ACCAGCCAAA TACTGTGCAG CCGCAGAATA TGCATATCAA	1620
	TGAGTTGGAG GTGATTATTC TCTGTAATC CTAATGATT GTTTTCTAAG CATTGTGGCT	1680
30	TCTCAGTGGC TTGACAGCAT CTTCTGGTT GTATGTGGCC TGTTTACATG ATGTATTGAA	1740
	TAATGTTGTT TGTGTGAGC ATCAATGCCT GTAACACCAA ACTAAACACG TGTTTTGGG	1800
35	ATATGTTTCC AATCTTTAAA TGACCTTGCC CTGTCCAATA AATAAATGAT TGTCTCACC	1860
	TGTTAAAAAA AAAAAAATT AAAAAAATG GNGGGGGGC CCGGTACN	1908

40

(2) INFORMATION FOR SEQ ID NO: 40:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 458 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 40:

	CCTCAAAAAA AAAAANGAAA GGAAAGAGGT CTCTACACAA GCCCGTGATT CTTTCATGGCA	60
	AGGGATAACA TCAGAAATGT TTCATTTYCK GCTATTAGTT TCCATTCTTT TCCCCATCCA	120
55	GGCATAAAGA GAAACAAAAG ACAATGATGG TATCTCTGT GTCTCAGCT TTGGCACTTT	180
	TGTTGATGTT GCTAAGGAGC AGTGACCTTG CTAAAAAGAC TGAATAATCC ACCCACTGAA	240
60	TAGCTAACCT GGGGAGGAAA TGAAATTTT CTTGTGGAT CTCCCCAAT CCATTGTTGT	300

CACCAGGCCC TCCCAGAACC TCCTCAGTTC CTTACAGTG CAACCCGTG TACTTGGCCC 360
 GCAACCCAAT AGTATTGTGC CTCACTTCAC CTTCCATGGG CAACTGCCCT CCCTTCTGGA 420
 5 CATAAACCT CATATTTTAA ATNAAGTTGA AATTTGAA 458

10 (2) INFORMATION FOR SEQ ID NO: 41:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1153 base pairs
 (B) TYPE: nucleic acid
 15 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 41:

20 GGCACAGAGC CTCGACCCA GGTGGTCTGG AGCCTGCCGG GAGAGTGGTG GCATCTGAGA 60
 GGCTGGTCGT GGACTGTGGT TGGGGGAGGT GGGAGCTGTT TTAACCGTGT GCCCCCTCTC 120
 CTGTGCCGGC GTGGGCATCC CCGGGGCGAG TGAACCCGG GCGCTCCTCC AGCTTCCGAG 180
 25 TCCAGCCAGC CTGGGCGCGG GCGCGCCCC GAGACACCCG AGGAGTCCGT TCCTCCCTGG 240
 TTACGTGGAC TGTGGAGCTG GTCTCTTG TGCTCAGCGC GTGCGGAGGT TGAAGCGTAC 300
 30 CTGCGGAGGT CGCACCAGG CGTGAGGAGG AGGAGGAAGG GCATGAGCCG AGCTTGAGGA 360
 ATCCGTGCTC CAAACTCTAC ACTCAAGGAT GCACTGCGCA ACTCTGGTGG CGATGGGCTG 420
 GGCAGATGT CCTTGGAGTT CTACCAGAAG AAGAAGTCTC GCTGGCCATT CTCAGACGAG 480
 35 TGCATCCCAT GGAAGTGTG GACGGTCAAG GTGCATGTGG TAGCCCTGGC CACGGAGCAG 540
 GAGCGGCAGA TCTGCCGGGA GAAGGTGGGT GAGAACTCT GCGAGAAGAT CATCAACATC 600
 40 GTGGAGGTGA TGAATCGGCA TGAGTACTTG CCAAGATGC CCACACAGTC GGAGGTGGAT 660
 AACGTGTTTG ACACAGGCTT GCGGGACGTG CAGCCCTACC TGTACAAGAT CTCCTTCCAG 720
 ATCACTGATG CCCTGGGCAC CTCAGTCACC ACCACCATGC GCAGGCTCAT CAAAGACACC 780
 45 CTGCCCTCTG AGCGTCGCTG GATCTCTGGG AGCTCCTTGA TGGCTCCCAG ACCTTGGCTT 840
 TTGGGAATTG CACTTTTGGG CCTTTGGGCT CTGGAACCTG CTCTGGGTCA TTGGTGAGAC 900
 50 TTGGAAGGGG CAGCCCCCGC TGGCTTCTTG GTTTTGTGGT TGCCAGCCTC AGGTCACTCT 960
 TTTAATCTTT GCTGACGGTT CAGTCTTGCC TCTACTGTCT CTCCATAGCC CTGGTGGGGT 1020
 CCCCCCTCTT TCTCCACTGT ACAGAAGAGC CACCACCTGG ATGGGAATA AAGTTGAGAA 1080
 55 CATGAGTTTG GGCTGAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA 1140
 AAAAAAAAAA AAA 1153

(2) INFORMATION FOR SEQ ID NO: 42:

- 5 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1983 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
10 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 42:

	GGCACGAGAG GGGCCGAGCC GACAAGATGT TCTTGCTGCC TCTTCCGGCT GCGGGGCGAG	60
15	TAGTCGTCCG ACGTCTGGCC GTGAGACGTT TCGGGAGCCG GAGTCTCTCC ACCGCAGACA	120
	TGACGAAGGG CCTGTGTTTA GGAATCTATT CCAAAGAAAA AGAAGATGAT GTGCCACAGT	180
20	TCACAAGTGC AGGAGAGAAT TTTGATAAAT TGTTAGCTGG AAAGCTGAGA GAGACTTTGA	240
	ACATATCTGG ACCACCTCTG AAGGCAGGGA AGACTCGAAC CTTTTATGGT CTGCATCAGG	300
	ACTTCCCCAG CGTGGTCTA GTTGGCCTCG GCAAAAAGGC AGCTGGAATC GACGAACAGG	360
25	AAAACTGGCA TGAAGGCAAA GAAAACATCA GAGCTGCTGT TGCAGCGGGG TGCAGGCAGA	420
	TTCAAGACCT GGAGCTCTCG TCTGTGGARG TGGATCCCTG TGGAGACGCT CAGGCTGCTG	480
30	CGGAGGGAGC GGTGCTTGGT CTCTATGAAT ACGATGACCT AAAGCAAAAA AAGAAGATGG	540
	CTGTGTCGGC AAAGCTCTAT GGAAGTGGGG ATCAGGAGGC CTGGCAGAAA GGAGTCCTGT	600
	TTGCTTCTGG GCAGAACTTG GCACGCCAAT TGATGGAGAC GCCAGCCAAT GAGATGACGC	660
35	CAACCAGATT TGCCGAAATT ATTGAGAAGA ATCTCAAAAG TGCTAGTAGT AAAACCGAGG	720
	TCCATATCAG ACCCAAGTCT TGGATTGAGG AACAGGCAAT GGGATCATTC CTCAGTGTGG	780
40	CCAAAGGATC TGACGAGCCC CCAGTCTTCT TGGAAATICA CTACAAAGGC AGCCCCAATG	840
	CAAACGAACC ACCCCTGGTG TTTGTGGGA AAGGAATTAC CTTTGACAGT GGTGGTATCT	900
	CCATCAAGGC TTCTGCAAAT ATGGACCTCA TGAGGGCTGA CATGGGAGGA GCTGCAACTA	960
45	TATGCTCAGC CATCGTGTCT GCTGCAAAGC TTAATTGACC CATTAATATT ATAGGTCTGG	1020
	CCCCCTTTTG TGAATAATATG CCCAGCGGCA AGGCCAACAA GCCGGGGGAT GTTGTTAGAG	1080
50	CCAAAAACGG GAAGACCAATC CAGGTTGATA ACACTGATGC TGAGGGGAGG CTCATACTGG	1140
	CTGATGCGCT CTGTTACGCA CACACGTTTA ACCCGAAGNT CATCCTCAAT GCCGCCACCT	1200
	TAACAGGTGC CATGGATGTA GCTTTGGGAT CAGGTGCCAC TGGGGTCTTT ACCAATTCAT	1260
55	CCTGGCTCTG GAACAACTC TTCGAGGCCA GCATTGAAAC AGGGGACCGT GTCTGGAGGA	1320
	TGCCTCTCTT CGAACATTAT ACAAGACAGG TTGTAGATTG CCAGCTTGCT GATGTTAACA	1380
60	ACATTGAAA ATACAGATCT GCAGGAGCAT GTACAGCTGC AGCATTCCTG AAAGAATTCG	1440

TAACTCATCC TAAGTGGGCA CATTTAGACA TAGCAGGCGT GATGACCAAC AAAGATGAAG 1500
 TTCCCTATCT ACGGAAAGGC ATGACTGGGA GGCCCACAAG GACTCTCATT GAGTTCTTAC 1560
 5 TTCGTTTCAG TCAAGACAAT GCTTAGTTCA GATACTCAAA AATGTCTTCA CTCTGTCTTA 1620
 AATTGGACAG TTGAACCTTA AAGGTTTTTG AATAAATGGA TGAAATCTT TTAACGGAGA 1680
 CAAAGGATGG TATTTAAAAA TGTAAGACAC AATGAAATT GTATGCCTTG ATTTTITTTT 1740
 10 CATTTACAC AAAGATTAT AAAGTAAAG TTAATATCTT ACTTGATAAG GATTTTAAAG 1800
 ATACTCTATA AATGATTAAA ATTTTATAGAA CTTCCTAATC ACTTTTCAGA GTATATGTTT 1860
 15 TTCATTGAGA AGCAAAATTG TAACTCAGAT TTGTGATGCT AGGAACATGA GCAAACTGAA 1920
 AATTACTATG CACTTGTGAG AAACAATAAA TGCAACTTGT TGTGCAAAAA AAAAAAAAAA 1980
 AAA 1983
 20

(2) INFORMATION FOR SEQ ID NO: 43:

25

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1406 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 43:

35 ATGATGATGA CTTTGAAGAC GATTTTATTC CTCCTCTCC AGCTAAGCGC CTTGAGGTTA 60
 ATAGTTGGAA AAGACTCTAT AGATATTGAC ATTTCTTCAA GGAGAAGAGA AGATCAGTCT 120
 TTAAGGCTTA ATGCCTAAGC NCTTGGTCTT AACTTGACCT GGGATAACTA CTTTAAAGAA 180
 40 ATAAAAAATT CCAGTCAATT ATTCTCAAC TGAAAGTTTA GTGGCAGCAC TTCTATTGTC 240
 CCTTCACCTA TCAGCATACT ATTGTAGAAA GTGTACAGCA TACTGACTCA ATTCCTAAGT 300
 CTGATTTGTG CAAATTTTTA TCGTACTTTT TAAATAGCCT TCTTACGTGC AATTCTGAGT 360
 45 TAGAGGTAAA GCCCTGTTGT AAAATAAAGG CTCAAGCAA ATGTGACAGT GATAGCAACT 420
 TTCCACACAG GACGTTGAAA ACAGTAATGT GGCTACACAG TTTTTTTAAC TGTAAGAGCA 480
 50 TCAGCTGGCT CTTTAATATA TGAATAACA ATAATTAAA ACAATCATA GTAGCAGCAT 540
 ATTAAGGGTT TCTAGTATGC TAATATCACC AGCAATGATC TTTGGCTTTT TGATTTATTT 600
 GCTAGATGTT TCCCCCTTGG AGTTTGTGCA GTTTCACACT GTTGTCTGGC CCAGGTGTAC 660
 55 TGTTTGTGGC CTTTGTAAAT ATCGCAAACC ATTGGTTGGG AGTCAGATTG GTTCTCTAAA 720
 AAAAAAAAAA AAAACGACAT ACGTGACAGC TCACTTTTCA GTTCATTATA TGTACCGAGG 780
 60 GTAGCAGTGT GTGGGATGAG GTTCGATACA GNCGTATTTA TTGCTTGTCA TGTAATTAA 840

5 AAACCTTGTA TTAACTCTT TTCAATCCTT TTAGATAAAA TTGTTCTTTG CAAGAATGAT 900
 TGGTGCTTAT TTTTTCAAAA ATTTGCTGTG AACACGTGA TGACAACAAG CAACATTTAT 960
 CTAATGAACT ACAGCTATCT TAATTTGGTT CTTCAAGTTT TCTGKTGCAC TTGTAAAATG 1020
 CTACAAGGAA TATTAAAAAA ATCTATTCAC TTAACTTAT AATAGTTTAT GAAATAAAAA 1080
 10 CATGAGTCAC AGCTTTTGTG CTGTGGTAAC CTATAAAAAA AGTTTGTCTT TGAGATTCAA 1140
 TGTAAGAAGC TGAAAACAAT GTATATGTTG TAAATATTG TGTGTTGTGA GAAATTTTGT 1200
 TCATAAGAAA TTAAAGAAGC TTACCAGGAA GGTMTTAAAG TTAGAAATAT TCCATGCCAA 1260
 15 TAAAATAGGA AATTATAAAT ATATAGTTTT AAGCCTGCAT CAGTGGGAGT CTTGGCTATG 1320
 TAGTTATGTA GTTATTATGN AACCACCAAG ATTTTTTGG CTATTACCG TAACCAAAGG 1380
 20 GGCCGATTAA NTGGTTTGAA GNCTTG 1406

25 (2) INFORMATION FOR SEQ ID NO: 44:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1391 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 44:

35 GGGCCTGAAG GCGGCRGCGC AGTCCCGAGC AGTGCTCGCT CCTGCTCGGG GCGCTGCGGC 60
 CCCGGGCGTC GCCATGACCA GTGAGCTGGA CATCTTCGTG GGAACACGA CCCTTATCGA 120
 CGAGGACGTG TATCGCCTCT GGCTCGATGG TTA CTGGTG ACCGACGCGG TGGCCCTGCG 180
 40 GGTGCGCTCG GGAATCCTGG AGCAGACTGG CGCCACGGCA GCGGTGCTGC AGAGCGACAC 240
 CATGGACCAT TACCGCACCT TCCACATGCT CGAGCGGCTG CTGCATGCGC CGCCCAAGCT 300
 45 ACTGCACCAG CTCATCTTCC AGATTCCGCC CTCCCGGCAG GCACTACTCA TCGAGAGGTA 360
 CTATGCCTTT GATGAGGCCT TTGTTGCGGA GGTGCTGGGC AAGAAGCTGT CCAAAGGCAC 420
 CAAGAAAGAC CTGGATGACA TCAGCACCAA AACAGGCATC ACCCTCAAGA GCTGCCGGAG 480
 50 ACAGTTTGAC AACTTTAAAC GGGTCTTCAA GGTGGTAGAG GAAATGCGGG GCTCCCTGGT 540
 GGACAATATT CAGCAACACT TCCTCCTCTC TGACCGGTTG GCCAGGGACT ATGCAGCCAT 600
 55 CGTCTCTTT GCTAACAACC GCTTTGAGAC AGGGAAGAAA AAATGCACT ATCTGAGCTT 660
 CGGTGACTTT GCCTTCTGCG CTGAGCTCAT GATCCAAAAC TGGACCCTTG GACCCGTCGA 720
 60 CTCACAGATG GATGACATGG ACATGGACTT AGACAGGAAT TTCTCCAGGA CTTGAAGGAG 780

CTCAAGGTGC TAGTGGCTGA CAAGGACCTT CTGGACCTGC ACAAGAGCCT GGTGTGCACT 840
 GCTCTCCGGG AAAGCTGGGC GTCTTCTCTG AGATGGAAGC CAACTTCAAG AACCTGTCCC 900
 5 GGGGGCTGGT GAACGTGCCG CCAAGCTGAC CCACAATAAA GATGTCAGAG ACCTGTTTGT 960
 GGACCTCGTG GAGAAGTTTG TGGAACCCTG CCGCTCCGAC CACTGGCCAC TCAGCGACGT 1020
 10 GCGGTTCTTC CTGAATCAGT ATTGACGCTC TGTCCAATCC CTCGATGGCT TCCGACACCA 1080
 GGCCCTCTGG GACCGCTACA TGGGCACCCCT CCGCGGCTGC CTCTGCGCC TGTATCATGA 1140
 CTGAGGTGCC TCCCAACGTC CGCCACGCT GACAATAAAG TTGCTCTGAG TTTGGAGACT 1200
 15 GGTCTCTGCT CCGGGGAGCA AGTGGGGGCG GTGCAGATGT GCCTGTGTCT GTCTCTGAGC 1260
 ACCTGGTGTC CGTGTAACAAG GATGGATGTG TNCNGTGGCT CCTTGGGAAC TGAGACATAT 1320
 CTCAGGAAT GGTGTCTGTG CTCAGCCCAT CCACCAGAAG AGTCTGCTCA CAAAAAAAAA 1380
 20 AAAAAAAAAA A 1391

25 (2) INFORMATION FOR SEQ ID NO: 45:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1569 base pairs
 30 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 45:

35 GGCACGAGTG GAGATGGCTG CGGCCGTGGC GGGGATGCTG CGAGGGGGTC TCCTGCCCCA 60
 GGCGGGCCCG CTGCCTACCC TCCAGACTGT CCGCTATGGC TCCAAGGCTG TTACCCGCCA 120
 40 CCGTCGTGTG ATGCACTTTC AGCGGCAGAA GCTGATGGCT GTGACTGAAT ATATCCCCC 180
 GAAACCAGCC ATCCACCCAT CATGCCTGCC ATCTCCTCCC AGCCCCCAC AGGAGGAGAT 240
 45 AGGCCTCATC AGGCTTCTCC GCCGGGAGAT AGCAGCAGTT TTCCAGGACA ACCGAATGAT 300
 AGCCGTCTGC CAGAAATGTG CTCTGAGTGC AGAGGACAAG CTCTTATTG CGACACCAGC 360
 TGCGGAAACA CAAGATCCTG ATGAAGGTCT TCCCCAACCA GGTCTTGAAA GCCCTTCTG 420
 50 GAGGATTCCA AGTACCAAAA TCTGCTGCCC CTTTTGTGG GGCACAACAT GCTGCTGGTC 480
 AGTGAAGAGC CCAAGGTCAA GGAGATGGTA CGGATCTTAA GGGACTGTGC CATTCCTGCC 540
 GCTGCTAGGT GGCTGCATTG ATGACACCAT CCTCAGCAGG CAGGGCTTTA TCAACTACTC 600
 55 CAAGCTCCCC AGCCTGCCCC TGGTGCAGGG GGAGCTTGTA GGAGGCCTCA CCTGCCTCAC 660
 AGCCCAGACC CACTCCCTGC TCCAGCACCA GCCCCCCAG CTGACCACCC TGTGAGACCA 720
 60 GTACATCAGA GAGCAACGCG AGRAAGGATT CTGTCATGTC GGCCAATGGG AAGCCAGATC 780

	CTGACACTGT TCCGGA CTG TAGCCAGCCT GTTTAGCCAG CCCTGCGCAT AAATACACTC	840
5	TGCGTTATTG GCTGTGCTCT CCTCAATGGG ACATGTGGAA GAACTTGGGG TCGGGGAGTG	900
	TGTTTGTCAC TTGGTTTTC A TAGTAATGA TATTGT CAGG TATAGGGCCA CTTGGAGATG	960
	CAGAGATT C CATTT CAGAT GTCAGTCACC GGCTTCGTCC TTAGTTTTCC CAACTTGGGA	1020
10	CGTGATAGGA GCAAAGTCTC TCCATTCTCC AGGTCCAAGG CAGAGATCCT GAAAAGATAG	1080
	GGCTATTGTC CCCTGCCTCC TTGGTCACTG CCTCTTGCTG CACGGGCTCC TGAGCCCACC	1140
15	CCCTTGGGGC ACAACCTGCC ACTGCCACAG TAGCTCAACC AAGCAGTTGT GCTGAGAATG	1200
	GCACCTGGTG AGAGCCTGCT GTGTGCCAGG CTTGTGCTG AGTGCTGTTA CATGTATTAG	1260
	TTCCMTTACT GCTGACCACA TTGTACCCAT TTCACAGAGA AGGAGCAGAG AAATTAAGTG	1320
20	GCTTGCTCAA GGTCAATG CAG TTAGTAAGTG GCAGAACAGG GACTTGAACC AAGCCCTCTG	1380
	CTCTGAAGAC CGCGTCTGA ATTTCTTCAC TAGAGCTTCC TCATCAGGTT ACCCAGAAGT	1440
25	GGGTCCCATC CACCATCCAG GTGTGCTTGG ATGTTAGTTC TCCACCCTCG AGGTGTACGC	1500
	TGTGAAAAGT TTGGGAGCAC TGCTTTATAA TAAAATGAAA TATATTCTAA AAAAAAAAAA	1560
	AAAAAAAAA	1569

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(2) INFORMATION FOR SEQ ID NO: 46:

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- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1924 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 46:

	GGGCCCCCCC WCGWKTTTTT TTTTTTTTTT TTAAATTAGG ATAATGCCTT TATTAACGAG	60
45	AATGAAACGT TCATTCTCTC TTCCACTCCT TCTCGTTGGT TTTCTGGACA CAGCTCACCT	120
	GATCCTGCTA GAAACGTTGT CAGTCTGCTT GTGGCTTCCC TCCTTGATTG ACTCACGCTG	180
50	TGTGATGTCT TGAGAAGTAT CTATCCACTT CATGTGAATG AGCACTCCAA TATCAGCCAA	240
	CATCAATCAT TCTTACCTAA AGAATAATAA GAAAAAGTTA ATATAAAGA CAAGGGTATA	300
	AAATAAAGGT TTGAAATGC TAGTCAACTT CAAAATTTAA AGAGTAAAAA TCCAGAGATA	360
55	AAGATTGGGG GTAAGTTACA GCATAAAAAA ATAGGAAGAA ACTTCATGGT GGGGGGGAAA	420
	TCTAAAATTA TTCTTACATA AAATAAGTAG ACACCTGAAT TAGAATGAAA ACTGTATTTT	480
60	CTTTAAATG TAAAAGCCTG ACTCTCAGTT TCACCAGTCT GAGCACAAAGT TTGACTGCAA	540

	CCCAAAATAT ACTATCCCTT ATGTGAAGGT ATGTGACAAC GTTGACCTCA CCAAATGAGT	600
	TTTAACATCA GCTCTTTTIT. CATATGAAAG CACATACCCT GCTCCCCATT CAAGTATGTC	660
5	TTCCATTGTC AGGCAGGCTG ACCACCTTCA GCAGGAGTCC TCCAAGAGTG CCCAACTCCC	720
	CTTCCACAG TACACAACGC TGTAGTTGTT GTCTTGCAAT CCTTGTATT TACCTCATT	780
10	TTTCCCATCT AAGTCTTCAC TGAGTTTAA AGTTAGGGCT GGAAAAGCTA TGCCTTACTG	840
	GGACAGCAAG GAACCAATTT TTTTCTGAGG GAGAAGACAT TCACCTTCAC TATATGCCTG	900
	GCAGGGCCAC AGTGACACAA ACAAGATCA GCCTTCATT AAGTTCCAGG TTTTCTTCC	960
15	TCCCTGAATG ATTACTGCAA AGGGTATATG AAGTAAGAGT TCCCTGTTGC ACATGTACCA	1020
	TCCATAAGGG ATACTATATC GTTTTGCAAT CTTCCTCCCA TTCTCCACAT TGTCTTATCT	1080
20	TAAGTCCAAG CCCTTTTCAC TCTCAAAAAA AAAAAAAAAA TATTTTTTTC AGCACTGGTG	1140
	TTCAAAAGCA ACGTTTTTAT GGTTAATGGT TTACCAGCAA CTGTTGAGAT TTCCAGTTGA	1200
	GTCTTAAAAA TTGCCAATCA TTATCTAGCA GCAATGACAG ATGATTAGGA GCAGTCAAAT	1260
25	CCTCTGAATT CTTCCTCTAA TAGGCAGCCA TTTGAGAACT GCACTAGCTG ACATCACTAA	1320
	AACATTATCA GCTAAAGCCA AAACCAAATA AAGGCCAGA CCAACATCCT GGCTCTCTAA	1380
30	AACCTGTCCA AAATCATTA GTGAAAGGCA GTAAATGCAG GACTGTGGAT CATGTCACTG	1440
	CAGCTGACAA TGATTAACAA TAGGAGACAT GCAACCCCA TTAAGGTTAA AAGTCCAAAA	1500
	CTAGTCACAC GCATCTCTTT ATTGGGGAAA AGTGAGACTA TTATGCATTC TTGGTAGGTT	1560
35	TGCAACCTTG CATGAAGAGC ACCCATGCA TTCTTTTCAT CTTCAGAAA GCACCGGTAT	1620
	CTGTTCCAAG GGCCTAACAG TACGAAAATA CATTCTGGCA TCACACCTCT GAACCAAGA	1680
40	CTGTTCTCAT TAAAAATAAT TTTGGTTTGT AACAAAATTA TGAAATACAA TGCAAGCACC	1740
	TCGGTATAGC ATTATTACTG AAACCACTTA ATTCAGCT TTTTGAGTTT TTTAAAAAAA	1800
	CCCACTGCAC TAAGATTCAC AATTCATTGC TACATACAAA TTAAAGCTAG TAAGAACACA	1860
45	CTAACGTCAC AAGTTTCTCA TTCTAAAGTG CAAAAGCCTA ATCATCTGAA AGTGAACAGG	1920
	GTAA	1924

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(2) INFORMATION FOR SEQ ID NO: 47:

- 55 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 475 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

60 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 47:

5 TGGTGTGGGG CCCAGAAAMC AAGGGACCAG TGAAAACAMC CCCAGAGACT TGTATCCGCC 60
 AGGAAAGCCA TTGCCAMTYC TGAGCCCTTG AAGGGCAAGG AGGGAAACAG TGTTACCAGA 120
 GCCCAGTAAG AACTGCTGTC ATGAAGGAGG GGCCACCTTG TAAGAGACAT CATTACTACC 180
 AGAACTGTGG TGCCAAATTG CTGGTGTCTC TCTTTGGAGA AACCAACCAG ATACATCTGC 240
 10 TGGAGACCCA GGTGGGCACA GAGAAGGAGT GAGAGAGAAT CTGGGAAGAG AAATGGAGAA 300
 TAAGCAGCAC AGTGTATATC ATTTCTGTAA ATTCTATGT AGAAGGCTCA GTGTTAGAAA 360
 TAAAGTTATT CTAAGTAGTTG CAAGTTAAGT GTTCTGTGTT GTTCTGCTTT CCTGTTAGCA 420
 15 TAAGTAAACT CCCTTGGAA CTACACAGGT ATGTCTCTCC TTCAACATGT GTGAA 475

20

(2) INFORMATION FOR SEQ ID NO: 48:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 346 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 48:

30 AAGGGACAGA GACCTGGATT CAGATCTCAT TTTACAATGA AGACCCCAAT GCAGAAAGTC 60
 ATGTCTGAAA TTCTGAGCTT ACTCTTCTGC CTGCTGGGAC CTGCTCTGGA TGAGAGAAGG 120
 35 GAGGAAAAGG ACTAATCAGA GGAGCCAATG AAGTCACTCC ATGAGTTTCC TGAACCCCTGC 180
 CCAGCTAGAG ATTAACGTYT GACCWPCAAC GTAGGACACT GTGCAGATGG CTACTTGCTG 240
 GCGCACATGA AGACCAAAGC CAGGACCAAG CCCCMA SCCT GCTWAACAG GCAGARTCTT 300
 40 GCCCAGCCMA CYTCTGTGAR AATCTGCTTC CCTCCACAGC TGACCC 346

45

(2) INFORMATION FOR SEQ ID NO: 49:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1366 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 49:

55 TAGGTGTCAG CCGCCACCCC CCCCCATAT GCAGATTTAC TSGGCATGGT AGTGGCCAGC 60
 TTCTAACACA GCTGGTATTT CAAGTCTCCT GGGACCTCAC TCAGGAATGA TACCCCTCA 120
 60 GTAGAAGCAG CAGGTGATCT TAACTCCTTT CAAAGAGCAG GCCTGTCTGG GAAGCCATGT 180

CCTCAGCAGG CACAGCAACC CCTCTGGAAA TGGATCACAA ACTCACTTCT CAGCCAGGCA 240
 5 GGCCAAGCTT CTATTGTAAC AGTAGGCACA GTATAGTCGG ATCATCACAT CAGCTGGGTT 300
 TTGGTTTAG TCATCTAGAG TCGTCTGGAC TAAAGGTCTT TCAGGTCTCC TTGCCCTGTG 360
 AGTGCGTGAA CCTCCCCACC CGAATTGCCT CAGTTGTCCT GAGCCTCATG TCTCTCCTGG 420
 10 TGGTGGGCCA GGCCCTGCA TGGGAAGGGA GCCTGCTGCG GGCAGGCCA GCTGGGGGTG 480
 CTCACCTATG CGCAATGANA GTTATTGAAG GACTGGTTGT TGATGTTGGT GAGCGTATCC 540
 15 TTCATGGCCA GCGCGAAGTC GGCCAGGTCA GCCAGGTGCT GCCAGCGCTC TCTCTCGGAC 600
 TTGTCTCCT GTGCCAGGG ACCGTGGAGA AAGTGTGAGG GGCCGCTCAC TGCAGCAGCC 660
 TGCTCTGCTG CCTTCCCTGG CAGTGTCTG GGGGTGGATT CCCTACAMCT AGATGTTCAA 720
 20 GGCTTACTT TTCCTCCAC AAAGGAGTCG CAGCCACGCT AGCTCTGACT TGCCACTGTG 780
 ACAAAGTICA CGTAGCAGGT CTAGGCAAAG ACTGGGCAAT TGAGCAGAGG AGACGGACCT 840
 25 GTGAGTCTGA CCRYGAGSCG GRCCCTTICA CCTTGGCTGG GCTGGTCTG GTCCTTAGGT 900
 TTGTGAGGT TGTCTTGT TGGATCCCTC AACTAGGTGA TAAGCACTGG AGGGGGATGA 960
 CCCGCTTGG ACGTGTCTT TTAACCTCAT CCATATAATA GGGCGTGG ATGTTGTAG 1020
 30 AGGTAAAGCA GGATGATGTT GTTTAAGAC CAGAGCTTGG GACCAGGGCT CCTACACCTA 1080
 ATTTTCTCTC CTGGTAGCTG AACAAAGTTC TAAATTAGCT TAACAAAAGA ACAGGCTGCC 1140
 35 GTCAGCCAGA GTTCTGAAG CCATGCTTTC AGTTTCCCTT GTTGACAATT GCTCTCCAGT 1200
 TCCTATGAAA GCACAGAGCC TTAGGGGCC TGGCCACAGA ACACAACCAT CTAGGCCTG 1260
 AGCTGTGAAC AGCAGGGGGT TGTGTGCTG TTCTGTTTCT CTGCTTGCCG AACTTTCTCA 1320
 40 ATAAACCTTA TTTCTATT ATAAAAAAA AAAAAAAA AAAAAA 1366

45 (2) INFORMATION FOR SEQ ID NO: 50:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1405 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 50:

55 GCAGTAATTC CTGTTAGCCA CTGCATCCAC CAAACTAGT TTATTTTTC CCTCAAATTC 60
 ATGATTTTGA CGTCTGTTAC AAAGGAATT TTGCTGATAG CTCTTTGGGT CCCACTGTTC 120
 60 CATTTTATGC TAATGATTC CATTCTAGGG CCCAGCCGTC TCTTGACTGA TGGTGTCCC 180

	TTTAACCCCTT GGCATGTATA ATAGAATTTT GGTGAATGAA AGAACCCAAA TAGGCCAGAT	240
	AGTCCCCCA GGCCTGATA TCCATAAAAG GCTTGGGAAT GCATTATGTA ATTGTCCTTA	300
5	GTCTTTTGT TGTTTTAGAA AAAAAACA AGATGGGCTC AGATGGATGC CTACGTAAAA	360
	ATGGTTCTTA GCTGTGTACT CATACTTTT CTTTGAATTG AGTAGTGAAA GGAAGGAGGA	420
10	GGAAAGGAAA TTAAATGTCC TTCTAGTATT CTCTGGACTC AAGTCTGACA TATGAGATAA	480
	TAACCTATAT TGAAATGCCA AGAATGTAT CTGAAACAAG AGAACAGTTT GACACATTTA	540
	TCATGCCTTC ATATTACATA TTAAGTAAA CCAATTAATA AACATATGAA ATATCCATTG	600
15	CACAAGGCAA AGGCACCTAA ACCTTTTGT TCTTTTCTA CATAGCAGAA ATTGATTTTT	660
	TTTTTATTTT TTTAGGGGAA CCTATATAAT TATGACCAG TGATGTCTTT TGGTGACTTA	720
20	AGCTTATGAA TTCAGGTAC AATTGAGTTG ATTCTAGATG GTTACTACCT TGAAAAGGAT	780
	GTTGGTGCCT TATGTGACAC GAGCCAGAGC CTGCTGGGA ATAAACAAAG CAGGTTTCAT	840
	GCCACACCA ACTCGTAGCT TTAGTGGGCA GATGGGGAGT GGTTCACAGA CTTCCCAAAA	900
25	TGTGGGGCT TTGGGATTTT CCACACCATC CCACGTGTGT TGTTCAATCT TCCTCTTTTC	960
	ACACTCTTGG ATGGATWATT TGRAAATGGT GRAAWYMCY YYKRAATTG CCCAATAGCC	1020
30	WTGRGCCACC ATTCTTWATG ACACCATAAC CAAATAGTTC CWTAAATGTTG AAATATTAGA	1080
	AACCTGTTAC CAGCCYKMA KTWACCCWVA WTTTCCCAT GTTGTGGAA TTGATATTGA	1140
	AATAGCAGGG CTAAGGAATT ACTGGCAAGT TTTAGCCTGT GGGTAATACC TTAGGGTTAT	1200
35	TTAAATATTT GTAATTTTAT TTAAATGTTT ATGAATGTTT GAAAGGAACA AAATTATCAG	1260
	GGATGGCTCT TTGCCATGGG TCTTATTTTC ACCCTCTTTT CTGTAAGAAA AAAGAACAAT	1320
40	GTCTTAATGT ATTTTAAAG TTTTGGTAT AGTTTCTAAT TCCAATTTTA ATAAAAGTTT	1380
	TWTRTAAAAA AAAAAAAAAA AAAAA	1405

45

(2) INFORMATION FOR SEQ ID NO: 51:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 504 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 51:

	CGGATTTTCT AGGACCCCAA AAAAAAAAAA AGGGNAAAAA AAACCCNCAA AACCANCCAA	60
	AACCCCAAAA AAAAAAAAAA TCCACAAAAA CAAAAAACT ATAAAAAGA AAGAATTAAA	120
60	AACTTTCAGA GAATTACTAT TTACTTTATT AACTTACGGA TTTATTATAT AAATATATAT	180

TCACCTAGCA ACATATCTCT GCCGTCTCTC CTGCTCTCAT AATGAAGACA TAGCCGATTC 240
 5 TCTGCCCGGG CCCCTTGCTG ATGCTCCTCC GGGTCTGCGT CGGGCGTGGG TCTCTGGGGA 300
 CCTCCAGAG GTGGAGGTGG GCTGATGGCC TGGCTGCCTG GTGGTTGATG GTTTTGCTCC 360
 CCTACCTTT TTTTTTGTAG TTTATCTGA TTGATTTTTT TTCTTGGTTT CTGGATAAAC 420
 10 CACCTCTGG GGACAGGATA ATAAACATG TAATATTTTT AAGAAGGAAA AAAAAAAAAA 480
 AAAAAACTNG GGGGGGGCCC CGAA 504

15

(2) INFORMATION FOR SEQ ID NO: 52:

20 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 777 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 52:

NAAGTATCTT GCCCAGTTTA TTACAGAGGA CGATAAATGA TTCCATGTGG ATAGGGCATA 60
 30 ACATACAGAG AATGAGACTA TGCCAGAAAT GGGAGGAGGC ATTTGAAACA ACATGAGTAT 120
 CTCAGGGACA GATGGATTGA TTCIGCTATT GGTAGGCCTG GAAGCAANGG TCAGAAGTAG 180
 CAAAAAATGG ATACCAAAG CACTATTWGT CACCCAAGCT AAGTGAATA GCTGGCCCAG 240
 35 TAGGAGAAAT GCAGGTTTTG CTCTACACTA AGTTCCTCAA CTCTTGATAA GCCTCCAAAA 300
 ACAATGTTA GGGGAAAAA ACGCAGCTGG TTATGAAAAG ATATATCTCA TTTCATTAAA 360
 AAATCAATGT CAATGCTGTT AATAGAATCC TTTTATCTTC AGGACAGAGG CAATGCCCTA 420
 40 AACAAACACC AGCTCAAGAG CCTCTGATGC CAACCTAGAG GGTACCCAAA CACAACTTA 480
 GCATAGAGGT AAGAATCTCT ATGTCTTTTG GTGGAGGCAA AGCCATTTGG TTGGTACTTC 540
 45 ACAGGAACAT CTTTCTACCA AGTCTTCATC ATATGGTATG TGCCACGAGT CTCCAGTTGT 600
 TTGCACCACT GTGTCATAGC TGAGAATACG CTGAAAGGTT AGTTTGTATC CTGGAAACCT 660
 50 ATTTACAATT GCCAGCTGAT GTCCCTGCTG CCACITAAAA AAGGCTTGGG TCTGGCATAG 720
 GCAGAMAGGC CTGTGGTCCC CTCGTGCCGA TTCTNGGCTC GAGGCCAATT NCCTTAT 777

55

(2) INFORMATION FOR SEQ ID NO: 53:

60 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 602 base pairs
 (B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 53:

5
 ATGACTACAG TGTATACCC TCCAATCTTT GCAGGTGGGC ATGGAACACT GCTGTATCA 60
 CTCTGTGCAC GGTATAAATC CATATATCCA CAAAAACACA CATCCATCCA TCAACATATA 120
 10 CATGGTTTGG GATGAGCAGG TCAATAGTTT TGAGAGGGAG TTTGTTCCCTT TTTTCTTCT 180
 CATTATACTC TTAAATTGTT GTCAGTTATC AAACAAACAA ACAGAAAAAT TGTTTGGAAA 240
 AACCTTGCAT ACGCCTTTTC TATCAAGTGC TTTAAAATAT AGACTAAATA CACACATCCT 300
 15 GCCAGTTTTT TCTTACAGTG ACAGTATCCT TACCTGCCAT TTAATATTAG CCTCGTATTT 360
 TTCTCACGTA TATTTACCTG TGACTTGTAT TTGTTATTTA AACAGGAAAA AAAACATTCA 420
 20 AAAAAAGAAA AATTAAGTGT AGCGCTTCAT TATACTATTA TATTATTATT ATTATTGIGA 480
 CATTTTGGA TACTGTGGA GTTTATCTC TTGCATATAC TTTATACGA AGTATTACGC 540
 CTTAAAAATA CGAAAATAAA TTTTACAAGG TTCCGGTTTT GGTGGTGGAA AGAGTAAATT 600
 25 GA 602

30

(2) INFORMATION FOR SEQ ID NO: 54:

(i) SEQUENCE CHARACTERISTICS:

35

(A) LENGTH: 1749 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 54:

40

AGTCACTGAC TTGGAGCCGC TCGGGGAAG TCCCGCCAG ACAGGCGGTG GGTGGGAATG 60
 CCTCACTTCA GTTTGAAGAG GTTCCGGATC CAAAGGGGTT AAAACGAGCG AACCCCGATC 120
 45 CCCGACCACA CTTCCCGCCT CCTAAAACG CACACCCCGC TAGCCATGGG CAGCCGCGAC 180
 CACCTGTTCA AAGTGTGTTT GTGGGGGAC GCCGAGTGG GCAAGACGTC GCTGGTGCAG 240
 GATTATTCCC AGGACAGCTT CAGCAAACAC TACAAGTCCA CGGTGGGAGT GGATTTTGCT 300
 50 CTGAAGGTTT TCCAGTGGTC TGACTACGAG ATAGTGCGGC TTCAGCTGTG GGATATTGCA 360
 GGGCAGGAGC GCTTCACCTC TATGACACGA TTGTATTATC GGGATGCCCTC TGCCTGTGTT 420
 ATTATGTTTG ACGTTACCAA TGCCACTACC TTCAGCAACA GCCAGAGGTG GAAACAGGAC 480
 CTAGACAGCA AGCTCACACT ACCCAATGGA GAGCCGGTGC CCTGCCTGCT CTTGGCCAAC 540
 AAGTGTGATC TGTCCCTTG GGCAGTGAGC CGGACCAGA TTGACCGGTT CAGTAAAGAG 600
 60

	AACGGTTTCA CAGGTTGGAC AGAAACATCA GTCAAGGAGA AAAAAATAT TAATGAGGCT	660
	ATGAGAGTCC TCATTGAAAA GATGATGAGA AATTCACAG AAGATATCAT GTCTTTGTCC	720
5	ACCCAAGGGG ACTACATCAA TCTACAAACC AAGTCCTCCA GCTGGTCC TGCTAGTAG	780
	TGTTTGCGCTT ATTTTCCATC CCAGTTCTGG GAGGCTTTTT AAGTCTCTTC CCTTTGGTTG	840
10	CCCACCTGAC CATTTTATTA AGTACATTG AATTGTCTCC TGACTIONGT CCAGTAAGGA	900
	GGGCCCAT TG TCACTTAGAA AAGACACCTG GAACCCATGT GCATTTCTGC ATCTCCTGGA	960
	TTAGCCTTTC ACATGTTGCT GRTACATTT AGTGCCAGTT AGTCCCTTCG GTGTAAGATC	1020
15	TTCTCATCAG CCCTCAATTT GTGATCCGGA ATTTTGTGAG AAGGATTAGA AATCAGCACC	1080
	TGCGTTT TAG AGATCATAAT TCTCACCTAC TTCTGAGCTT ATTTTCCAT TTGATATTCA	1140
20	TTGATATCAT GACTTTCAAT TGAGAGGAAA ATGAGATCAA ATGTCATTTT CCAAATTTCT	1200
	TGTAGGCCGT TGTTCAGAT TCTTCTGTG TTGGAATGTA AACATCTGAT TCTGGAATGC	1260
	AGAAGGAGGG GTCTGGGCAT CTGTGGATTT TTGGCTACTA GAAGTGTCCC AGAAGTCACT	1320
25	GTATTTTGA AACTTCTAAC GTCATAATTA AGTTTCTCTT GTCTTGGCAT CAAGAATAGT	1380
	CAAGTTTTTT GGCCGGGCAT GGTGGCTCAT GCGKGTAA TC CCAGCACTTG GGGAGGCCAA	1440
30	GGCAGGCGGA TCACATGAGG CCAGGAATTC GAGACCAACC TGGTCAGCAT GGCAAAACCC	1500
	CGTCTCTACT AAAAGTACAA AAATTAGCCA GCGTGATGG CACGTGTCTG TAATCCCAGC	1560
	TACTCTGGAG ACTGAGGTGG GAGAATCGCT TGAGACTGGG AGGCAGAGGT TGCAGTGAAC	1620
35	CGAGATCATG CCACCGCACT TCAGCCTGGG TGACAGAGAA GGACTCCGTC TCAAAAAAAA	1680
	AAAAAAAAA AAAACTCGAG GGGGGGCCG GTACCCAAAT CGCCSTGATA GTGATCGTAW	1740
40	ACAATCNAA	1749

45 (2) INFORMATION FOR SEQ ID NO: 55:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1896 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 55:

55	AAAGAGATGG GCTCTTTATT TTCTCGAAAA ACCAATTTGG AGTIACTCAT TTTTCCATAA	60
	CATTAAATTT CTTACAGTGA ACTACATATT GTCCATAAGT GCTTCATCAG GACTCATCGC	120
	CCTCTGTCT ACTGGCTCCA AATAGACCAT GTCAGCTTCA CCCCTGGCT TTGTGTCTAT	180
60	GGGTGGCCTG TGGTATATGG AAAAGTAGCA GGGTGGTCAG GGTGGGAGAC ACAAGATGTT	240

	TTTATAGTCT AGAGCCTTTA AAAAACCAG CAGAATGTAA TTCAGTATTT GTTTATTGGC	300
5	TGTTTTTTGA CAGATTGTTG AAATTAAATG AATTGAAAGG GAAACTCAGA GACTAGGAC	360
	GTTTATTAAA AGGAAAAAAA TGTCTTGCAA TGTGCTGTAA TCACAAGAGG AGAAAATAAC	420
	TTGTTTCCTT GATCTGTCAG AGGTCACAGT AACCTGGGCC GAGCTGTTAT TATTTATTAT	480
10	ATAATAGTAG TAGGAAGTTA ATAACGGTT CTCTGTGTC CAAGCACAAT ATTACAACCT	540
	CTTTTGAACC GTAAATATCA GAATGAATCC TCTTCCCAGG GGATTGAACA GAAGCTTAAT	600
15	GTTTACAAGT GTTTGAATTT GTGATCTGAA ATAACACAAA ATTAAAAACA TGATTTCTCT	660
	AATTTTCCAA CTAGAGGAAG AGAACTTGT GAAAAGTTC TTTTTTTTC TTTTTTTTTT	720
	CTTAAAGAAG GGCAGCCAAG GTAGTAACCT AAAAATAGTG CCCAGGCATA TGAGAGTTGT	780
20	CCTACGAGGT TAAAGAACAC ACTGTTCCAC TGTATGGCTT TGGCCCTGAG TGGCCAGGGA	840
	GGTCAACTTG ACCCTGCCAT GTTGGTTTGA CTTACTAAGA CACAGGAATC ATTGTTTTC	900
25	TTGACCAGGG TCTCACACCC TGGAGGAATG TTAAGTAAGA GAAAGAACCT CTTTCTGAA	960
	TATTGACATG TAAAAGACCA AAGTAATTTT TCTGAACTTC TGCAATTCTG AGAACTCTCC	1020
	AAGGAATTTA CAGTGATTTT AGTGCTGTC AGCATTTTTC CATGAGGACT TTCATACATT	1080
30	TGACTCTTTA GTTCACAGGT TCCCATTGAT TGTGAGCAAG ATATTTATCT CTTTAGCCCT	1140
	TGGGGATCCA GCTGAGAGCA ATCTCTTGCA TTTTTTTACC CGTGTATGTA CAGATATCAT	1200
35	TTCTTGTTGA TGCCATGACT TGAAAAAGTT TGGGAAGCTC TTTAGCAATA TCAGCTAAAA	1260
	GGATATGAAA TCACAGGTGA TAGCAGTTGT CATTCAGTAA TTTCTACAA GCAGCACCCC	1320
	AAAGGAAATA TAGTCCTAAT CTTTACTATC CACTTCTAAA TTTAATGTGA ATTTCATACA	1380
40	TGTTATTAGT TGTMTTCTTT ATAATTTTAT AAAAATTATT CATCGGAGT TTAACCTCCA	1440
	CTTCCATGCT ATCGGATGTG TTGGGCTCCA TGCAAGAACT TGGAAGAAAA ACAGGCAGGA	1500
45	ATGCATTTGC ATAATGACCC AGATCATCAT TTTCTGCAAC TGAGAATTAT ATTTTCATCAT	1560
	TGCTTCTAGA AGTCTGCAAT TCTTTACTTT TCTTTGGTGC ATTATTATCT AGGTGCCATC	1620
	ACTGGATAAT GTGGAGTGAC TAGAGAAGTC AYATATCACT GTAAGGTACA GTTAGGGTA	1680
50	ACACTTTAGA GGTMTATTAT TTTTAAAAA CTTTCTTGA ACTCCTGGGC CAACATGGGT	1740
	GAAACCCCGT CTTCTTACTT AAAAATACCC AAAATTAGGC CAGGGCCGTG GATGGGTGGG	1800
55	GTGCCTGTTA ATCTTCAGCT ACTTNGGGGA GGGCTTGAAG CCAGGGAGGA ACTGCCCTGG	1860
	ANCCCCGGG NGGCCAGNA GGTGTGCCAG TTGAGT	1896

(2) INFORMATION FOR SEQ ID NO: 56:

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 1753 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 56:

10 TCTTTTAAAT ATAGACATTT GTGGGCTCA CACAATATAT GAAATAGTAC CCTCTAAAAA 60
 AGAGAAAAAA AAAATCAGGC GGTCAAACCT AGAGCAACAT TGTCTTATTA AAGCATAGTT 120
 15 TATTTCACTA GAAAAAATTT AATATCAAGG ACTATTACAT ACTTCATTAC TAGGAAGTTC 180
 TTTTAAAT GACACTTAAA ACAATCACTG AAAACTTGAT CCACATCACA CCCTGTTTAT 240
 20 TTTCTTAAAT CATCTTGGA GCCTAAGCTT CTGAGAATCA TGTGGCAAGT GTGATGGGCA 300
 GTAAATACC AGAGAAGATG TTTAGTAGCA ATTAAAGGCT GTTGCACCT TTAAGGACCA 360
 GCTGGGCTGT AGTGATTCTT GGGGCCAGAG TGGCATTATG TTTTACAAA ATAATGACAT 420
 25 ATGTCACATG TTTGCATGTT TGTGCTTG TTGAATTTT GAACAGCCAG TTGACCAATC 480
 ATAGAAAGTA TTACTTTCTT TCATATGGTT TTTGGTTCAC TGGCTTAAGA GGTTCCTCAG 540
 AATATCTATG GCCACAGCAG CATAACAGTT TCCATCCTAA TAGGAATGAA ATTAATTTTG 600
 30 TATCTACTGA TAACAGAATC TGGGTCACAT GAAAAAAAT CATTTTATCC GTCTTTTAAG 660
 TATATGTTTA AAATAATAAT TTATGTGTCT GCATATTGCA GAACAGCTCT GAGAGCAACA 720
 35 GTTTCCTCATT AACTCTTTCT GACCAATAGT GCTGGCACCG TTGCTTCCTC TTTGGGAAGA 780
 GGAAAGGGTG TGTGAACATG GCTAACAATC TTCAAATACC CAAATTGTGA TAGCATAAAT 840
 AAAGTATTTA TTTTATGCCT CAGTATATTA TTATTTAATT TTTTAGGTAA TGCCTATCTC 900
 40 TTGGTCTATT AAGGAAAGAA GCAATCAGTA GAGAATTCAG GATAGTTTGT TTTAAATTTCT 960
 TGCAGATTAC ATGTTTTTAC AGTGGCCTGC TATTGAGGAA AGGTATTCTT CYATACAACT 1020
 45 TGTTTTAACC TTTGAGAACA TTGACAGAAA TTATGCAATG GTTTGTTGAG ATACGGACTT 1080
 GATGGTGCTG TTTAATCAGT TTGCTTCCAA AGTGGCTTAC TCAAGAGGCC CTAAGACTGG 1140
 TAGAAATTAA AAGGATTTCA AAAACTTTCT ATTCCTTTCT TAAACCTACC AGCAAACCTAG 1200
 50 GATTGTGATA GCAATGAATG GTATGATGAA GAAAGTTTGA CCAAATTTGT TTTTGTGTG 1260
 TTGTTGTGTG TTTGAATTG AAATCATCTT TATTCCTTTT AAGAATGTTT ATGTATGAGT 1320
 55 GTGAAGATGC TAGCGAACCT ATGCTCAGAT ATTCATCGTA AGTCTCCCTT CACCTGTTAC 1380
 AGAGTTTCAG ATCGGTCCT GATAGTATGT ATTTCTTTAG TAAGAAATG TTTAAATTAC 1440
 AATGATCTTT TAAAAAGATG ATGCAGTTCT GTATTTATTG TGCTGTGTCT GGTCTTAAGT 1500
 60

GGAGCCAATT AAACAAGTTT CATATGTATT TTTCCAGTGT TGAATCTCAC ACACTGTACT 1560
 TTGAAAATTT CCTTCCATCC TGAATAACGA ATAGAAGAGG CCATATATAT TGCCTCCTTA 1620
 5 TCCTTGAGAT TTCACTACCT TTATGTTAAA AGTTGTGTAT AATTGTTAAA ATCTGTGAAA 1680
 GAATAAAAAG TGGATTTAAA TTAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA 1740
 AAAAAAAGG GGG 1753
 10

(2) INFORMATION FOR SEQ ID NO: 57:
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- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1220 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 20 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 57:

GCGGAAGTTA CTGCAGCCGC GGTGTGTGC TGTGGGAAG GGAGAAGGAT TTGTAAACCC 60
 25 CGGAGCGAGG TTCTGCTTAC CCGAGGCCGC TGCTGTGCGG AGACCCCGG GTGAAGCCAC 120
 CGTCATCATG TCTGACCAGG AGGCAAAACC TTCAACTGAG GACTTGGGGG ATAAGAAGGA 180
 30 AGGTGAATAT ATTAACTCA AAGTCATTGG ACAGGATAGC AGTGAGATTC ACTTCAAAGT 240
 GAAAATGACA ACACATCTCA AGAACTCAA AGAATCATAC TGTCAAAGAC AGGGTGTTC 300
 AATGAATTCA CTCAGGTTTC TCTTTGAGGG TCAGAGAATT GCTGATAATC ATACTCCAAA 360
 35 AGAACTGGGA ATGGAGGAAG AAGATGTGAT TGAAGTTTAT CAGGAACAAA CGGGGGGTCA 420
 TTCAACAGTT TAGATATTCT TTTTATTTT TTTCTTTCC CTCAATCCTT TTTTATTTT 480
 40 AAAATAGTT CTTTGTAAAT GTGGTGTCA AAACGGAATT GAAACTGGC ACCCATCTC 540
 TTTGAAACAT CTGTAATTT GAATCTAGT GCTCATTATT CATTATTGTT TGTTTTCATT 600
 GTGCTGATTT TTGGTGATCA AGCCTCAGTC CCTTCATAT TACCTCTCC TTTTAAAAA 660
 45 TTACGTGTGC ACAGAGAGGT CACCTTTTTC AGGACATTGC ATTTCAGGC TTGTGGTGAT 720
 AAATAAGATC GACCAATGCA AGTGTTTATA ATGACTTTCC AATTGGCCCT GATGTTCTAG 780
 50 CATGTGATTA CTTCACTCCT GGACTGTGAC TTTCACTGGG AGATGGAAGT TTTTCAGAGA 840
 ACTGAACTGT GGAAAAATGA CCTTTCCTTA ACTTGAAGCT ACTTTTAAAA TTTGAGGGTC 900
 TGGACCAAAA GAAGAGGAAT ATCAGGTGTA AGTCAAGATG ACAGATAAGG TGAGAGTAAT 960
 55 GACTAACTCC AAAGATGGCT TCACTGAAGA AAAGGCATTT TAAGATTTTT TAAAAATCTT 1020
 GTCAGAAGAT CCCAGAAAAG TTCTAATTTT CATTAGCAAT TAATAAGCT ATACATGCAG 1080
 60 AAATGAATAC AACAGAACAC TGCTCTTTT GATTTTATTT GTACTTTTGT GCCTGGGATA 1140

TGGGTTTAA ATGGACATTG TCTGTACCAG CTTCAATTAA ATAAACAATA TTTGTAAAAA 1200

TCAWAAAAA AAAAAAAAAA 1220

5

(2) INFORMATION FOR SEQ ID NO: 58:

10

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1049 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

15

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 58:

20

TCGCGCCTGC AGACACAGCA TCTACTCAGC GTGGGTCACC TCTGTGAACA TCACTGACTG 60

CAAGCCTCCC TCAATTTCTG GTGCAGCCCA TCAGGGACCC ACAGCGCCTG GGAGGATGGT 120

GCGGATCTTG GCCAATGGGG AAATCGTGCA GGACGACGAC CCCCAGGTGA GGACCACTAC 180

25

CCAGCCACCA AGAGGTAGCA TTCTCGACA GAGCTTCTTC AATAGGGGCC ATGGTGCTCC 240

CCCAGGGGGT CCTGGCCCCC GCCAGCAGCA GGCAGGTGCC AGGCTGGGTG CTGCTCAGTC 300

30

CCCTTCAAT GACCTCAACC GGCAGCTGGT GAACATGGGC TTTCCGAGT GGCATCTCGG 360

CAACCATGCT GTGGAGCCGG TGACCTCCAT CCTGCTCCTC TTCTGCTCA TGATGCTTGG 420

TGTTCTGTGC CTCTCCTGG TTGGCCTTGT CTACCTGGTG TCCCACCTGA GTCAGCGGTG 480

35

ACCTCTGAGG GCTGATAGGG GTGGGTTTGT TGAGAGGGAC TTGCTGGGCC TTGGTGTGAG 540

AGCAGGCATA TTTGGAGGGG ATCTGGTGGT GCCTTGAAGG TATGATCAGA GAGGGGACCA 600

CAGGTGTGTG TTTCCCCCTT GTGTTAAGCG TGAGGCAGAG GGAGACGTTA GTCCCAGCAT 660

40

TTCCCAAAGT GTGGGTGGGT CGTTGGTTC CCGATACT TTTAGGTGGT ATGGGGCCTG 720

CATTAAAGTG CACAAAATCA GAGCAAGAAA GCGATGCCCT TCCCAATTCT CTCAATCCTT 780

45

TTATGCCGAG AAGATCTCAG CTGGATGCCA ACATGTTCCG ATGCCTGTGG AAGACATGCC 840

GACGTCTCCT CTGCCTAGGG AGCAGGACTT GGGCTTAGGG CAGGTGAAA AAATTCCAGA 900

50

CTTTTTTAGC ACTGTTTTTG TTTAATGGT ATATTTTAT TGGCTACTTT ATTGTTTAGG 960

ACAAGTGGA GTGGCATTCCT ATTTATTGTG ACCTTTCAA TAAATAGATT TAAGTAAAAA 1020

AAAAAAAAA AAAACTCGAG GGGGGGCC 1049

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(2) INFORMATION FOR SEQ ID NO: 59:

60

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1776 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 59:

	AAAGAGGATG TGMAGCTAGA GGTCCCCGAT GGCTGGTCGG ATGGGAAGCA CAAGGCTGAG	60
10	GGACTGGATT GTAAAGGCAC TAAGTCGTTT TCGGGTGAGA ATCAGACATG GGGGACCTCT	120
	AGCTTCACAT CCTCTTTCCT TGCAGSTCTG GACATCCTGA GCCCAAGTCC CCCACACTCA	180
15	GTGCAGTGAT GAGTGGCGAA GTGAAGGTGA CAGGGCAGAA CCAGGAGCAA TTTCTGCTCC	240
	TAGCCAAGTC GGCCAAGGGG GCAGCGCTGG CCACACTCAT CCATCAGGTG CTGGAGGCCC	300
	CTGGTGCTTA CGTGTTTGGA GAACTGCTGG ACATGCCCAA TGTTAGAGAG CTGGCTGAGA	360
20	GTGACTTTGC CTCTACCTTC CGGCTGCTCA CAGTGTTTGC TTATGGGACA TACGCTGACT	420
	ACTTAGCTGA AGCCCCGAAT CTTCTCCAC TAACAGAGGC TCAGAAGAAT AAGCTTCGAC	480
25	ACCTCTCAGT TGTACCCCTG GCTGCTAAAG TAAAGTGAT CCCATATGCA GTGTTGCTGG	540
	AGGCTCTTGC CCTGCGTAAT GTGCGGCAGC TGAAGACCT TGTGATTGAG GCTGTGTATG	600
	CTGACGTGCT TCGTGCTCC CTGGACCAGC GCAACCAGCG GCTCGAGGTT GACTACAGCA	660
30	TCGGGCGGGA CATCCAGCGC CAGGACCTCA GTGCCATTGC CCGAACCCCK AANAAAAACC	720
	ATTAAAGTTA CGACGCGAGC AGCAGCCGCA GCCACATCTC AGGACCCTGA GCAACACCTG	780
35	ACTGAGCTGA GGAACCCAGC TCCTGGCACC AACCAGCGCC ASCCAGCAAG AAAGCCTCAA	840
	AGGCAAGGG GCTCCGAGGG ANCGCCAAGA TTTGGTCCAA GTCGAATTGA AAGRACTGTC	900
	GTTTCTCTCC TGGGGATGTG GGGTCCCAGC TGCCTGCCTG CCTCTTAGGA GTCCTCAGAG	960
40	AGCCTTCTGT GCCCCTGGCC AGCTGATAAT CCTAGGTTCA TGACCCTTCA CCTCCCCTAA	1020
	CCCCAAACAT AGATCACACC TTCTCTAGGG AGGAGKCAAA TGTAGTCAT GTTTTGTGTG	1080
45	GTACTTTCTG TTTTGTGTGA CTTTCATGTG TCCATGTGCT CCCGCTGCCA TGCTCTCTCC	1140
	CTTGTTTCCT TAAGAGCTCA GCATCTGTCC CTGTTTCATTA CATGTCAATTG AGTAGGTGGG	1200
	TAGCCCTGAT GGGGTGCGCT CTGTCTGGAG CATAACCCAC AGGCGTTTTT TCTGCCACCC	1260
50	CATCCCTGCA TGCCCTGATCC CCAGTTCCTA TACCCTACCC CTGACCTATT GAGCAGCCTC	1320
	TGAAGAGCCA TAGGGCCCCC ACCTTTACTC ACACCCTGAG AATTCTGGGA GCCAGTCTGC	1380
55	CATGCCAGGA GTCACCTGAC ATGTTTCATCC TAGAATCCTG TCACACTACA GTCATTTCTT	1440
	TTCTCTCTC TGGCCCTTGG GTCCTGGGAA TGCTGCTGCT TCAACCCAG AGCCTAAGAA	1500
	TGGCAGCCGT TTCTTAACAT GTTGAGAGAT GATTCTTTCT TGGCCCTGGC CATCTCGGGA	1560
60	AGCTTGATGG CAATCCTGGA AGGGTTTAAT CTCCTTTTGT GAGTTTGGTG GGAAGGGAA	1620

GGGTATATAG ATTGTATTAA AAAAAAAAAAG GTATATATGC ATATATCTAT ATATAATATG 1680
 ACGCAGAAAT AAATCTATGA GAAATCTATC TACAAAMWAA AAAAAAAAAA AAAAAAAAAA 1740
 5 AGGAATTCGA TNTCAAGCTT ATCGATACCG TCNACC 1776

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(2) INFORMATION FOR SEQ ID NO: 60:

(i) SEQUENCE CHARACTERISTICS:

15

- (A) LENGTH: 443 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 60:

20

ACAGATAAAT AAATAAATAA TAAATTAAAT TAAATAAAAA ATCTGAGCTA ATCTGAATAA 60

ATTGAGAGAT TTCACATGAA AGCCAGGATT TCTGGCTTCC CAGGAACAGT CAGAAGAGCT 120

25

AGCTAGCAAC ACTGGTCTGC TTGGCTACCT TCTTTGGAAC AACATGAAAT CTAGCTCCCT 180

TTTTTTTTTT TTTTGGCCC ACTTCATCCA TTCACATGAC CTGCCTGGCC TCTGCAGGTA 240

30

AGTGAGTATG CAACAAAAAT GTAGCACAGG TTTTGTGCGT GAACTACGTG GTTTCAGGTC 300

CAGCTCTGCC ACTTGCTAGC ATGACCTCGT GCCGAATTCC NGCACGAAGT TTTTTTTTTT 360

TTTTTCAGTG CTCCAGTCCC CCTATTGGAG AATCCTGCCC CCCCCTGGGA CAGAATGTTC 420

35

ACCCTGGCCC CGCGANTCCC TGA 443

40

(2) INFORMATION FOR SEQ ID NO: 61:

(i) SEQUENCE CHARACTERISTICS:

45

- (A) LENGTH: 2888 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 61:

50

TTAATGTTGT CAATAACCAC CAGGCCAAAC AGAATTTATA TGACCTGGAT GAAGATGATG 60

ATGGTATAGC TTCGTTCTCT ACTAACAGA TGAAGTTTGC AGCCTCAGGC GNCCTTCTCC 120

55

ACCACATGGC TGGGCTAAGC AGTTCCAAGC TTTCCATGTC CAAGGCCCTC CCTCTCACCA 180

AAGTGGTTCA GAATGATGCA TACACAGCTC CTGCTCTCCC TTCCTCTATT CGAACAAAAG 240

CCTTGACCAA CATGTCCCGG AACTGGTGA ACAAGGAAGA ACCCCCCAAA GAGCTGCCAG 300

60

CTGCTGAGCC TGTCTCAGC CCATTGGAAG GCACCAAGAT GACTGTGAAT AATCTGCACC 360

	CTCGAGTCAC TGAGGAGGAC ATTGTTGAGC TTTTCTGTGT GTGTGGGGCC CTCAAGCGAG	420
5	CTCGACTGGT CCATCCTGGG GTAGCGGAGG TGGTGTTTGT GAAAAAGGAC GATGCCATCA	480
	CCGCATATAA GAAGTACAAC AACCGGTGTC TGGACGGGCA GCCGATGAAG TGCAACCTTC	540
	ACATGAATGG GAATGTTATC ACCTCAGACC AGCCCATCCT GCTGCGGCTG AGTGACAGCC	600
10	CATCAATGAA AAAGGAGAGC GAGCTGCCTC GCAGGGTGAA CTCTGCCTCC TCCTCCAACC	660
	CCCTGCGYGA AGTGGACCTT GACACCATCC TGAAGGCACT CTCAAGTCC TCAGGGGCCT	720
15	CTKTGACCAC GCAGCCCACA GAATTCAAAA TCAAGCTTTG AGCAGGGGAG TGAGGCAGCC	780
	AGAAGTGGGG GCAGAGGAGG GTGGCTCTGT TTCCCCAAGG CAAAGCTTAT GACCAATGGG	840
	CCATCGGACT GGAGACCCCT GATGTGTTGA AGGGTGTCCA GGGATAAAGA GCTTCCTCAC	900
20	TGGATGGGAC CCGCCTTTCT GTGTTGTGTT CTGCCCTGTG CTCTCTCTC TACGTTAACG	960
	TTTCCTGTAG TATGTTTCTT CATCTCATCG CCAAGGTAGG CTTGTGTTTT TCAGTGTGTG	1020
25	CCTCCCCGAG CCTCAGCCCC AAGCTGATTT CTTATCTGGA AATGGTACAC TGAATTCTCT	1080
	GGGTGGCTTT CTTGTGGCCC CATGGGATGC AGCGTGGGGG CTGTCTGAAG GACCTGCTT	1140
	TTCCAGGGG CCGAGGGGCT GCCTTTCCTT TGTGTGTATT AAGCTTTTCA AACAAATGGAG	1200
30	GGGATGGAGA GCCCTGGTGT CCGTACGGGA GCCAGGTCGG CCTGAGAGCT GTGCCGCTCC	1260
	TCTGTCTTGT CAGTGGAGGT GCCTGGGTGG GGAGCAGGTC TCAGGCCTCT TGTCTCTCC	1320
35	CCAGTGGCTC CAGGCCTCAC TAGTGGCAAG GGCAGGATGA GGCTGCACCG CTGGGAAGAG	1380
	TCTATCTAAG YTCCTGGCTT GGAGTCCCGT GTCGTCTCCR CCCAGAGGAA GTTCTCCAGA	1440
	GTTACCTTT CCCTTTTCTT TGAGTTGTGC TGAATGCCCC ACCCCAGCTC TCTTTCCCTT	1500
40	CTGGGTGTCT TTGCTGGGAG GGGGCTGTGT TGTGAGCCCT CCCGGTCTC ACCTCGCCTG	1560
	GCACTTAACC ACACCTGGT TTTGTGTAGC CGCCAGCTCT CTTCTGGTTG GGCCTTTGAA	1620
45	AGGCTCAGCC TCCCATTGTG CAGTGCCTGG GTTTGGAGCT TATTTGAATG GAAGAGGTCA	1680
	GTTGTCTCCT GGCTCTCCAT TTCTGGCCTC AGTTGTCTAC AGGACAGTGG TCAGGGATGC	1740
	CTGGAGGCAT ATATCCAGCT GCCACCAAGG GGCAGTGTG GTTCCCACTT ATGTGAGTGA	1800
50	CCCCATCCAT CCATGACCAG AGGATTATTT TCCTGCCTTG GCAGAGGAGG AGGAGTCAAG	1860
	GGAGCAGGGC AGCTCTACCA GGCAAGGTGT TTCCCCAGCA TAGGCGCAGA CAGTTGGGAC	1920
55	GAAACTTCAG AGCCCAGGCA GTCCCTGAAT GACCAGGCCA GTGTGTCTAC TGAGTGGTCC	1980
	CCTGCTGGTT GGGAGTGAAG AGAATCCAGG CTGGCAGAGC TGGAGCCAGT TGGGGAGCAC	2040
	GGTCTGGGA GCTCTGCAAA ATCAGTAGCA AGTGTGGAA AAGGCACATG CCGAAGATAC	2100
60	TCAAGAGCTC CCAAGATTTG CTTGAGGCTA GCCCAGTGAA RAAAACCAGA GACTCATGTT	2160

	TCCAGGGGTC AGTCTGTGAG GCAGGAAGGA CCCAGGATTT GAACCCAGCT TCAGTGTGCA	2220
5	GGCTCTGAGG CTGCCAGGA CGGAAAGTC CAAGGAAGGG GCCTGGTGGT GCTCCACTTG	2280
	CAGTTCCTTTA AAGAATGCTG CTTTTTATTC TCCTAACCCCT TTCAAGTGGG TGCAGACTTC	2340
	TCGTTAGCAG CTGGAAGACA TTCCTCCAC ACTTTTCCCT TCCTGGCCA AGAGAGCATC	2400
10	CAGAAGGCAG TAGGACCTGG TTTTTCAGGT ACTGGGAGCC GGGGGCTCAC TGCTTGCACT	2460
	GTGCTTAGGG TAGGGATGGT AAATATCCTC CTGCATGGC TTTATCCTCC CTCTCATCCC	2520
15	AAAGCAGGTA TCTTCTGGTT GTCACAGAGT TTCATTGAGT CCAGCTGCAG CCACGTGGCC	2580
	ATCTGGAGCT GGTGCTATAG GTGACCATCT GGTACATTGA GGGGACCTGT TTGCCTCCTC	2640
	CACTCTATAA GCAGTCATCT TGGGAGACCG GGAGGAGAAG GTGGTGGGCT AGTCCTGTGT	2700
20	CCTCCTCCAC TTCCCATGCC TCTATGTTAC CCATCTGTGT CTCCTGTGCA GAAGGAGAGG	2760
	AAGGGGCATT AAGAGATGAA GGGTGATTAT GTATTACTTA TCCATTTCTG AATAAACATT	2820
25	TGTTATTCCT AAAAAAAAAA AAAAAAACT CGAGGGGGG CCCGWAACC AWATCGCCSK	2880
	AAAGTGAG	2888

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(2) INFORMATION FOR SEQ ID NO: 62:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1851 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

35

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 62:

	CACTAGTATA ATTTATAATT ATAACCTATT CTGATTCTTT TTCAAATATT AGGTGTCCTA	60
	GTGCTTATG AAGGTTTGCC ACTTCATCTT GCACTGTTCC CCAAACCTTG GACTGAGCTA	120
45	TGCCAGACTC AGTCTGCTAT GTCAAAAAC TGCATCAAGC TTTTGTGTGA AGATCCTGTT	180
	TTTCGAGAAT ATATTAAATG TATCCTAATG GATGAAAGAA CTTTTTTAAA CAACAACATT	240
50	GTCTACACGT TCATGACACA TTTCTTCTA AAGGTTCAA GTCAAGTGT TTCTGAAGCA	300
	AACTGTGCCA ATTTGATCAG CACTCTTATT ACAAACCTGA TAAGCCAGTA TCAGAACCTA	360
	CAGTCTGATT TCTCCAACCG AGTTGAAATT TCCAAGCAA GTGCTTCTTT AAATGGGGAC	420
55	CTGAGGGCAC TCGCTTTGCT CCTGTCAGTA CACACTCCCA AACAGTTAAA CCCAGCTCTA	480
	ATTCCAACCTC TGCAAGAGCT TTTAAGCAA TGCAGGACTT GTCTGCAACA GAGAACTCA	540
60	CTCCAAGAGC AAGAAGCCAA AGAAAGAAAA ACTAAAGATG ATGAAGGAGC AACTCCCAAT	600

	AAAAGGCGGC GTGTTAGCAG TGATGAGGAG CACACTGTAG ACAGCTGCAT CAGTGACATG	660
	AAAACAGAAA CCAGGGAGGT CCTGACCCCA ACGAGCACTT CTGACAATGA GACCAGAGAC	720
5	TCCTCAATTA TTGATCCAGG AACTGAGCAA GATCTTCCTT CCCCTGAAAA TAGTTCGTGT	780
	AAAGAATACC GAATGGAAGT TCCATCTTCG TTTTCAGAAG ACATGTCAAA TATCAGGTCA	840
10	CAGCATGCAG AAGAACAGTC CAACAATGGT AGATATGACG ATTGTAAAGA ATTTAAAGAC	900
	CTCCACTGTT CCAAGGATTC TACCCTAGCC GAGGAAGAAT CTGAGTTCCC TTCTACTTCT	960
	ATCTCTGCAG TTCTGTCTGA CTTAGCTGAC TTGAGAAGCT GTGATGGCCA AGCTTTGCCC	1020
15	TCCCAGGACC CTGAGGTTCG TTTATCTCTC AGTTGTGGCC ATTCCAGAGG ACTCTTTAGT	1080
	CATATGCAGC AACATGACAT TTTAGATACC CTGTGTAGGA CCAITGAATC TACAATCCAT	1140
20	GTCGTCACAA GGATATCTGG CAAAGGAAAC CAAGCTGCTT CTTGACATTA GGTGTAGCAT	1200
	GTCTACTTTT AAGTCCCTCA CCCCCAACC CCATGCTGTT TGTATAAGTT TTGCTTATTT	1260
	GTPTTTGTGC TTCAGTTTGT CCAGTGCTCT CTGCTTGAAT GGCAAGATAG ATTTATAGGC	1320
25	TTAATTCCTG GTCAGGCAGA ACTCCAGATG AAAAAAAGT GCATCTTCAG TATACTTCCT	1380
	AAAGGGCAAT CAGATAATGG ATATGTTTTA TGTAATTAAG AGTTCACITT AGTGGCTTTC	1440
30	ATTTAATATG GCTGTCTGGG AAGAACAGGG TTGCCTAGCC CTGTACAATG TAATTTAAAC	1500
	TTACAGCATT TTTACTGTGT ATGATATGGT GTCCTCTGTG CCAGTTTTGT ACCTTATAGA	1560
	GGCAGATTGC CTCGATCGC TGTGGTCTT ATPATCAAAA TTAAGTTTAC TTGTATACGG	1620
35	AACAACCACA AGAAATTTGA TTCTGTAAAG AATCCTCTTT AGCTGTGGCC TGGCAGTATA	1680
	TAAATGGTGC TTTATTTAAC AGAATACCTG TGGAGGAAAT AAAGCACACT TGATGTAAAA	1740
40	ATAATTGTTT TATTTTATT GACATGACTG APTGATTGCT ATTCTGTGCA CTTAATTAAA	1800
	CTGATTGTGA TGACTTWAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA A	1851

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(2) INFORMATION FOR SEQ ID NO: 63:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 3542 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

50

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 63:

55

	TCCAATGCTG ATGAGCGTCT TCGCTGGCAG GCCAGCTCCT TGCCTGCTGA TGACCTTTGC	60
	ACAGAAAATG CCATCATGCT GAAACGATTC AATAGGTATC CGCTGATCAT TGACCCCTCT	120
60	GGACAGGCCA CAGAATTCAT TATGAATGAA TATAAGGATC GTAAGATCAC ACGGACCAGC	180

	TTCTTGGATG ACGCCTTCAG AAAGAACTTA GAGAGTGCAC TGAGATTTCG TAACCCCTT	240
5	CTGGTCCAGG ATGTGGAAAG CTACGATCCA GTTTTGAACC CGGTGCTGAA CCGTGAAGTG	300
	CGGCGAACAG GGGGAGAGT GCTGATCACT CTCGGGGACC AGGACATAGA CCTGTGCGCA	360
	TCGTTTGTC TCTTCTGTG CACCCGGGAT CCAACTGTG AGTTCCACC AGATCTCTGT	420
10	TCCCGGGTTA CTTTGTGAAA CTTCACAGTT ACCCGTAGCA GTTTACAAAG CCAGTGCTTA	480
	AATGAAGTAC TTAAAGCAGA AAGACCTGAT GTGGACGAGA AACGATCTGA TCTTCTTAAA	540
15	CTTCAAGGGG AATTTCAGCT CGTTTTCGT CAGCTGGAAA AATCTCTACT ACAAGCTCTG	600
	AACGAGGTGA AAGGCGCAT TTTGGATGAC GACACGATCA TAACCACTCT GGAGAACCTG	660
	AAGAGAGAGG CTGCAGAGT CACCAGGAAA GTTGAGGAGA CGGACATTGT CATGCAGGAG	720
20	GTGGAGACCG TGTCCAGCA GTACCTCCCG CTCTCCACCG CCTGCAGCAG CATCTACTTC	780
	ACCATGGAGT CCCTCAAGCA GATACACTTC TTGTACCAGT ACTCCCTCCA GTTTTTCCTG	840
25	GACATTTATC ACAACGTCCT ATACGAGAAC CCGAACCTGA AGGGTGTAC CGACCACACA	900
	CAGCGCCTGT CCATTATAAC AAAGGACCTC TTCCAGGTGG CGTTTAACCG AGTGGCTCGA	960
	GGCATGCTGC ATCAGGACCA CATTACCTTT GCCATGCTGC TGGCAAGAAT CAAACTGAAG	1020
30	GGCACCCTGG GGGAGCCAC CTACGATGCA GAATTCCAGC ACTTCTTGAG AGGAAATGAG	1080
	ATTGTCTTGA GTGCTGGCTC CACCCCAGG ATCCAGGCC TGACTGTGGA GCAGGCGGAG	1140
35	GCGGTGGTGA GGCTGAGCTG CCTTCCCGCG TTAAAGGACT TGATTGCAA GGTTCAGGCA	1200
	GACGAGCAAT TTGGCATCTG GCTGGACAGC AGCTCCCCGG AGCAGACTGT GCCCTACCTC	1260
	TGGAGTGAAG AAACACCTGC AACACCCATT GGCCAGGCCA TCCACCGCCT GCTCCTGATC	1320
40	CAGGCTTTCC GGGCGATCG CCTGTGGCC ATGGCCACA GTTTGTGTTT AACAAACCTT	1380
	GGGAGTCTT TCATGTCCAT CATGGAGCAG CCGCTCGACC TGACCCACAT TGTGGSCACA	1440
45	GAGGTGAAGC CCAACACTCC TGTCTTAATG TGCTCTGTGC CTGGTTATGA TGCCAGTGGA	1500
	CATGTCGAGG ACCTTGACAG CGAGCAGAAC ACGCAGATCA CTTCAATTGC AATCGGCTCT	1560
	GCAGAAGGCT TTAACCAAGC AGATAAGGCA ATAAACACCG CTGTAAAGTC GGGCAGGTGG	1620
50	GTGATGCTGA AGAATGTGCA TCTGGCCCCA GGGTGGCTGA TGCAGCTGGA GAAGAAGTTG	1680
	CATTCCCTGC AGCCGCATGC CTGCTTCCGA CTCTTCTCA CCATGGAGAT CAACCCCAAG	1740
55	GTGCCCTGTA ATCTGCTCCG TCGGGCCGC ATCTTTGTGT TCGAGCCACC GCCAGGKGTG	1800
	AAGGCCAACA TGCTGAGGAC GTTCAGCAGC ATTCCCGTCT CACGGATATG CAAGTCTCCC	1860
	AACGAGCGTG CCCGCTTGTA CTTCTGCTG GCCTGGTTTC ATGCGATCAT CCAAGAACGC	1920
60	TTACGATACG CACCACTGGG GTGGTCAAAG AAGTATGAAT TTGGAGAGTC TGACCTGCGG	1980

	TCANYTTGCG ATACGGTGGA CACGTGGCTG GATGACACGG CCAAGGGCAG GCAGAACATC	2040
5	TCACCGGATA AGATCCCGTG GTCTGCACTA AAGACCTTAA TGGCCCAGTC CATTTATGGC	2100
	GGGCGCGTGG ACAACGAGTT TGACCAGCGT CTGCTCAACA CCTTCCTGGA GCGCCTGPMC	2160
	ACAACCAGGA GTTTCGACAG TGAGTTTAAG CTGGCATGCA AGGTGACGAG ACATAAAGAC	2220
10	ATTCAAATGC CAGATGGCAT GCAGGCGAGA GGAGTTTGTG CAGTGGGTGG AGTTGCTCCC	2280
	CGACACCCAG ACGCCCTCCT GGCTGGGCCT GCCCAACAAC GCCGAGAGAG TCCTCCTTAC	2340
15	CACACAGGGT GTGGACATGA TCAGTAAAT GCTGAAGATG CAGATGTTGG AGGATGAGGA	2400
	CGACCTGGCC TACGCAGAGA CTGAGAAGAA GACGAGGACA GACTCCACGT CCGACGGGCG	2460
	CCCTGCCTGG ATGCGGACAC TGCACACCAC CGCGTCCAAC TGGCTGCACC TCATCCCCCA	2520
20	GACGCTGAGC CACCTCAAGC GCACCGTGGA GAATATCAAG GATCCTTTGT TCAGGTTCCTT	2580
	TGAGAGAGAA GTGAAGATGG GCGCAAAGCT GCTTCAGGAC GTTCGCCAGG ACCTTGCGA	2640
25	TGTCGTCCAG GTGTGCGAAG GAAAGAAGAA GCAGACCAAC TACTTGCGCA CGCTGATCAA	2700
	CGAGCTAGTG AAAGGGATCT TGCTCGGAG CTGGTCCAC TACACGGTGC CTGCCGGCAT	2760
	GACCGTCATC CAGTGGGTGT CCGACTTCAG CGAGAGGATC AAACAGCTGC AGAACATCTC	2820
30	ACTGGCAGCT GCATCTGGTG GCGCCAAGGA GCTAAAGAAC ATCCACGTGT GCCTGGGTGG	2880
	CCTGTTCTGT CCTGAGGCGT ACATCACTGC CACCAGGCAG TATGTGGCCC AGGCCAACAG	2940
35	CTGGTCCCTG GAGGAGCTCT GCCTGGAAGT CAACGTCACC ACCTCACAGG GCGCCACCCT	3000
	TGACGCTTGC AGCTTCGAG TCACGGGTTT GAAACTTCAA GGGGCCACGT GCAACAACAA	3060
	CAAGCTGTCA CTGTCCAATG CCATCTCAAC CGCCCTTCCC CTGACGCAGC TCGCTGGGT	3120
40	CAAGCAGACA AACACCGAGA AGAAGGCCAG TGTTGTAACC TTACCTGTCT ACCTGAACTT	3180
	CACCCGTGCA GACCTCATCT TCACCGTGGA CTTCGAAATT GCTACAAAGG AGGATCCTCG	3240
45	CAGCTTCTAC GAGCGGGGTG TCGCAGTCTT GTGCACAGAG TAAACTTTTC TAGCTGCCCC	3300
	TTTCTGTAAT AGTGAAAGTT GGTATTTAAC ATTTATTCAT TTTTAAAATA TTTGGAAGGT	3360
	CTGAGCTTGT GAAAAGAAAG TGGTTGGTCT GAGGTGGAG GAAGCTGAAT GGAATCTGAC	3420
50	GGTTGGGAGT GGTGGAATT GGAAGGATAC CAGGAGGTAT TTGGGAAGGC CAATGGCGTG	3480
	GCTCCTTTGA GGAATAAAAA CACTAAGCAT GAAAAAATA AAAAACTTA CAANCCNCAA	3540
55	GG	3542

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 883 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 64:

10 AGGTGATTTT AATGATAGGT GTCATATATA GGACGGATAA TCTGTTTACA TTCTGTTCCTT 60
 CTCGATGCAC TCACAAGCGG GTAAC TAGGT GACAAGAAAA CAAAGATCTT ATTCAAAAGA 120
 GGTCTTACAG CAACCCAACG TCTCATCTTC CCATAGTAAA GATGACGGCG CCTTGAGGTA 180
 15 AGCTACAGGC AACACCACTT CCGCGTTTCT CTGCGCCCT GGTCCAAGAT GCGGATGAA 240
 GCCACGCGAC GTGTGTGTC TGAGATCCCG GTGCTGAAGA CTAACGCCGG ACCCCGAGAT 300
 CGTGAGTTGT GGGTGCAGCG ACTGAAGGAG GAATATCAGT CCCTTATCCG GTATGTGGAG 360
 20 AACACAAGA ATGCTGACAA CGATTGGTTC CGACTGGAGT CCAACAAGGA AGGAACTCGG 420
 TGGTTTGGAA AATGCTGTA TATCCATGAC CTCCTGAAAT ATGAGTTTGA CATCGAGTTT 480
 25 GACATTCCTA TCACATATCC TACTACTGCC CCAGAAATTG CAGTTCCTGA GCTGGATGGA 540
 AAGACAGCAA AGATGTACAG GGGTGGCAAA ATATGCCTGA CGGATCATTT CAAACCTTTG 600
 TGGGGCCAGG AATGTGCCA AATTGGACT AGCTCATCTC ATGGCTCTGG GGCTGGGTCC 660
 30 ATGGSTGGCA GTGAAATCC CTGATCTGAT TCAGAAGGGC GTCATCCAAC ACAAAGAGAA 720
 ATGCAACCAA TGAAGAATCA AGCCACTGAG GCAGGCAGA GGGACCTTTG ATAGGCTACG 780
 35 ATACTAWTTT CCGTGTGATC AACTTAACCT CATCTAAGT TTCCCCGGAC ANCTCCACT 840
 CTAGTTGTTA CTAAGTANTG CAGTAGCATT NTGGGAAGA ACA 883

(2) INFORMATION FOR SEQ ID NO: 65:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1541 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 65:

55 GGCACGAGGT GGCCTCTACC CTGGGCTCAT CTGGCTACAC AGGGACTCTA AACGCTTCCA 60
 GATTCCCTGG AAACATGCCA CCCGGCATAG CCCTCAACAA GAAGAGGAAA ATACCATTTT 120
 TAAGCCTGG GCTGTAGAGA CAGGAAGTA CCAGGAAGG GTGGATGACC CTGACCCAGC 180
 TAAATGGAAG GCCCAGCTGC GCTGTGCTCT CAATAAGAGC AGAGAATTCA ACCTGATGTA 240
 60 TGATGGCACC AAGGAGGTGC CCATGAACCC AGTGAAGATA TATCAAGTGT GTGACATCCC 300

	TCAGCCCCAG GGCTCGATCA TTAACCCAGG ATCCACAGGG TCTGCTCCCT GGGATGAGAA	360
5	GGATAATGAT GTGGATGAAG AAGATGAGGA AGATGAGCTG GATCAGTCGC AGCACCATGT	420
	TCCCATCCAG GACACCTTCC CCTTCCTGAA CATCAATGGT TCTCCCATGG CGCCAGCCAG	480
	TGTGGGCAAT TGCAGTGTGG GCAACTGCAG CCCGGAGGCA GTGTGGCCCA AAACCTGAACC	540
10	CCTGGAGATG GAAGTACCCC AGGCACCTAT ACAGCCCTTC TATAGCTCTC CAGAACTGTG	600
	GATCAGCTCT CTCCCAATGA CTGACCTGGA CATCAAGTTT CAGTACCGTG GGAAGGAGTA	660
15	CGGGCAGACC ATGACCGTGA GCAACCTCA GGGCTGCCA CTCTTCTATG GGGACCTGGG	720
	TCCCATGCCT GACCAGGAGG AGCTCTTTGG TCCCGTCAGN CTGGAGCAGG TCAAATTCCT	780
	AGGTCTGAG CATATTACCA ATGAGAAGCA GAAGCTGTTT ACTAGCAAGC TGCTGGACGT	840
20	CATGGACAGA GGACTGATCC TGGAGGTCAG CGGTCATGCC ATTTATGCCA TCAGGCTGTG	900
	CCAGTGCAAG GTGTACTGGT CTGGGCCATG TGCCCCATCA CTGTGTGCTC CCAACCTGAT	960
25	TGAGAGACAA AAGAAGGTCA AGCTATTTTG TCTGGAAACA TTCTTAGCG ATCTCATTGC	1020
	CCACCAGAAA GGACAGATAG AGAAGCAGCC ACCGTTGAG ATCTACTTAT GCTTTGGGGA	1080
	AGAATGGCCA GATGGGAAAC CATGGAAG GAAACTCATC TTGGTTCAGG TCATTCCAGT	1140
30	AGTGGCTCGG ATGATCTACG AGATGTTTTC TGGTGATTTC ACACGATCCT TTGATAGTGG	1200
	CAGTGTCCTC CTGCAGATCT CAACCCAGA CATCAAGGAT AACATCGTTG CTCAGCTGAA	1260
35	GCAGCTGTAC CGCATCCTTC AAACCCAGGA GAGCTGGCAG CCCATGCAGC CCACCCCCAG	1320
	CATGCAACTG CCCCTGCCG TGCCTCCCCA GTAATTGTGA ATGCCATCTT CTTCTTCTC	1380
	TTTTTTATAA TATTGTACAT ATGGATTTT TTATTGTTTA GATTTAACCA GCTTTTAAAT	1440
40	CTCTGTTTTC TGTGACAGTG TTAGAAGTTT GTGATCTCC AAATATGCCT AGATTTAAAG	1500
	CTGATTTAAT TTATGGAAAA AAAAAAAAAA AAAAAAAAAA A	1541

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(2) INFORMATION FOR SEQ ID NO: 66:

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- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 732 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 66:

	AGAAAATGAA TGTTAGAAGG TGCTGCCGA GCGGGACAG AGTGTTCCT CGCGCTGGAG	60
60	AAGGCTCTGC TCAGCCCTGA GAGTCCCTTC CTGCCCCACC GATACTGGCA CTTTAAAAAG	120

GAAGCTGACC GCACAGTGTG CAGACGAATT GGCCCCAGA AGATGGGGAG TTCTGTCTTG 180
CCCTTCTGTG TCTGCGTGAC CTCACCCAGC CTAGGAGGGA GGTGCATTCA GGGTAGATTT 240
5 GCCTCTCATT CAAAGTTCTG GGGCTTTGGG CGGAAAACAG CCAGCTTTGG CGCTGTGGG 300
GAGACTCTTC CAGACCAGGA ACCCCAGAAG GAGACAGAGC CTGCCACATC CTCCCACGCC 360
10 AGGCCCTGGG CCAGGGTGAT TGGACTGAGA ATTTGGCCAC AACCAAATG ATGCTGGCTG 420
GAACCAGAGG CCAGAAAGCC TGGCCTTGTC CCCATGTGGG AGCCCTGTCC TCAGCCCTCT 480
TGTCCCTTG AGCTCAGTGA ATTCCACCA GGTGCCACA GCTCCTGGAC TTCAAATTCT 540
15 ATATATTGAG AGAGTTGGAG AGTATATCAG AGATATTTT GGAAAGGAGT TGGTCTATGC 600
AATGTCAGTT TGAATCTTC TTGAAAGTTT AATGTTTTTA TTAGGAGATT TAAAGAAAAT 660
AAAGGTCTAC AATATCAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA 720
20 AAAAAAAAAA AA 732

25

(2) INFORMATION FOR SEQ ID NO: 67:

(i) SEQUENCE CHARACTERISTICS:
30 (A) LENGTH: 629 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 67:

35 TTAAGGAATT CGGCMGATC CCGCAAGTA ACATGACTAA AAAGAAGCGG GAGAATCTGG 60
GCGTCGCTCT AGAGATCGAT GGGCTAGAGG AGAAGCTGTC CCAGTGTGG AGAGACCTGG 120
40 AGGCCGTGAA CTCCAGACTC CACAGCCGGG AGCTGAGCCC AGAGGCCAGG AGGTCCCTGG 180
AGAAGGAGAA AAACAGCCTA ATGAACAAAG CCTCCAATA CGAGAAGGAA CTGAAGTTTC 240
TTCGGCAAGA GAACCGGAAG AACATGCTGC TCTCTGTGGC CATCTTTATC CTCCTGACGC 300
45 TCGTCTATGC CTACTGGACC ATGTGAGCCT GGCACCTCCC CACAACCAGC ACAGGCTTCC 360
ACTTGGCCCC TTGGTCAGGA TCAAGCAGGC ACTTCAAGCC TCAATAGGAC CAAGGTGCTG 420
50 GGGTGTTCCT CTCCCAACCT AGTGTTCAG CATGGCTTCC TGGCGGCCCA GGCCTTGCCT 480
CCCTGGCCTG CTGGGGGGTT CCGGTCTCC AGAAGGACAT GGTGCTGGTC CCTCCCTTAG 540
CCCAGGGAG AGGCAATAAA GAACACAAAG CTGAAAAAA AAAAAAAAAA AACTCGTAGG 600
55 GGGGGCCCGT ACCCAATCGC CCTNCTGTG 629

60

(2) INFORMATION FOR SEQ ID NO: 68:

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 1751 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 68:

10 CTGCTAGCCG GCCGGCGCAG GCTGCCGAGC GGGTGAGCGC GCAGGCCAGG CCAAAGCCCT 60
GGTACCCGCG CGGTGCGGGC CTCAGTCTGC GGCCATGGGG GCGTCCGCGC GGCTGCTGCG 120
15 AGCGGTGATC ATGGGGGCCC CGGGCTCGGG CAAGGGCACC GTGTCGTGCG GCATCACTAC 180
ACACTTCGAG CTGAAGCACC TCTCCAGCGG GGACCTGCTC CGGACAACA TGCTGCGGGG 240
CACAGAAATT GGCCTGTTAG CCAAGGCTTT CATTGACCAA GGGAAACTCA TCCCAGATGA 300
20 TGTCATGACT CGGCTGGCCC TTCATGAGCT GAAAAATCTC ACCCAGTATA GCTGGCTGTT 360
GGATGGTTTT CCAAGGACAC TTCCACAGGC AGAAGCCCTA GATAGAGCTT ATCAGATCGA 420
25 CACAGTGATT AACCTGAATG TGCCCTTTGA GGTCAATPAA CAACGCCTTA CTGCTCGCTG 480
GATTCATCCC GCCAGTGGCC GAGTCTATAA CATTGAATTC AACCTCCCA AACTGTGGG 540
CATTGATGAC CTGACTGGGG AGCCTCTCAT TCAGCGTGAG GATGATAAAC CAGAGACGGT 600
30 TATCAAGAGA CTAAAGGCTT ATGAAGACCA AACAAAGCCA GTCCTGGAAT ATTACCAGAA 660
AAAAGGGGTG CTGGAAACAT TCTCCGAAC AGAAACCAAC AAGATTTGGC CCTATGTATA 720
35 TGCTTTCCTA CAACTAAAG TTCCACAAAG AAGCCAGAAA GCTTCAGTTA CTCCATGAGG 780
AGAAATGTGT GTAATATTA ATAGTAAGAT GGGCAACCTT CCTAGTCCCT GCATTTAGAA 840
GCTGCTTTTC CTAAGACTTC TAGTATGTAT GAATTCCTTG AAAATTATAT TACTTTTATT 900
40 TCTACTGATT TTATTTTGA TACTAAGGAT GTGCCAAATG ATTCGGATAC TAAGATGCAT 960
CGTTTGAAAT CATCTAGTGT GTGTATGCA GTTATCCTCA AAAACATCAG CGATGTCTGA 1020
45 ACCTTTAAAA CATCTGTTAG AGCAAAATTA AAAGAGCATT TGGTAGTAAT CTAACTTTTT 1080
GTTTCAGTAA TAAGTGGTTG ATAAAGTTTC CATATTTTTC TGGAAAAGTT AAAAAAGTT 1140
ACATGTCATT TGGAGAAAAT ACGTAATCAG AAATTTGTGC ATAGATTGAT GCCAAAAAG 1200
50 ACATTTCCAG CATGTGGAA CATGGTGAGA CACTATATAA AATTCCAGAA AGAAAGCAAC 1260
TGGATTTACA GATTTATTGT GAGACACAAA TTCACTGCTG CCTTTACACT AAGAAATGTA 1320
55 TATGTTAACC ATATATGCTG TATTTATTTT GTCGTTAAGC ATACTTTCAG TTTACTCAGA 1380
ATTTTCAATT TGCTATAAAG ATGTATCAAT TAGCATATAG AAAAATATTA CTTTAAGATG 1440
ACTTGTTCCT TTTGAAAATA CCTGTGTACT GAGGGTTATG ATTTGTGTCA AAAATTGACA 1500
60

TAAGTGCTTT TACAAGCACC AAAGTTGAAT GAATTTTCAA CAAAATGTAA TTAAAGTCTA 1560
TGTTTTTCAGT TATGACTCAG GTTAAGAAAT GTGTTTTAGG ATCTACTTGC TGGTTTTTCT 1620
5 TTTTGATCCA AATGTGTGAT CTGCCCTGAT AAATAACAAG TTATNGTACC ATCTCCCCCG 1680
CCAATAAAAA AAAAAAAAAA AAAAAAAAAAC TCGAGGGGGG GCCCGGTACC CAATTCTCCG 1740
NAATAGGNAG T 1751
10

15 (2) INFORMATION FOR SEQ ID NO: 69:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 508 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
20 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 69:

GGCACGAGAT TATGTATTAA AATGTTTTTG AATTGTGAAA TATTAGAATA TTGTTACTAT 60
25 TTGACCCAAC TCAAAATCTC CATGGGAAAA TACCTGTGCA TACCCACAGT ATTGTTGAAA 120
ATAATCAGAT GCAGTATCAC AGCTGTGTCA GACTCTAGTA CCAGTTGGGC AATCAAGGCA 180
30 CAGCTAAAAA TTGAAAACAA AGATCTGGAC AACAAAACAG CCAAAGGTGG GGGTCAAGAA 240
GCTCTGACGT GTACCTAGCT GTAGAATGCT ATGCACACGT GCCAGGTGTA GTGTGCATAT 300
CCAGGAAAAA CTGCAGAGAG CCCAGTCTT CACCTCTGGT TGACCATGAG CTCTGTGTAA 360
35 GCAGGAAGTG AAGGCTAAGG CAGATTAAAG CTCTGAAAGC ATTCCACAAC ATACACACAA 420
ATCGTGCAAA GCATTAAGGA AATCTTGTTA CTGCTAAGTG TTGCTGACCC AGGAACAAC 480
40 CCTACTCAGC TGGACTTAAA AATAAAAA 508

45 (2) INFORMATION FOR SEQ ID NO: 70:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 245 base pairs
(B) TYPE: nucleic acid
50 (C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 70:

TACATAGAGC AAAGAGAAAT TTCCAGAATT TCTARAATTC TGGAAAGAGA ATTTTCCTGA 60
GATTGCAGAT TTGCTTGTGT CCTCAGGTGA TGATGAGGCG TGTTTTCCCC TGTGTCTCTT 120
TCCTCACACT CATGCTTCCT CTCCTAGAGT GTCTGGTTGG CATGATCATG TGCTACCTAG 180
60

GCATTTCTTT CACTGATACA AGGAAACTG CAGGGTTAAA AAAAAAAAAA AAAAAAAAAA 240
NCNCG 245

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(2) INFORMATION FOR SEQ ID NO: 71:

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- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 361 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 71:

ATGTTCTCA TGAGGATGCA CTGTGCTTC TGCAAGTATT GCTGCAGCTT CATAGTGACT 60
20 CCCACCAGCA CCAGCAATAC AGCTAGCTAC CTGTGGCCTT GGATCTCAGC CAGCATGGCT 120
GGGAGAGGGA GCAGCTGGGC ATGTACCTTA AATGCTGTTA CCAGGGAAGG ACTCCAGAG 180
TGAAGACAAG TAGGGACTTC CTGCAGAGGT GGTACATGTG CTCTCTGTAT CCATACTTTT 240
25 TTTTTTTTTT TTTTGAGATA GAGTTTCACC CTTGTTGCCC TGGCTGGAGT GCAATGGTGC 300
GATCTCAGCT CACTGCAACC TCTCTGCCTC CCGGGTTCAA GTGATTCTCC TGCCTCAGCC 360
30 T 361

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(2) INFORMATION FOR SEQ ID NO: 72:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 713 base pairs
(B) TYPE: nucleic acid
40 (C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 72:

45 AGGATCACAC AATAGAGAAC ACTGTAGTAA CATTTTCGGTC TGCTCACAAG ACCCAGAACA 60
TTGATCAGTT TTTGTTGTTG GTTATATATT TTTCTGTAA AAAATTGTGA AAAGTTTGT 120
TTAGCTAGAT GATATTTTAA TAGCTGCGAG TGCITTTGGAA CTATAAAGAT GTCACTACTT 180
50 AACACACATA CCTTATGTTT TGTTTTGTTC TGTTTTACAC TCAGTATAAA TCAGGAGAAG 240
TTAGCCAACC ATCTAGCAIT TAGAATCCTC TTTTATTATG TCTTCTAAGG ATATGGATGT 300
55 TCCCATAACA GCAACAAAAC AGCAACAAA ACATTTTATA AATATCACTT GATAGACTGT 360
AAGCACTGC TTAACTTTGT GTCCCAAATA TTTAGTGIGT ATATATATAT ATATATATAC 420
60 ACACACACAC ACATATATAT TCAACAAATA AAGCAAATA TAACATGCAT TTCACATTTT 480

GTCTTTCCCT GTTACGATTT TAATAGCAGA ACTGTATGAC AAGTTTAGGT GATCCTAGCA 540
TATGTTAAAT TCAAATTAAT GTAAACAGA TTAACAACAA CAAAGAACT GTCTATTTGA 600
5 GTGAAGTCAT GCTTCTATT ATAATAACTT GGCTTCGGTT ATCCATCAA TGCACACTTA 660
TACTGTTATC TGATTGTTTA TAATAAGAA TACTGTACTT ATAAAAAAAA AAA 713

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(2) INFORMATION FOR SEQ ID NO: 73:

(i) SEQUENCE CHARACTERISTICS:
15 (A) LENGTH: 862 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 73:

GAAAGTCAGA GCTGTCCAAT CCCTCAGCAC CTTTTAGATT TGCTCCAAAT TAGAAACGTG 60
GGGACTATGT GTTCTGGGCA ATCAGAGGTC TGGAAATGG CTCTGCAGGC TCTTGATAGT 120
25 GAGACAGTGG TCATCTTACC AGACATGCAT CTGATTTTAA GCCTCAGGCT AATCCACAAT 180
GCTCGGCCAT GCCTATGATT AACAAACAAA AGCAAAATCT GCTTTTATAG TTTAGGAAAC 240
30 CTGGATAGAA CAGTATTTTT CAGCATTCTT GGATAAAGCA GTTCTGCATT TTTAAATTGG 300
GACTGCAGAA GTGACTGTCT ATAGTTGTGA AATACAAAAA ATGGTATGTT TGATCAGAAA 360
AGGAAGCCCG TGCCTGGCAC TTGGAAAGAT ACTGAGCATC ATAACCCTAA TGAGAAAATG 420
35 TAGGCTCTGT GAATGTTAAC TACAAATCAG GTTAGGAAAG CATATGACAC CCTTTGTCAA 480
ACTAAGCTTC ACTAGGAGGA CCTGTGCTCA TAGAAGAATA TGCTTTAAAA GTATCAATTT 540
40 TCCACAGTCG ATGATGGAGA AAAGTTCATT TGCACCAGAA TGCTGATAGT CACAATACAC 600
AGCCTGACAT ATATAACAAT ACAGTTTCTT GTAAACAGAA GTTCTTCCTC TTCCAATTCA 660
GGAGTCAGTC AGAGCATAAA TATTGCATGT TTCACTTTAG AAAGTGATTC ATTTTAGAAA 720
45 GCAGATCTGG ATTATTTTGC AGGGTAGAAA TGAAGGCTAT TTCTGGCATT CTTGCTCAAA 780
AAGTCAATAT ATGTACATTA AGTATAAAAA AGGGTCTCTT TCACCTCTTT TGTTCGTAG 840
50 CATTGCTAC ATAACCTGTG CC 862

55 (2) INFORMATION FOR SEQ ID NO: 74:

(i) SEQUENCE CHARACTERISTICS:
60 (A) LENGTH: 4602 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 74:

5	GCGAGGGGGC GKGGGGAGCA GCGCCGARGC CGCCGCCTCC GCCTCCGCCG CCTAGGACTA	60
	GGGGGTGGGG GACGGACAAG CCCGATGCC GGGGAKACG GAAGAGCCGA GACCCCGGA	120
10	GCAGCAGGAC CAGGAAGGGG GAGAGGCGGC CAAGGCGGCT CCGGAGGACC CGCAACAACG	180
	GCCCCCTGAG GCGGTGCGG CGGCGCTGC AGGGACCACT AGCAGCCGCG TGCTGAGGGG	240
	AGGTGGGAC CGAGCCGGG CCGCTGCGRC CGCCGCGCMG CAGCTGTGTC CCGCCGGAGA	300
15	AGGCCGAGTA TCCCCGCCG CGAGGAGCAG CCCAGCGCC AGGCCTCCCG ACGTCCCCGG	360
	GCAGCAGCCC AGGCCGCGAA GTCCCCGTCT CCAGTTCAGG GCAAGAAGAG TCCGCGACTC	420
20	CTATGCATAG AAAAAAGTAAC AACTGATAAA GATCCCAAGG AAGAAAAAGA GGAAGAAGAC	480
	GATTCTGCCC TCCCTCAGGA AGTTTCCATT GCTGCATCTA GACCTAGCCG GGGCTGGCGT	540
	AGTAGTAGGA CATCTGTTTC TCGCCATCGT GATACAGAGA ACACCCGAAG CTCTCGGTCC	600
25	AAGACCGGTT CATTCAGCT CATTTGCAAG TCAGAACCAA ATACAGACCA ACTTGATTAT	660
	GATGTTGGAG AAGAGCATCA GTCTCCAGGT GGCATTAGTA GTGAAGAGGA AGAGGAGGAG	720
30	GAAGAAGAGA TGTTAATCAG TGAAGAGGAG ATACCATTCA AAGATGATCC AAGAGATGAG	780
	ACCTACAAAC CCCACTTAGA AAGGGAAACC CCAAGCCAC GGAGAAAATC AGGGAAGGTA	840
	AAAGAAGAGA AGGAGAAGAA GGAAATTAAA GTGGAAGTAG AGGTGGAGGT GAAAGAAGAG	900
35	GAGAATGAAA TTAGAGAGGA TGAGGAACCT CCAAGGAAGA GAGGAAGAAG ACGAAAAGAT	960
	GACAAAAGTC CACGTTTACC CAAAAGGAGA AAAAGCCCTC CAATCCAGTA TGTCCGTTGT	1020
40	GAGATGGAAG GATGTGGAAC TGTCTTGCC CATCCTCGCT ATTTCAGCA CCACATTAAA	1080
	TACCAGCATT TGCTGAAGAA GAAATATGTA TGTCCCCATC CCTCCTGTGG ACGACTCTTC	1140
	AGGCTTCAGA AGCAACTTCT GCGACATGCC AAACATCATA CAGATCAAAG GGATTATATC	1200
45	TGTGAATATT GTGCTCGGC CTTCAAGAGT TCCCACAATC TGGCAGTGCA CCGGATGATT	1260
	CACACTGGCG AGAAGCATT AATGTGAGA TCTGTGGATT TACTTGTCGA CAAAAGGCAT	1320
50	CTCTTAATTG GCACATGAAG AAACATGATG CAGACTCCTT CTACCAGTTT TCTTGCAATA	1380
	TCTGTGGCAA AAAATTGAG AAGAAGGACA GCGTAGTGGC ACACAAGSCA AAAAGCCACC	1440
	CTGAGGTGCT GATTGCAGAA GCTCTGGCTG CCAATGCAGG CGCCCTCATC ACCAGCACAG	1500
55	ATATCTTGGG CACTAACCCA GAGTCCCTGA CGCAGCCTTC AGATGGTCAG GGTCTTCCTC	1560
	TTCTTCCTGA GCCCTTGGGA AACTCAACCT CTGGAGAGTG CTTACTGTTA GAAGCTGAAG	1620
60	GGATGTCAAA GTCATACTGC AGTGGGACGG AACGGGTGAG CCTGATGGCT GATGGGAAGA	1680

	TCTTTGTGGG AAGCGGCAGC AGTGGAGGCA CTGAAGGGCT GGTATGAAC TCAGATATAC	1740
	TCCGTGCTAC CACAGAGGTT CTGATTGAAG ATTCAGACTC TGCCGGACCT TAGTGGACAG	1800
5	GAAGACTTGG GGCATGGGAC AGCTCAGACT TTGTATTTAA AAGTTAAAAA GGACAAAAAA	1860
	AAAATCTAAA GCATTTAAAA TCTAGTGAAA TAACTGAAGG GCCTGCTCTT TCCATTGTGG	1920
10	ATCACAGCAC ACACATACAT ACACCTCCA CCTCCCCATC CCCTGTCTC CCTCTGTTC	1980
	TCCCCTTATA AAATTGATGT TGTCCTTACC AGAAAGGTAG ACAAAAAAGA AGCAGCAGCA	2040
	GCTCTTAAAG TGAGGGTTAT TCTCATACTC GGTCCAGCC ATCAGCAGAC TTCCTGCTCA	2100
15	TCGGCAGATC CCCCTTTCCA ACCTGTAACCT CTGATGTGCT CTGGATCAGC TTTTAACTTT	2160
	TAATCATATA TTAGTGTCTT CTAAATCCCT TCTCTCTCTC TACTGCTGCC CTATGGTCT	2220
20	GGCTCCTACC CCCTGCGGCA CACTTATCTT CAAATACCAT AGAATCTTAA TCTCTGAAAT	2280
	CATAGCTCTC CAGTGGCTTT TAAAGAAAGC TGGTCTCAG CACTAACAAA ATCACTACAA	2340
	TAGCCTAGTG CTTTMTTGA AGCCTMTTGA GGAAGAATG TTAGGTTTCAT GGTAAC TAGT	2400
25	ATGCTCTTTG AGATTTTTAC AGTGTGAAA CTTAAGAATT TTGAGAGGGT GAGGAGGGTT	2460
	GTCAGAATC TAAATTACAG ATAGATGATT GTTCTTTGTG AATTTGTTTC TTTTCTTTT	2520
30	TTTTTGTCCT TACCATTTC TTACATTTCC CTTGGGGCCC ATCTCTGGCT CCTTGCTTTT	2580
	TGTTCTTTC TTTGCTTTAT CAGTTCATTC CAGCTCCCTG TTAGTGAAGG AACTGCTGT	2640
	TAGTGAAGGA ACAAAGTCTA TGAGTCTTAA AATTTTAAGT CAAAGAAAAC TGCTCTGTTT	2700
35	CCCCTTTAGT AACACTTCTG AAGAGGAAAA ACTTCAATAG CCAAAGTTAA TAATCCTATA	2760
	TAATAATTGC TTTGGCTTTC ACCTAAAATT CTGGGCATCA CAATTTCTTT GGGATAGAGG	2820
40	TTGTGTGGG GAATAGATTG CTTATTGCTG TTCACTGGAG AGAAAAGGTA GTGTTTTTGT	2880
	ACAAGGTCAT ACCGCCAGAA GCCCCAAATC CTATTTTGGC TCATCTTCAG GTAAAGAGTA	2940
	ATTCCTATCC TGTGTGCTC AGAAGCTAGA ATCGAAGGCT TACCCTATTC ATTGTTTATT	3000
45	GTCAGAAATG CATGATGGCT CTTGAAAGA ATGACGTTTT GCTGGAAAAA AAAAAAARA	3060
	CMGTTTGTGT TTCACAAACA TGGCTTATCA ATTTTTCATC AGAATTCCTT TTTCCCAAAA	3120
50	AGAGGAGTAA CAAAATGTCA TTTCTGAAAG AGGCTTACTT TATACCAACT AGTGTGAGCA	3180
	TTTGGGATGC CAGGGAACAG AGAGTGAGAC ACCTACAATC ACCAGTCTCA AATGCGCTAT	3240
	TGTTTCTTTT CAGAGTGTG CAGATTTGCC ATTTCTCCAT AATATGGGGA TAGAAAATGG	3300
55	AATAAAGATA GAAGGGATGT AGAATATGCT TTCCTGCCAA CATGGTTTGG AGTCGACTTT	3360
	GGTATATTGA CTAGATTGA AAATACAAGA TTGATTAGAT GAATCTACAA AAAAGTTGTC	3420
60	CTCTCTCAG GTCCCTTTTA CACTTTTGA CTAAGTAGCA TCTATATTCC AACTTAGCT	3480

TTTTGTGCAC ACTTATCCTT TGTCTCCGTA AATTTTCATTT GCAGTGGTTA GTCATCAGAT 3540
 ATTTTAGCCA CCTACACAAA AGCAAACGTC ATTTTAAAA ATCTTTCTGA GATGGGAGAA 3600
 5 AATGTATTCT CCTTCTCTAT ACCGCTCTCC CAACAAAAA ACAACTAGTT AGTTCTACTA 3660
 ATTAGAAACT TGCTGTACTT TTTCTTTTCT TTTAGGGGTC AAGGACCCTC TTTATAGCTA 3720
 10 CCATTTGCCT ACAATAAATT ATTGCAGCAG TTTGCAATAC TAAAATATTT TTTATAGACT 3780
 TTATATTTTT CCTTTTGATA AAGGGATGCT GCATAGTAGA GTTGGTGTA TAAACTATC 3840
 TCAGCCGTTT CCTGCTTTC CCTTCTGCTC CATATGCCTC ATTGTCCTTC CAGGGAGCTC 3900
 15 TTTTAATCTT AAAGTTCTAC ATTTTCATGCT CTTAGTCAA TTCTGTTACC TTTTAATAA 3960
 CTCTCCAC TGCAATTTT CATCTGAAT TGGTGGTTCT AAATTCGAA ACTGTAGTTG 4020
 AGATACAGCT ATTTAATATT TCTGGGAGAT GTGCATCCCT CTTCTTTGTG GTTGCCCAAG 4080
 20 GTTGTMTTG GTAACGAGA CTCCTTGATA TGCTTCAGAG AATTAGGCA AACACTGGCC 4140
 ATGGCCGTGG GAGTACTGG AGTAAATAA AAATATCGAG GTATAGACTA GCATCCACAT 4200
 25 AGAGCACTTG AACCTCCTTT GTACCTGTTT GGGGAAAAAG TATAATGAGT GTACTACCA 4260
 TCTAACTAAG ATTATTATAG TCTGGTGTG TGAAATACCA TTTTTTCTC CTTTGTGTT 4320
 TTTCCCACTT TCCAATGTAC TCAAGAAAT TGAACAAATG TAATGGATCA ATTTAAATA 4380
 30 TTTTATTTCT TAAAGCCTT TTTGCTGTG TGTAATGTG AGGACCCTTC TCCTTTTCATG 4440
 GGAGAGACAG GTAGTTACCT GAATATAGGT TGAAAAGGTT ATGTAAAAG AAATTATAAT 4500
 35 AAAAGGATA CTTTGCTTTT CAAATCTTTG TTTTCTCTTA TTCTAGGTAA GGCATATTAA 4560
 AAATAAATAT GTAAAGAAGA AAAATAAAG TTGTCCTCAT GG 4602

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(2) INFORMATION FOR SEQ ID NO: 75:

45 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1255 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 75:

CGCGCCCCGG GCCGGCGGGT TTCTCTAACA AATAACAGA ACCCGCACTG CCCAGGCGAG 60
 CGTTGCCACT TTCAAAGTGG TCCCCTGGGG GAGCTCAGCC TCATCCTGAT GATGCTGCCA 120
 55 AGGCGCACTT TTTATTTTAA TTTTATTTT ATTTTTTTT TAGCATCCTT TTGGGGCTTC 180
 ACTCTCAGAG CCAGTTTTTA AGGGACACCA GAGCCGAGC CTGCTCTGAT TCTATGGCTT 240
 60 GGTGTGTTACT ATAAGAGTAA TTGCCTAACT TGATTTTCA TCTCTTTAAC CAACTTGTG 300

	GCCAAAAGAT ATTTGACCGT TTCCAAAATT CAGATTCTGC CTCTGCGGAT AAATATTTGC	360
5	CACGAATGAG TAACTCCTGT CACCACTCTG AAGGTCCAGA CAGAAGGTTT TGACACATTC	420
	TTAGCACTGA ACTCCTCTGT GATCTAGGAT GATCTGTTC CCCTCTGGAT GAACATCCTC	480
	TGATGATCAA GGCTCCCAGC AGGCTACTTT GAAGGGAACA ATCAGATGCA AAAGCTCTTG	540
10	GGTGTATTATT TAAAATACTA GTGTCACTTT CTGAGTACCC GCCGCTTCAC AGGCTGAGTC	600
	CAGGCCTGTG TGCTTTGTAG AGCCAGCTGC TTGCTCACAG CCACATTTCC ATTTGCATCA	660
15	TTACTGCCTT CACCTGCATA GTCACCTCTT TGATGCTGGG GAACCAAAAT GGTGATGATA	720
	TATAGACTTT ATGTATAGCC ACAGTTCATC CCCAACCCCTA GTCTTCGAAA TGTTAATATT	780
	TGATAAATCT AGAAAAATGCA TTCATACAAT TACAGAAATC AAATATTGCA AAAGGATGTG	840
20	TGTCCTTCTC CCGAGCTCC CCTGTTCCCC TTCATTGAAA ACCACCACGG TGCCATCTCT	900
	TGTGTATGCA GGGCTATGCA CCTGCAGGCA CGTGTGTATG CACTCCCCGC TTGTGTTTAC	960
25	ACAAGCTGTG GGGTGTACG CATGCCTGCT TTTTTCACCT AATAATACAG CTTGGAGAGA	1020
	TTTTTGATC ACATTATAAA TCCCCTCGC TCTTTTGTAT GGCCACATAA TAACTACTGC	1080
	ATAATATGGA TACGCCCTTAT TTGATTTAAC TAGTTCCTTA ATGATGGACT TTTAAGTTGT	1140
30	TTCCCTTTTTT TTCTTTTTT GCTACTGCAA ACGATGCTAT AATAAATGTC CTTATCAAAA	1200
	AAAAAAAAA AAAAAAAAAA AAAAAANCCC NGGGGGGGG CCCC GGGAAC NCAAT	1255

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(2) INFORMATION FOR SEQ ID NO: 76:

- 40 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 475 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 76:

	GGCAGGAGAG AAATGTTTGA TTCTCTTCC TATTTTAAGG GATCTTCTCT CTTGTTGATG	60
50	TTGAAAACCT ACCTTAGTGA AGATGTGTTT CAACATGCTG TTGTCCTTTA CCTGCATAAT	120
	CACAGCTATG CATCTATTCA AAGTGATGAT CTGTGGGATA GTTTTAATGA GGTCACAAAAC	180
	CAACACTAG ATGTAAAGAG AATGATGAAA ACCTGGACCC TGCAGAAAGG ATTTCTTTTA	240
55	GTGACTGTTT AAAAGAAAGG AAAGGAACCT TTTATACAAC AAGAGAGATT CTTTTTAAAT	300
	ATGAAGCCTG AAATTCAGCC TTCAGATACA AGGTACATGC CCTCTTCTCT TTCATGCCAT	360
60	CTCTTTTGCA CTCTCAGGTG GAAATATTTT GAAGTGTTTT ATAATCATAA GTTCTGTGTA	420

AACCTAACAA GATTATCCCT TCCTAAGAAT ACTTAACCTT CCTACCAAAT TAAAA

475

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(2) INFORMATION FOR SEQ ID NO: 77:

(i) SEQUENCE CHARACTERISTICS:

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- (A) LENGTH: 465 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 77:

15

TTCTCTCTGC TCTTCGACTG CACCGCACTC GCGCGTGACC CTGACTCCCC CTAGTCAGCT 60
CAGCGGTGCT GCCATGGCGT GCGGGCGGCG CGAACCRGCG TCGGGGCTCG CGGCGTGTG 120
GCTCTGGCGT TGCTCGCCCT GGCCCTGTGC GTGCCCGGGG CCGGGGGCCG GGCTCTCGAG 180
TGGTCTCCG CCGTGGTAA CATCGAGTAC GTGGACCCGC AGACCAACCT GACGGTGTGG 240
AGCGTCTCGG AGAGTGGCCG CTTGGGCGAC AGCTCGCCCA AGGAGGGCGC GCATGGCCTG 300
GTGGGCGTCC CGTGGGCGCC CGGCGGAGAM CTCGARGGCT KCGCGCCCGA CACGCGCTTC 360
TTCGTGCCCC AGCCCCGGCG CCGAGGGGCC GCGCCCTGGG TCGCCCTGGT GGTCTGTTGG 420
GCTGCACCTT TCAAGGACAA AGTGCTGGTG GCGGCGCNGA ANGAA 465

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(2) INFORMATION FOR SEQ ID NO: 78:

(i) SEQUENCE CHARACTERISTICS:

40

- (A) LENGTH: 1907 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 78:

45

ACATGCAGCC CAACTACAGA TTCTTATGGA ATTCTCAAG GTTGCAAGAA GAAATAAGAG 60
AGAGCAACTG GAACAGATCC AGAAGGAGCT AAGTGTTTGT GAAGAGGATA TTAAGAGAGT 120
GGAAGAAATG AGTGGCTTAT ACTCTCCTGT CAGTGAGGAT AGCACAGTGC CTCAATTGTA 180
AGCTCCTTCT CCATCACACA GTAGTATTAT TGATTCCACA GAATACAGCC AACCTCCAGG 240
TTTCAGTGGC AGTCTTCAGA CAAAGAAACA GCCTTGGTAT AATAGCACGT TAGCATCAAG 300
ACGAAAACGA CTTACTGCTC ATTTTGAAGA CTGAGAGCAG TGTTACTTTT CTACAAGGAT 360
GTCTCGTATC TCAGATGACA GTCGAAGTGC AAGCCAGTTG GATGAATTTT AGGAATGCTT 420
GTCCAAGTTT ACTCGATATA ATTCAGTACG ACCTTTAGCC ACATTGTCAT ATGCTAGTGA 480

60

TCTCTATAAT GGTTCAGTA TAGTCTCTAG TATTGAATTT GACCGGGATT GTGACTATTT 540
 TGGGATGCT GGAGTTACAA AGAAGATTAA AGTCTATGAA TATGACACTG TCATCCAGGA 600
 5 TGCAGTGGAT ATTCATTACC CTGAGAATGA AATGACCTGC AATTCGAAAA TCAGCTGTAT 660
 CAGTTGGAGT AGTTACCATA AGAACCTGTT AGCTAGCAGT GATTATGAAG GCACTGTTAT 720
 10 TTTATGGGAT GGATTCACAG GACAGAGGTC AAAGGTCTAT CAGGAGCATG AGAAGAGGTG 780
 TTGGAGTGTT GACTTTAATT TGATGGATCC TAAACTCTTG GCTTCAGGTT CTGATGATGC 840
 AAAAGTGAAG CTGTGGTCTA CCAATCTAGA CAACTCAGTG GCAAGCATG AGGCAAAGGC 900
 15 TAATGTGTGC TGTGTTAAAT TCAGCCCCTC TTCCAGATAC CATTTGGCTT TCGGCTGTGC 960
 AGATCACTGT GTCCACTACT ATGATCTTCG TAACACTAAA CAGCCAATCA TGGTATTCAA 1020
 AGGACACCGT AAAGCAGTCT CTTATGCAAA GTTGTGAGT GGTGAGGAAA TTGTCTCTGC 1080
 20 CTCAACAGAC AGTCAGCTAA AACTGTGGAA TGTAGGGAAA CCATACTGCC TACGTTCTTT 1140
 CAAGGGTCAT ATCAATGAAA AAAACTTTGT AGGCCTGGCT TCCAATGGAG ATTATATAGC 1200
 25 TTGTGGAAGT GAAAATAACT CTCTCTACCT GTACTATAAA GGACTTTCTA AGACTTTGCT 1260
 AACTTTTAAG TTTGATACAG TCAAAAGTGT TCTCGACAAA GACCGAAAAG AAGATGATAC 1320
 AAATGAATTT GTTAGTGCTG TGTGCTGGAG GGCATACTA GATGGGGAGT CCAATGTGCT 1380
 30 GATTGCTGCT AACAGTCAGG GTACAATTAA GGTGCTAGAA TTGGTATGAA GGGTTAACTC 1440
 AAGTCAAATT GTACTTGATC CTGCTGAAAT ACATCTGCAG CTGACAATGA GAGAAGAAAC 1500
 35 AGAAAATGTC ATGTGATGTC TCTCCCCAAA GTCATCATGG GTTTTGGATT TGTTTTGAAT 1560
 ATTTTTTTCT TTTTTTCTTT TCCCTCCTTT ATGACCTTTG GGACATTGGG AATACCCAGC 1620
 CAACTCTCCA CCATCAATGT AACTCCATGG ACATTTGCTG TCTTGGTGGT GTTATCTAAT 1680
 40 TTTTGTGATA GGGAAACAAA TTCTTTTGAA TAAAAATAA TAACAAAACA ATAAAAGTTT 1740
 ATTGAGCCAC AGTTGAGCTT GGAAAGTTTT TGTCAAATGC NGCAAGAGAT AACTCTTTTT 1800
 45 ANGAAGTAGC ATATGTGAAC TATAATGTAA CAGTGAATAA TTTGTAAAGT TCGTATTTC 1860
 CAACCTCTTT GGAATTACA CATATCAATA TAAACAAAAT ATAAAGT 1907

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(2) INFORMATION FOR SEQ ID NO: 79:

55 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1168 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

60 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 79:

5 GCTGGGGTGT CCCCKCSGCC ACCATCGTCA TCGCTTACTT GATGAAGCAC ACTCGGATGA 60
 CCCATGACTG ATGCTTATAA ATTTGTCAAA GGCAACGAC CAATTATCTC CCCAAACCTT 120
 AACTTCATGG GGCAGTTGCT AGAGTTCGAG GAAGACCTAA ACAACGGTGT GACACCGAGA 180
 ATCCTTACAC CAAAGCTGAT GGGCGTGGAG ACGGTGTGTG GACAATGGTC TGGATGGAAA 240
 10 GGATGCTGC TCTCCATTAG GAGACAATGA GGAAGGAGGA TGGATTCTGG TTTTCTTCT 300
 TTCTTTTCTT TTTTGTAGTT GGGAGTAAGT TTGTGAATGG AAACAAACTT GTTTAAACAC 360
 TTTATTTTTA ACAAGTGTA GAAGACTATA ACTTTTGATG CCATTGAGAT TCACCTCCCA 420
 15 CAAACTGACA AATTAAGGAG GTTAAAGAAG TAATTTTCTT AAGCCAACAA TAAAAATATA 480
 ATACAACCTG TTTCTCCCCC TTTTCTTTT AAGCTATTTG TAGAGTTTAT GACTAAATAG 540
 20 TCTGTGCAGG TTCATAGACC GAAGATACTA CACACTTTAA ACCAATTAAG AAGAACCAAA 600
 AGTAAATAGA AAAGACATTG AATCACCAG GCCTGGGATC AACCTGGGCT GTCCACACAG 660
 AAAACAAAAA CCCAACCAAA CCAAGCCCTG TTGTGCTCAC TGGTGCAAAG AGAAGATCAG 720
 25 GGCAGCTTAA GTGGTCTAAG RATCCTTCAG GCATTCTTTA AGGAGAAAAA GGATACCTTT 780
 GATTTTGTGT GTTTCATGCT CTGGATTCTT TTTTCTTCTC CTCTCTGGG TTTAAGAGAT 840
 30 TTTTCTTGAA ATAGTGAGGA ACTGACCATT ATATGCCTTC ACTGGCTTCT TGTGCAATAA 900
 TATGATGTTT TAAGTGTGCA AACAAGTTAG AGCTGGCAGC TGAATGATAG ACAATAGTG 960
 CAAATTTGCC AGCTTGGAGA TAGAAAGGAA TTCAACAATA TATCAAATAC TTTCTTCCC 1020
 35 ACCTTTTCCC TTTTCTTCTG TTTTCTTCTG TTTGATTCTG GTTACAGTGC CATAAACCTT 1080
 GTTACATATG TATATCAGAA TGTAAAGAAA AAAAATTTAT TTAATAATAT TTTTCGCAAA 1140
 40 AAAAAANNA AAAAATCGA GGGGGGCC 1168

45 (2) INFORMATION FOR SEQ ID NO: 80:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1285 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 80:

55 AGAAAAATCAC ATCCTAACAA AGAAGTCTGT CTAAGACAGT ACATCTCCTG TTGAACCTGC 60
 ATCTTTCCAC AGGACTTTCT GTTTTAGGG ATGAGACTAT TCTCTGCTTC ATCAAGGAAA 120
 60 GAGAAATGTT CAGGGTTGTA GGGATGGCAC ACTTATTAGT TCTGCCTGTC TGAAAGGTTT 180

	CTGCAGGACA GTTTGGTCAG AGCTGCAATT CTTAGTCCAT GGTCTAATGC TTGAGTATCT	240
	CTTCTTTCCC TTCTCTGTCT CAGGAATCAG CTGAGAATTC ATTGATTGT CATGCCCTCA	300
5	GCCCCTACT GTGATTTGTT GGTGCACTT TCATTTGCTT TAGTTCTAGA ATCACCTGTT	360
	GACTCCTCAG ACTTCACCTA ACTTTGAAA CTCTCTTTTG GAGGCTTCTC ATTTCCCCCT	420
10	AATTCTGTGC TGCCTGAGCC CTAGAATTTT CCCACCAACG AATTATTCCA GGTAGATCCT	480
	AAGTTGCTGG ATCTAGTTGA TATTTAAACA ATATCTAGTT GATATTTCTC ATTCAGTTGG	540
	ATCCAGAAAC CAGTATCTCT NAAAAACAAC CTCTCATACC TTGTGGACCT AATTTTGTGT	600
15	GCGTGTGTGT GTGCGCGCAT ATGTATATAG ACAGGCACAT CTTTMTTACT TTGTAAAAAG	660
	CTTATGCCCTC TTTGGTATCT ATATCTGTGA AAGTTTAAAT GATCTGCCAT AATGTCTTGG	720
20	GGACCTTTGT CTCTGTGTGA AATGGTACTA GAGAAAACAC CTATATTATG AGTCAATCTA	780
	GTTGGTTTTA TTCGACATGA AGGAAATTTC CAGATAACAA CACTAACAAA CTCTCCCTTG	840
	ACTAGGGGGA CAAAGAAAAG CAAACTGAC CATAAAAAAC AATTACCTGG TGAGAAGTTG	900
25	CATAACAGA ATTAGGTAGT ATATTGAAGA CAGCATCATT AAACAGTTAT GTGTCTCTCC	960
	TTGCAAAAAA CATGTACTGA CTTCCTGTTG AGTAATGCCA AGTTGTTTTT TTTATTATAA	1020
30	AACTTGCCCT TCATTACATG TTTCAAAGTG GTGTGGTGGG CCAAAATATT GAAATGATGG	1080
	AACTGACTGA TAAAGCTGTA CAAATAAGCA GTGTGCCTAA CAAGCAACAC AGTAATGTTG	1140
	ACATGCTTAA TTCACAAATG CTAATTTTCAT TATAAATTGT TTTGCTAAAA TACACTTTGA	1200
35	AACTATTTT CTGTATTCCA AGAGCTGAGA TCTTAGATTT TATGTAGTAT TAAGTGAAAA	1260
	AATACGAAAA TAATAACAT TGAAG	1285

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(2) INFORMATION FOR SEQ ID NO: 81:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1290 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 81:

	TCTCCAGCCC CAATTTCTAC GCGCACCGGA AGACGGAGGT CCTCTTTCCT TGCCTAACGC	60
	AGCCATGGCT CGTGGTCCCA AGAAGCATCT GAAGCGGGTG GCAGCTCCAA AGCATTGGAT	120
55	GCTGGATAAA TTGACCGGTG TGTTTGCTCC TCGTCCATCC ACCGGTCCCC ACAAGTTGAG	180
	AGAGTGTCTC CCCCTCATCA TTTTCTGAG GAACAGACTT AAGTATGCCC TGACAGGAGA	240
60	TGAAGTAAAG AAGATTTGCA TGCAGCGGTT CATTAATATC GATGGCAAGG TCCGAAGTGA	300

	TATAACCTAC CCTGCTGGAT TCATGGATGT CATCAGCATT GACAAGACGG GAGAGAATTT	360
5	CCGTCTGATC TATGACACCA AGGGTCGCTT TGCTGTACAT CGTATTACAC CTGAGGAGGC	420
	CAAGTACAAG TTGTGCAAAG TGAGAAAGAT CTTTGTGGGC ACAAAGGAA TCCCTCATCT	480
	GGTGACTCAT GATGCCCGCA CCATCCGCTA CCCCAGTCCC CTCATCAAGG TGAATGATAC	540
10	CATTTCAGATT GATTTAGAGA CTGGCAAGAT TACTGATTTT ATCAAGTTCC ATTCACCCAG	600
	CCAGGTGGTC TCGTCACCTC AGAGGCTCCG CAGACTCCTG CCCAGGCCAG GACTGAGGCA	660
15	AGCCTCAAGG CACTTCTAGG ACCTGCCTCT TCTACCAAG ATGAACTCAC TGGTTTCTTG	720
	GCAGCTACTG CTTTCTCTCT GTGCCACCCA CTTTGGGGAG CCATTAGAAA AGGTGGCCTC	780
	TGTGGGAAT TCTAGACCCA CAGGCCAGCA GCTAGAATCC CTGGGCCTCC TGGCCCCSGG	840
20	GGAGCAGAGC CTGCCGTGCA CCGAGAGGAA GCCAGCTGCT ACTGCCAGGC TGAGCCGTCG	900
	GGGGACCTCG CTGTCCCCGC CCCCCGAGAG CTCCGGGAGC CCCCAGCAGC CGGGCCTGTC	960
25	CGCCCCCAC AGCCGCCAGA TCCCCGCACC CCAGGGCGCG GTGCTGGTGC AGCGGGAGAA	1020
	GGACCTGCCG AACTACAAC TGAACCTCTT CGGCCTGCGC TTCGGCAAGC GGGAGGCGGC	1080
	ACCAGGAAC CACGGCAGAA GCGCTGGCG GGGCTGAGGG CGCAGGTGCG GGGCAGTGAA	1140
30	CTTCAGACCC CAAAGGAGTC AGAGCATGCG GGGCGGGGG GGGGGCGGG GACGTAGGGC	1200
	TAAGGGAGGG GCGCTGGAG CTTCCAACCC GAGGCAATAA AAGAAATGTT GCGTAACTCA	1260
35	AAAAAAAAA AAAAAAANC TCGGGGGGG	1290

(2) INFORMATION FOR SEQ ID NO: 82:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 684 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 82:

50	TTTATGTAT TCTGTAAC TAAGAACTTCT ATTTWATTCT TTTTGGACT TGCTAAGTTG	60
	TCTTTWATGG TTTTWAGTTC CATGCTGAAG TTTTCAGTAT TGAATTATCC CCTTGAACAT	120
	GAGTGTGTTT ATAGACTCTR ATGATTCAAA AATCTTACAT CTTTGGTAG TCTCTTTCAT	180
55	TGTGYCACTG TTTCTGTGA TTCTWACTCA TGGTATTTTA ATTCTTCGTT WTTTTTTTTC	240
	TGTTWAGAWA CATTTCTTGA AAAATAATTT GGAGGAATAT TTGATTCTTA TGAACAAGGC	300
60	ATTACTCACC AGAGAAGATT TTTTGTGTTT ACCARGTGCC TARGAATGCT AACAGTCTGG	360

GAMCACATAG AMCACCAGGT GATGAGACAA TCCTGGGART CCTGTTTTAC TTTGGSCCAT 420
 CTTTCTCCC AACCTGTGG GAATATCAT YCATATCCTA RCTGCAGGCT ARAAGGTGGT 480
 5 TTATCAGAGC CCAACTTCGA GGGCTCTGGG CTTTAGCTAC TGTCACCCCA TCATAACTGA 540
 GCTTCATGGA TTGATTCTCT TTTTATCTTT CAGATTTTCT TTTAAAAATC TTTGTTTTTT 600
 TTTTCTTCC GAAAGATTCC CCCAACATTA CCATTCCCCA CCTTCCGTTG AATTTTITTG 660
 10 GCTCTCATTT TGAATTTTTC AAGA 684

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(2) INFORMATION FOR SEQ ID NO: 83:

(i) SEQUENCE CHARACTERISTICS:

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- (A) LENGTH: 2024 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 83:

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CTGCAGGAAT TCGGCACAGC TGCCTGGAG GCTTCATCTT TGCCGCGCT GCCGTGCGCT 60
 TCCTGGGATT GGAGTCTGA GCTTCTTCG TTCGTCGYC GCGGGTTCG CGCCCTTCTC 120
 30 GCGCTCGGG GCTGCGAGGC TGGGAAGGG GTTGGAGGG GCTGTTGATC GCCGCGTTTA 180
 AGTTGCGCTC GGGGCGCCA TGTCGGCCGG CGAGGTCGAG CGCCTAGTGT CGGAGCTGAG 240
 CGGCGGGACC GGAGGGGATG AGGAGGAAGA GTGGCTCTAT GGCGATGAAA ATGAAGTTGA 300
 35 AAGGCCAGAA GAAGAAAATG CCAGTGCTAA TCCTCCATCT GGAATTGAAG ATGAAACTGC 360
 TGAAAATGGT GTACCAAAAC CGAAAGTGAC TGAGACCGAA GATGATAGTG ATAGTGACAG 420
 40 CGATGATGAT GAAGATGATG TTCATGTCAC TATAGGAGAC ATTAAAACGG GAGCACCACA 480
 GTATGGGAGT TATGGTACAG CACCTGTAAA TCTTAACATC AAGACAGGGG GAAGAGTTTA 540
 TGGAACTACA GGGACAAAAG TCAAAGGAGT AGACCTTGAT GCACCTGGAA GCATTAATGG 600
 45 AGTTCCACTC TTAGAGGTAG ATTGGGATTC TTTTGAAGAT AAACCATGGC GTAAACCTGG 660
 TGCTGATCTT TCTGATTATT TTAATTATGG GTTTAATGAA GATACCTGGA AAGCTTACTG 720
 50 TGAAAAACAA AAGAGGATAC GAATGGGACT TGAAGTTATA CCAGTAACCT CTAATACAAA 780
 TAAATACG GTACAGCAGG GAAGAACTGG AAATCAGAG AAAGAACTG CCCTTCCATC 840
 TACAAAAGCT GAGTTTACTT CTCTCCTTC TTTGTTCAAG ACTGGGCTTC CACCGAGCAG 900
 55 GAGATTACCT GGGCAATTG ATGTTATCGG TCAGACTATA ACTATCAGCC GAGTAGAAGG 960
 CAGGCGACGG GCAATGAGA ACAGCAACAT ACAGGTCCTT TCTGAAAGAT CTGCTACTGA 1020
 60 AGTAGACAAC AATTTTAGCA AACCACCTCC GTTTTCCCT CCAGGAGCTC CTCCCACTCA 1080

	CCTTCCACCT CCTCCATTTC TTCCACCTCC TCCGACTGTC AGCACTGCTC CACCTCTGAT	1140
5	TCCACCACCG GGTTCCTCTC CTCCACCAGG CGCTCCACCT CCATCTCTTA TACCAACAAT	1200
	AGAAAGTGA CATTCTCTG GTTATGATAG TCGTTCTGCA CGTGCAATTC CATATGGCAA	1260
	TGTTGCCTTT CCCCATCTTC CTGGTTCTGC TCCTTCGTGG CCTAGTCTTG TGGACACCAG	1320
10	CAAGCAGTGG GACTATTATG CCAGAAGAGA GAAAGACCGA GATAGAGAGA GAGACAGAGA	1380
	CAGAGAGCGA GACCGTGATC GGGACAGAGA AAGAGAACGC ACCAGAGAGA GAGAGAGGGA	1440
15	GCGTGATCAC AGTCCTACAC CAAGTGTTTT CAACAGCGAT GAAGAACGAT ACAGATACAG	1500
	GGAATATGCA GAAAGAGGTT ATGAGCGTCA CAGAGCAAGT CGAGAAAAAG AAGAACGACA	1560
	TAGAGAAAGA CGACACAGGG AGAAAGAGGA AACCAGACAT AAGTCTTCTC GAAGTAATAG	1620
20	TAGACGTCGC CATGAAAGTG AAGAAGGAGA TAGTCACAGG AGACACAAAC AAAAAAATC	1680
	TAAAAGAAGC AAAGAAGGAA AAGAAGCGG CAGTGAGCCT GCCCCTGAAC AGGAGAGCAC	1740
25	CGAAGCTACA CCTGCAGAAT AGGCATGGTT TTGGCCTTTT GTGTATATTA GTACCAGAAG	1800
	TAGATACTAT AAATCTTGTT ATTTTCTGG ATAATGTTTA AGAAATTAC CTTAAATCTT	1860
	GTTCTGTTTG TTAGTATGAA AAGTTAACTT TTTTCCAAA ATAAAAGAGT GAATTTTCA	1920
30	TGTTAAGTTA AAAATCTTTG TCTTGTAATA TTTCAAAAAT AAAAAGACAG CAATGACTTT	1980
	ATATCCAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAGGGC GGCC	2024

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(2) INFORMATION FOR SEQ ID NO: 84:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 931 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 84:

	CGCGCCMATA GCCGGACGGG GATCTGAGCT GGCAGGATGA ATGTGGGGGT GGCACACAGC	60
50	GAAGTAAACC CCAACACCCG AGTGATGAAT AGCCGAGGCA TCTGGCTGGC CTACATCATC	120
	TGTTAGGAT TGCTGCATAT GGTCTACTC AGCATCCCCT TCTTCAGCAT TCCTGTTGTC	180
	TGGACCTGA CCAACGTCAT CCATAACCTG GCTACGTATG TCTTCCTTCA TACGGTGAAA	240
55	GGGACACCTT TTGAGACTCC TGACCAAGGA AAGGCTCGGC TACTGACACA CTGGGAGCAA	300
	ATGGACTATG GGCTCCAGTT TACCTCTTCC CGCAAGTTCC TCAGCATCTC TCCTATTGTG	360
60	CTCTATCTCC TGGCCAGCTT CTATACCAAG TATGATGCTG CGCACTTCCT CATCAACACA	420

GCCTCATGTC TAAGTGACT GCTGCCGAAG TTGCCCCAGT TCCATGGGGT TCGTGCTTTT 480
 GGCATCAACA AATACTGAGG GATGGGTTTT GGGACAGCTC CATGGGCATG GGAAGGCAC 540
 5 TGAAACAGAG GACTATAAAA CATCCTTCTC TTATTCTCCA TACTGTCTTC TACACCTTTA 600
 AAGCCTGAGA ACTATACAAC CTTTCCCAGA CTCCCAAGAA GAGAAGAGAT TGGCAAATGG 660
 GGCTCCTGGG CCCAGTCTCG CTAGTGGCAA GTTCTTTTGA ATCAGGAAGG CAGGTGAGGT 720
 10 AAGGGCCAAA TCACTCTCCT CCATAGCAGG AAGCCATTG GGCAGCTCCT TTGGTGATTA 780
 CATCTTTCCA TATCTTTTAC ACTTACCACC TTCCAGCTCT GTTTTGCTGT GTATTTTCT 840
 15 TACAATAATT TTTTTCAGCT ATAGCTGCAG TTPAATCAGG ATGGGTAGAG AGCTGTCCTC 900
 ATAAGGCTGG GGGTGGGAAG ATGAATACT G 931

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(2) INFORMATION FOR SEQ ID NO: 85:

25 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 825 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 85:

CGGGGCCGGC GGGGTCTTCA GGTACCGGG CTGGTTACAG CAGCTCTACC CCTCAGACG 60
 CAAACATGGC AGCGCAGAAG GACCAGCAGA AAGATGCCGA GCGGAAGGG CTGAGCGGCA 120
 35 CGACCTGCT GCCGAAGCTG ATTCCCTCCG GTGCAGGCCG GGAGTGGCTG GAGCGCGCC 180
 GCGCGACCAT CCGGCCCTGG AGCACCTTCG TGGACCAGCA GCGCTTCTCA CGGCCCCGCA 240
 40 ACCTGGGAGA GCTGTGCCAG CGCCTCGTAC GCAACGTGGA GTACTACCAG AGCAACTATG 300
 TGTTCGTGTT CCTGGGCTC ATCCTGTACT GTGTGGTGAC GTCCCTATG TTGCTGGTGG 360
 CTCTGGCTGT CTTTTTCGGC GCCTGTTACA TTCTCTATCT GCGCACCTTG GAGTCCAAGC 420
 45 TTGTGCTCTT TGGCCGAGAG GTGAGCCCAG CGCATCAGTA TGCTCTGGCT GGAGGCATCT 480
 CCTTCCCCTT CTCTGCGTG GCTGGTGGG GCTCGGCCGT CTCTGGGTG CTGGGAGCCA 540
 50 CCTGGTGGT CATCGGCTCC CACGCTGCCT TCCACCAGAT TGAGGCTGTG GACGGGGAGG 600
 AGCTGCAGAT GGAACCGGTG TGAGGTGTCT TCTGGGACCT GCCGGCCTCC CGGGCCAGCT 660
 GCCCCACCCC TGCCCATGCC TGTCTGCAC GGCTCTGCTG CTCGGGCCCA CAGCGCCGTC 720
 55 CCATCACAAG CCCGGGGAGG GATCCCGCCT TTGAAAATAA AGCTGTTATG GGTGTCATTC 780
 AGGAAAAAAA AAAAAAAGG GGGGCCCTC TAGGGGTCAA AGTTA 825

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(2) INFORMATION FOR SEQ ID NO: 86:

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(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1238 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 86:

CATGTAAAAG GATGAAATGT GACTTCTGGT GTTTTTTTAT TTCTATGGAG GGACTTTCTG	60
GGGACGGTTT CTGGCTCTCA GGCTCTGAGA AGCTGCAGTT TATGAGTGGC TCTGTGTGTG	120
CTGCCACCTA CTGGAGAAGC CATAAGCTGC AGCTTTAGGA AAAGGGAACC CGGGGCAGAG	180
TGTGGGGAAG TGGGATGGCA GCATGGCAGG GCTTTGGAAA ATGAGAGGTG AGAGTKTKTC	240
CAGGAAGGGT GTAAGGAGAG GATGGATCCT GATACATGGA TTCAGGATCA TTAGGGTCCT	300
GTCTGGGACA CTGGCCTTCC TGCTTACCTG CTCTTTCCTT CCTCCTTGGT CGGAGGAGGG	360
GCTGGCTCAC TGCTCTGGCT TCATTTTCCA GAGCTGCCTG CTGCAGTCAC ACTTAGGTCA	420
TCTTCTCTCA CTTTTCTCCT TTTGCCGATT AGTGGACGTG ACAGAGATGT GAATGGGGCA	480
GGGATGTCCT TTGATGGCAT CAAGACTTTA GCTTCTGGTG CGCTGTGTCC CAGCTCTGAT	540
TTCACTTGCA GCCGTGATGG AMAGTTNGCA TGGAAGCTGA GACTCTCACT GACAGTGAAA	600
CCCTCAAATG AACACAATCC CTGCTTTCCT GCCAAGGATC CTTGTAGGGT NCCCCCAGCT	660
TCCCCACTTT TTTTCTGTGT CCTGACAAAG AAACACAGAG TAACTTGATT GCCCTGTGAC	720
CTGGCCAGTT GCATTTCCCC TGCAGGCTTG AGCCCAAGCC AGAGCCTTGA AAAGGTATTG	780
AGGTGTGTC CCAAACACT GAAAAAACT GCCCTGGCCC TGAACCAAAT ACCTTGAACC	840
CTCGTAAACT CCATACCCCTG ACCCCCTTGT TTTGGATATA CCCAGGTAGA ACAACTCTCT	900
CTCACTGTCT GTTGTGAGGA TACGCTGTAG CCCACTCATT AAGTACATTG TCCTAATAAA	960
TGCTTTGGAC TGATCACCCCT GCCAGTCTTT TGCTTTGGGC AATCTATACT TTTNCTCAGA	1020
GGTTCCCAAG GCCTACTGAA GGGACTTAAC ATACTCTTAA TGGCTTTCCT CTCTCTTGTG	1080
TTACCTTATG CCCTCACTTC CTGAGTTAAC CTCCCAAATA CAGGATTACAC CTGTACCCAA	1140
GCCCTTAGCT TCAAGAATAC AGGATCACCT GTACCCAAGC CCTTAGCTCA AGCTCTGCTT	1200
TGGAAGAACC CAAACTAAGA CAGTGCTCCT GGTCGCCCT	1238

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(2) INFORMATION FOR SEQ ID NO: 87:

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(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1460 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 87:

	ATTGCCTTCT GGTCCCTGGT GACACTGGGG TCATCCTTCA TCCCCGAGA GCATTCTCTG	60
10	CTGCTCCTCC TGACCCGGGG CCTGGTGGGG GTCGGGGAGG CCAGTTATTG CACCATCGCG	120
	CCCCTCTCA TTGCCGACCT CTTGTGGGCC GACCAGCGCG ACCGGATGCT CAGCATCTTC	180
15	TACTTTGCCA TTCCGGTGGG CAGTGGTCTG GGCTACATTG CAGGCTCCAA AGTGAAGGAT	240
	ATGGCTGGAG ACTGGCACTG GGCTCTGAGG GTGACACCGG GTCTAGGAGT GGTGGCCGTT	300
	CTGTGCTGT TCTGGTAGT GCGGGAGCCG CCAAGGGGAG CCGTGGAGCG CCACTCAGAT	360
20	TTGCCACCCC TGAACCCAC CTCGTGGTGG GCAGATCTGA GGGCTCTGGC AAGAAATCCT	420
	AGTTTGTCC TGTCTTCCCT GGGCTTCACT GCTGTGGCCT TTGTACGGG CTCCCTGGCT	480
25	CTGTGGGCTC CGGCATTCCCT GCTGCGTTCC CGCGTGGTCC TTGGGGAGAC CCCACCCTGC	540
	CTTCCCGGAG ACTCCTGCTC TTCCTCTGAC AGTCTCATCT TTGGACTCAT CACCTGCCTG	600
	ACCGGAGTCC TGGGTGTGGG CCTGGGTGTG GAGATCAGCC GCCGGCTCCG CCACTCCAAC	660
30	CCCCGGGCTG ATCCCCTGGT CTGTGCCACT GGCCTCCTGG GCTCTGCACC CTTCTCTTTC	720
	CTGTCCCTTG CCTGCGCCCG TGGTAGCATC GTGGCCACTT ATATTTTCAT CTTTATTGGA	780
35	GAGACCCCTC TGTCCATGAA CTGGGCCATC GTGGCCGACA TTCTGCTGTA CGTGGTGATC	840
	CCTACCCGAC GCTCCACCGC CGAGGCCTTC CAGATCGTGC TGTCCACCT GCTGGGTGAT	900
	GCTGGGAGCC CCTACCTCAT TGGCCTGATC TCTGACCGCC TGCGCCGAA CTGGCCCCC	960
40	TCCTTCTTGT CCGAGTTCCG GGCTCTGCAG TTCTCGCTCA TGCTCTGCGC GTTGTGTGGG	1020
	GCACTGGGCG GCGCACTTCC TGGGCACCGC CATCTTCATT GAGGCCGACC GCCGGCGGGC	1080
45	ACAGCTGCAC GTGCAGGGCC TGCTGCACGA AGCAGGGTCC ACAGACGACC GGATTGTGGT	1140
	GCCCAGCGG GGCCGCTCCA CCCGCGTGCC CGTGGCCAGT GTGCTCATCT GGAGAGGCTG	1200
	CCGCTCACCT ACCTGCACAT CTGCCACAGC TGGCCCTGGG CCCACCCAC GAAGGGCCTG	1260
50	GGCCTAAACC CCTTGGCCTG GCCCAGCTTC CAGAGGGACC CTGGGCGGTG TGCCAGCTCC	1320
	CAGACACTAC ATGGGTAGCT CAGGGGAGGA GGTGGGGGTC CAGGAGGGG ATCCCTCTCC	1380
55	AACAGGGGCA GCCCAAGGG CTCGGTGCTA TTTGTAACGG GATTAAAATT TGTAGCCAGA	1440
	AAAAAAAAA AAAAAAAAAA	1460

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(2) INFORMATION FOR SEQ ID NO: 88:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1395 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 88:

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CAGGTGCAAA GTGGGAAGTG TGAGTCCTCA GTCTTGGGCT ATTGGGCCAC GTGCCTGCCG 60
 GACATGGGAC GCTGGAGGGT CAGCAGCGTG GAGTCCTGGC CTMTTGGCTC CACGGGTGGG 120
 AAATTTGGCCA TTGCCACGGC GGGAACTGGG ACTCAGGCTG CCCCCCGGCC GTTCTCATC 180
 CGTCCACCGG AYTCTGGGCG GCTCGCACTG GCGCTGATGT AGTTTCCTGA CCTCTGACCC 240
 GTATTGTCTC CAGATTAAAG GTACGACATT TGGAGGCCCC AGCGAGAAAC GTCACCGGGA 300
 GAAACGTAC CGGGCGAGAG CGGKCCCGCT GTGTGCTCCC CCGGAAGGAC AGCCAGCTTG 360
 TAGGGGGGAG TGCCACCTGA AAAAAAATT TCCAGGTCCC CAAAGGGTGA CCGTCTTCCG 420
 GAGACAGCGG ATCGACTACC ATGTGGGTGC CCACAAAAAT TYCACCTYTG AGTCCTCAAC 480
 TGCTGACCCC GGGGTCACTT CCAGAGAGAA GGAATCCCTC CTGCTTGGA GAGACCTCAC 540
 ACCGTCATCA CGATGCCAAC GGCTCTGAAG GTGGATGGCA TTCCTGCGTG GATTCATCAC 600
 TCCCGCATCA AAAAGGCCAA CRGAGCCCAA CTAGAAACAT GGGTCCCAG GGCTGGGTCA 660
 GGCCCTTAA AACTGCACCT AAGTTGGGTG AAGCCATTAG ATTAATTCTT TTTCTTAATT 720
 TTGTAAACA ATGCATAGCT TCTGTCAACT TATGTATCTT AAGACTCAAT ATAACCCCTT 780
 TGTTATAACT GAGGGAATCA ATGATTTGAT TCCCCAAAA CACAAGTGGG GAATGTAGTG 840
 TCCAACCTGG TTTTACTAA CCTGTTTT AGACTYTCCC TTTCCTTTAA TCACTCAGCC 900
 TTGTTCCAC CTGAATTGAC TCTCCCTTAG CTAAGAGCGC CAGATGGACT CCATCTTGGC 960
 TCTTTCNACT GGCAGCCGCT TCCTYCAAGG ACTTAACTTG TGCAAGCTGA CTCCCAGCAC 1020
 ATCCAAGAAT GCAATTAACT GATAAGATAC TGTGGCAAGC TATATCCGCA GTTCCCAGGA 1080
 ATTCGTCCAA TTGATTACAC CCMAAAGCCC CGCGTCTATC ACCTTGTAAAT AATCTTAAAG 1140
 CCCCTGCACC TGGAACATTT AACGTTCTTG TAACCATTTA TCCTTTTAAAC TTTTMTGCCT 1200
 ACTTTATTTC TGTAATAATTG TTTTAACTAG ACCCCCCCTC TCCTTTCTAA ACCAAAGTAT 1260
 AAAAGCAAAT CTAGCCCTT CTTCAGGCCG AGAGAATTTC GAGCGTTAGC CGTCTCTTGG 1320
 CCACCAGCTA AATAAACGGA TTCTTCATGT GTAAAAAAA AAAAAAAA CTCGGAGGGG 1380
 GGGCCCGGTA CCAA 1395

(2) INFORMATION FOR SEQ ID NO: 89:

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 1186 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 89:

10 GGCACGAGCC GGCAAGCCGA GCTAGGGTGA AAAC TGGGGG CGCACCAGGA TGTNNGACAG 60
 AAAAGCAGAA GATGAGACTC TGTTCATICA CTTTTCCTAG CCCCATCCTG TGGTCATCTT 120
 15 TCCCCCTCCC ATCATACCTC CTCCTTCCTG GAGCCTCTGC CGGCTTGGCT GTAATGGTGG 180
 CACTTACCTG GATATTTTCA TGGGAGGATG AAAGGCGAGA CTCACCCTAC GCGGTGGGAC 240
 20 AGATGGGGAG AGGAAAAAGG CAGAGATGGC CAGGAGAGGG GTGCAGGACA AACCAGAGAG 300
 GTTGGGTCAG GGGAAAAGG TGGGAGAGAA GAGGGGTGCA GGCCCTGCAG GCCGGTTAGC 360
 CAGCAGCTGC GGCCCTCCCG GGCCCTTGGC ATCCAAC T C GCAGACAGG TACCAGCCTC 420
 25 CTGGTGTGTA TCATAGGATT TGTTCACATA GTGTATGCA TGATCTTCGT AAGGTTAAGA 480
 AGCCGTGGTG GTGCACCATG ACATCCAACC CGTATATATA AAGATAAATA TATATATATA 540
 30 TGTATGTAAA TTATGGCAG AGAAATTATA GCACTGAGGG CCCTGCTGCC CTGCTGGACC 600
 AAGCAAACT AAGCCTTTTG GTTGGGTAT TATGTTTCGT TTTGTTATTT GTTGTGTTTT 660
 GTGGCTGTC TTATGTCGTG ATAGCACAAG TGCCAGTCGG ATTGCTCTGT ATTACAGAAT 720
 35 AGTGTMTTAA ATTCACTAAT GTTCTAGTTA ATGTCTACCT CAGCACCTCC TCTTAGCCTA 780
 ATTTTAGGAG GTTGCCCAAT TTGTCTCTT CAATTTTACT GGTTACTTTT TTGTACAAAT 840
 40 CAATCTCTTT CTCTCTTTCT CTCTCCCCA CCTCTCACC TTGCCCTCTC CATCTCCCTC 900
 TCCCGCCCTC CCTCTCTCC TCTGGCTCCC CGTCTCATTT CTGTCCACTC CATCTCTCTT 960
 CCTCTCTCC TGCCTCTGTC TGCCCCCTCC CCAGCCCACT TCCCGAGTT GTGCTTGCCG 1020
 45 CTCTCTATCT GTTCTAGTTC CGAAGCAGTT TCACTCGAAG TTGTGCAGTC CTGGTTGCAG 1080
 CMTCCGCAT CTGCCTTCGT TTCGTGTAGA TTGACGGTT TCTTTGTAAT TTCAGTGTTT 1140
 50 CTGACAAGAT TTAATAAAAA AAAAAGGAAA AAAAAAAAAA AAAAAA 1186

(2) INFORMATION FOR SEQ ID NO: 90:

(i) SEQUENCE CHARACTERISTICS:

- 55 (A) LENGTH: 1821 base pairs
 (B) TYPE: nucleic acid
 60 (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 90:

5	AAAACATGCT TTCAGGGCGT CCCCTATGTA TTCGGGGGGC CCACGGACAC TCAGGCTGGA	60
	KATCCGTCCT CACTGCGCTC AAGATGGCCT CAGCAGACAC CAGTTACCCA GCTGAAAGTC	120
	ACAATCCCTC CCAGAAGTCT CCCAACACTA GTGCTGACCA GAGGTGGGGC TCTCAGGCTA	180
10	GGAGTTTCAC ACACAATGAC AGGCTGCTGG GGGACATTGC AGGACCCCTT TTCCTYTCCT	240
	CTCCATGCTA GAAGCCAGCC CTAGGMAGCT GCAGTTACTC CCTGTGACTC AGCAGCAGGC	300
15	TGATTCAACA CAGCTGCCCA CACAAAGCCA GTGGTAATAC ATCTGTTTAC CTTTCCCTAT	360
	CACCCAGACA CAAGCCCTT TCCCAGGTCA AACCACAGGC CGATGCATCT CCAGTTTGAC	420
	AGTCAAAATCA CTACTTCCAT TGCTACTTTA GATCAGCCAA AGTGGTGACT GCTGCAGTGT	480
20	GTGGCTATCC CTACAAGGCC CACCCAGGG ATGCCCAAAG CCCAACCTTC TCCAGGGCTG	540
	CAGCAGNAGC AACCCACCA GCCTAAGTCC AGCAGAGGAC CTCCCACCCA ATGTCTTGTT	600
25	CTAATTAGAA GGGGAAGTGA GCCACAGAAA ATCAACTTAT CTATAATTAC AAAATTCTCT	660
	TGACTCACCT TAAAGTTCCT ATTGACATCT ACTGCTTTTA AACCTATTTG AAAACTCTGA	720
	TACTAAAACA AATGACACTC TAAGAAAGTT TGGGAGCCCC ATGCTGAGAA CCATTTCTGT	780
30	GCAGTGAGGA TGTTCACAGA AGCTACTTAC CTACATGTGA ATGTGCCATT TTCCTTCCTT	840
	TTGTAGAGAA AATCCCTTT ACTTTTGGGA ACAGTAATGG CAGCTTCTAG TACAGCCATT	900
35	ACAGTTTCAT ATGAGAAAAA TTAAGAATAA CTATAAAAT GITAAAATAT CCAATAATGG	960
	ATAATGATGG CCAGAAGATT TAACATACAA AGTAATTCTC AATGTAAAGC TATTCAGCTC	1020
	TTCCAGGTG AATGCCCTGT AACCCACCT GACCTTCCAC ATCATCTTCA AAAAGCAGTT	1080
40	TCTCTGTTC CCATGATTCT CCTATAAGGT AACTCTTTAG TCCTCCATTT AGCACATTTT	1140
	AAATCCTCCA AAGAATAAGT ATCATGTGAT TATTTTAGCT TTACAAAAA AAAGTTGAAT	1200
45	GGCGTTTAT TTTTCATGGC TATAAGCAGG TACCTTAGTA GGCAGATAT AGGAAAAACA	1260
	AATTAGAGCA AAACAAATCC TCTACAAATC CAAGGCAGGA AAAGTGGTGG CAGAGTGACT	1320
	CATTCTCTG TCCCTCCAT CAGGTCAAAT CAGGAGGCTG CAGTGAATGC CTGTTCTTTG	1380
50	AATGTGTAGC AGTTGTTCTT GTAACCTTTT AAACTTGGC TATAGGCTGT TTAGCACAGT	1440
	ACAGATTAAA GATACAGTTA CGTAAACAGC AAAGTAATTT TATAGTGCTT CATCCATTTA	1500
55	TCATGCTTTG GTTTGCTAAT TTTTTCACAT ACCTTTTCT ATCACAGTCT GTTGCTTTTG	1560
	TACACATTTT TCATATTGGG GTTCGACAGG TAAACACAAA CTGCTATTTT AGTAGAAAAA	1620
60	GTTATTGTTA TGGAATATTA AACCCAATAA ATTGTATAAA GGGTAAAAA AAAAAAAAAA	1680

AAAAAAAAA AAAAAAAAAA AAAAAATTC CTGCGGGCCG CANGCTTTTT CCCTTTGGGT 1740
GAGGGGTTAT TTTNGGCTTG GGCAGTGGGC CCTTCGTTTT TACAACGTCG TGANGGGGGG 1800
5 AACCCGGGGG GGGTTTCCCC C 1821

10 (2) INFORMATION FOR SEQ ID NO: 91:

(i) SEQUENCE CHARACTERISTICS:

- 15 (A) LENGTH: 862 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 91:

20 TGCCCTTTTT CCCACCGATT CGGGGNTGG TGAAGGTGGG AGATGTGAAC TCCAATTAAG 60
GGACTGGAGA GAGGTGAAGA ATTTTGCAGG TGGGAGATTT GGATTTGAAT GTGGACTTGT 120
AAATGACTTG ACCTTGCCAT CTGTGTTCAA GGTACGGTT TGCTGTGGGG TTCTTGGGAG 180
25 AGCTTACTCA CCCCGGAGTC TTTCTTTCT CTGTCTCAA GAAGAGCCCT GTTGGTGCTT 240
TACCACCGCT TGGAGTCTCC CGAGGACACA AACAGGCAGA GAGGGACGTG TAGGGAGAGT 300
30 TCTTTCCTGT TTTCTGTGCT TTCCTTTTTA CAGGACTCCC GGAAGGCCAC TCATGGCCAT 360
GCCAGGAGCT TTCTCAGAAA CAGTCATAAA CGATCTCTTG AGTCTCTTTC TTGTCTCTCC 420
AGCTGAGCTT TCTTATCCA CCTTTCTGG TGTCTATAGG AATGCATGAG AAGACCTTGG 480
35 GACGTTTTTC TGCTCTCTC TGGCCCTCCA TGGAGCCATG GGCTCGGCC TCGGCGGCTC 540
CTCACCTCA CAATTTATTT CCTCCTCCCG TGCCAGCCCT TCTTTTGTGT CTGAAACCGG 600
40 TTTTAAAATG TGACTCTCCC AGAGAAGAAG CCGCTGGCTG TATGAAACTT GACGGCGCTT 660
TTGTAAGGTG CCACCCCAA ACTTTAAGGT AGCTAAACCA ATTTTAAAA GATTCAATGG 720
CTTGTTCATC CTCCAGATGT AGCTATTGAT GTACACTTCG CAACGGAGTG TCTGAAATTG 780
45 TGGTGGTCCT GATTTATAGG ATTCATAAT TAAAATGTCT GCTGAATAAA AAAAAAAAAA 840
AAAAACTCGA GGGGGGCCCG GT 862

50

(2) INFORMATION FOR SEQ ID NO: 92:

55 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 696 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
60 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 92:

CTGAGGCGAG TGAAGTGGAC TCTGAGGGCT ACCGCTACCG CCACTGCTGC GGCAGGGGCG 60
 5 TGGAGGGCAG AGGGCCGCGG AGGCCGCGAGT TGCAAACATG GCTCAGAGCA GAGACGGCGG 120
 AAACCCGTTC GCCGAGCCCA GCGAGCTTGA CAACCCCTTT CAGGAGCCAG CTGTGATCCA 180
 GCACCGACCC AGCCGGCAGT ATGCCACGCT TGACGTCTAC AACCCCTTTG AGACCCGGGA 240
 10 GCCACCACCA GCCTATGAGC CTCCAGCCCC TGCCCCATTG CCTCCACCCT CAGCTCCCTC 300
 CTTGCAGCCC TCGAGAAAGC TCAGCCCCAC AGAACCTAAG AACTATGGCT CATACAGCAC 360
 15 TCAGGCCTCA GCTGCAGCAG CCACAGCTGA GCTGCTGAAG AACAGGAGG AGCTCAACCG 420
 GAAGGCAGAG GAGTTGGACC GAAGGACGA GAGCTGCAGC ATGCTGCCCT GGGRGGCACA 480
 GCTACTCGAC AGAACAAATG GCCCCCTCTA CCTTCTTTTT GTCCAGTTCA GCCCTGCTTT 540
 20 TTCCAGGACA TCTCCATGGA GATCCCCCAA GAATTTGAGA AGACTGTATC CACCATGTAC 600
 TACCTCTGGA TGTGCAGCAC GSTGGNTCTT CTCTGAAYT TCMTGSGCTG CCTGGCCAGT 660
 25 TCTGTGTGGA AACCAACAAT GGCGAGGCTT TGGGTT 696

30 (2) INFORMATION FOR SEQ ID NO: 93:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1886 base pairs
 (B) TYPE: nucleic acid
 35 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 93:

40 CAGGCCACTG ACGCTTCTTT GCGAGGGATG CAGGAGGTCC TACAGAGAAA GGCGCTTCTT 60
 GCATKTCAGA GGGCCACAG CCGTCACCC ACAGATCACC AAGCAGCTTT CTACCTGGCT 120
 CTGCAGCTTG CCATCTCCAG ACAGATCCCA GAGGCTCTGG GGTATGTCCG CCAAGCTCTT 180
 45 CAGCTTCAAG GTGACGATGC CAACTCCCTG CACCTCCTTG CCTCCTGCT GTCAGCACAG 240
 AAGCATPACC ATGACGCTCT GAACATCATC GACATGGCCC TGAGTGAATA CCCAGAAAAT 300
 50 TTCATACTAC TGTTTTCCAA AGTGAAGTTG CAGTCACTCT GCGAGGCCC GGACGARGCA 360
 CTGCTGACTT GTAAGCACAT GCTGCAGATA TGGAAATCCT GCTACAACT CACCAACCCC 420
 AGTGATTTCTG GACGTGGGAG CAGCCTCTTA GATAGAACCA TTGCTGACAG ACGACAGCTT 480
 55 AATACAATTA CTTTGCCAGA CTTCAGCGAT CCCGAGACAG GCTCCGTCCA TGCCACATCG 540
 GTAGCAGCCT CAAGAGTGGG GCAGGCACTG TCGGAAGTGG CTTGCTCTCT GCAGAGCATG 600
 60 CCCCTAAGCA GGGCCCGCTG CACCCCTGGA TGACGCTGGC ACAGATCTGG CTCCATGCAG 660

CTGAAGTCTA TATCGGCATC GGAAGCCTG CAGAAGCCAC AGCCTGTACC CAAGAAGCTG 720
 CCAACCTCTT CCCAATGTCC CACAATGTCC TCTACATGCG CGGCCAGATT GCTGAGCTCC 780
 5 GGGGAAGCAT GGACGAGGCG CGGCGGTGGT ATGAAGAGGC CTTAGCCANT CAGCCCCACC 840
 CACGTGAAGA GCATGCAGCG ACTTGGCCCT GATCCTTCAC CAGYTAGGCC GYTACAGTYT 900
 10 GGGGAGAAG ATCTCCGGG ACGCGGTGCA GGTGAACCTG ACAGCCCACG AGGTCTGGAA 960
 CGGGCTGGGC GAGGTCTCC AAGCTCAGGG CAACGATGCG CGGGCTACGG AGTGCTTCCT 1020
 GACAGCCTTG GAGCTGGAGG CCAGCAGCCC CGCGTGCCC TTCACCATCA TCCCCCGCGT 1080
 15 GCTCTGAGCA GGGCCTGCC AGCCTCACCT GCCGCTCAGC CTNCAGAGGC CCTGCCGGGC 1140
 ACCAGGGCTT GTGCCATCCG CCAAGGGGA TGAATCTGCC GCACTGAGGC CAGGGACGAG 1200
 20 TGTTCAGTGG GCCACAGTGA ACCAACC AAA CCAACCCGA ATCATCGCTC TCGCCATGTG 1260
 CGTTTCTCTT GTTTTTTTTG CCAGCCCAAT GGTAGTTTCT GAACCTATTG ACATTGTTCA 1320
 AAATGGATCA TGTGCCATAT TTTGTAGTT GACATCTGAG TTTTCAGTAA AATGATTATG 1380
 25 GAATTAATCA GCAAATGTAG AAGAATATAT TCAAAGTTAA AATTCAGTGG CAGCACAGAT 1440
 TATTTTTATC AGAGCTGTAA AGAAAACAAC TGTCCTTTTC TCCCCACCAC CCCTCCTGCC 1500
 30 CCACCTTTGGC CCAGAAACCA AATGTGAAC TCTGTCTCC CACCTCAGCA CTAGTCCATG 1560
 CCAGGACACC AGCTGACAAT TTCTTGGTTT TACTGTCAAT AATTGTACCA TGTGATCAAT 1620
 TACTGTCTC ACTTAGAACA AAGCCTGAGT CCGAGAATAT TTATATTTTA CCAATATATG 1680
 35 CCTGTTACAA GAGAAGGAAA TATGAGTTAT TTAAGTTTAA CTTTTTTATG TGAATTCAGA 1740
 GTTTATTTAT CGAGGGAAAT ATGTACAAAG AAGCTTCAA TGGAATATTT ACCGACATTC 1800
 40 CTTATACATG ACAGACACTT GGCTACATGG GAAGATGATG TTAATAATAA AATGATTTTT 1860
 AAATGGAAAA AAAAAAAAAA AAAAAN 1886

45

(2) INFORMATION FOR SEQ ID NO: 94:

50 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1774 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 94:

CTCAGCTACC GTATACAGTA GGACATAACC CCATTTTACA TGCACTACAC TGAGACTTGC 60
 60 CTCTCTCTCC CCCACATTGA AGATGTTCTT TTTTCATAAC TATATACTAT TCCATTGCAT 120

	GAATATTCTG TAATTTATTT AATCCCCTAT GGATTGATAA TTAGGTTTCAT TATAGATAGA	180
	AGTGTAATTA ACATTCCTGT ACATGTATTT TGCTACTTGT GTGGGTATTT CTGTAGGATG	240
5	AATAACTAGA AATTTATTTG ATCAGGTTTC ACATTTGCAG TTTTGAAAAC TACTACCAAA	300
	AAGATTTCAC CAATTTACAA CTCCATCATT AGTAAGAATG CCTGTTTGCC TATAGTCTGC	360
10	CAACCTGAA TCCTTAAAAA TTTTGGCCAA TCTGGTAGGC AAAATTTCTT TCTTTTCTTT	420
	GAATATTAAT GAGGAGGAAC ATCTTTTCAT GTTCTTTGGC CATTTCATT TCCTATTATG	480
	AATTGCTTTT GCCCATTTTC CTTTPTTTAA TTATGAAAGT CTAATGACTA CCTTCTCATT	540
15	GTATAAAAAA CACAGTTCTT TGAATAGAGA GACCCPTTTC TCCAATGCTA CCAATCACAT	600
	TCCACTTACC ACAGTTTAAC ATACATCCTC TAGTCACCTT TCCGTACGAA TATACATACA	660
20	CATAAAAAA CTTTTTACAT AAATAGGATC TCATATTCG TAGCTTTTAA AAATTTGGT	720
	CTCAAAAAA GATAACAGGT CTTTAAATTT CTTAATGGT TGAATATGAT TAAATACTAT	780
	GAAAATGCCA TTATTTATTC CCTTAATTTT TTTCTCTCG CTATTACATT GCCAAAGTAA	840
25	ACATCCTATT CAGATGTCTT TGTGCATGTG TGTGAATATT TCTTTAGTCT GGAGTCCAGT	900
	AAGGTGGATT TTTGGATCAA AGGGTTTGT TCTGTCCAC CTTTCAGTCT CCCAAAGGCC	960
30	TTTCATAACTG TATTTTCACC AAGTGTATGG AGAATGTTCA TTTCCCCATA TAACCATACC	1020
	TACACTTGAT AGTTTTATC TGTGGGGCGA AAAAGAACCT TTTCTTATTT TGCATTTCCC	1080
	TGATTATAAA AAAAAATGGT GAGATTGGGG TTATTTTCAT GTTTATTGGC CATTTATAGT	1140
35	TTACTGTGGA TTGTTTGAT CCCTACCTG CTTTCTATTG GGTATGTGT GGATATATTG	1200
	TTTTTATTG TTCAGCATCT CCTCCCCAT CTCTGGTAA CACAACCTT ATTTATTTGT	1260
40	GGGGAACCTA TTCCCTGTGG CTTAGGTGAG CATGTGACCA GGCCTGGCCT CCTGAGTCCC	1320
	ACAGCTTCCT AGCCACAGTG ATAAAAGAAT GGTATATAA CTTAAGCCAG GCTAAGGAAA	1380
	GCCCTTAACA GAACCTCTGC TGGAACTACT GGAAAGAAG CTTTATGGAG ATCCCAGGAA	1440
45	CCAAGGACCA TGTAAGCCTG AATTTGTGCC ATGTGGAGAG AGTCTGTCTG AGGAGAACT	1500
	CGGATGCTAG CAGAAATGGA AAGAGAACTA AGTTCTGATG TCATTTTCTT GGAGGCCCTA	1560
50	GATCCAGCTG TGCCTAAAGC CTGCCCTACT CCGGACTTTA AAGTTTTGTG AGCCAATAAA	1620
	GTCCCTTTCT TGTTAAGAT AATTGAATG AGTTTCTGTT CTGATTAATA TAGGTTATTT	1680
	GTATTTTCTT ATTGATTTGT AGAAAACCTT TGTAATTTA AATCTAGAC TTTATGCACT	1740
55	ATATAAGTTA ATAAAATTAG CATGGCCTTC CATG	1774

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2503 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 95:

10	GGCACGAGCG AAGGCAAGGG GGCACCAGCT CAGGACTGCA TCTGCCTGCC ATTTCCCTTC	60
	CACTCCTCCT TTCTGGAGTC TGACATTAGA AAGCCAGCGA GAAGGAAGAT TCAAACAACC	120
15	AACCCGTGATT TCCTGCTTCT CCTTTTCATG AGTGTTCCTG TGGTCTCTGC ACCTCCTTTC	180
	TGTCCCCCGG CAGAGGGCAG TAGAGATGGC CGGCCCAAGG CCTCRGTGGC GCGACCAGCT	240
	GCTGTTCATG AGCATCATAG TCCTCGTGAT TGTGGTCATC TGCTGATGT TATACGCTCT	300
20	TCTCTGGGAG GCTGGCAACC TCACTGACCT GCCCAACCTG AGAATCGGCT TCTATAACTT	360
	CTGCCTGTGG AATGAGGACA CCAGCACCCT ACAGTGTAC CAGTTCCTG AGCTGGAAGC	420
25	CCTGGGGGTG CCTCGGGTTG GCCTGGGCCT GGCCAGGCTT GGCCTGTACG GGTCCCTGGT	480
	CCTCACCTC TTGCCCCC AGCCTCTCCT CTTAGCCAG TGCAACATG ATGAGAGAGC	540
	GTGGCGSCTG GCAGTGGGCT TCCTGGCTGT KTCTCTGTG CTGCTGGCAG GCGGCCTGGG	600
30	CCTCTTCCTC TCCTATGTGT GGAATGGGTC ARGCTCTCCC TCCCGGGGCC TGGGTTCCTA	660
	GCTCTGGGCA GCGCCAGSC CTTACTCATC CTCTTGCTTA TAGCCATGGC TGTGTTCCCT	720
35	CTGAGGGCTG AGAGGGCTGA GAGCAAGCTT GAGAGCTGCT AAAGGCTTAC GTGATTGCAA	780
	GGGTTCAGTT CCAACCATGG TCAGAGGTGG CACATCTGCT CAGCCATCTC ATTTTACAGC	840
	TAACGCTGAT CTCCAGCTCC AGCGATGGAA CCCACTACAG AGGAGGTGGG GCCCCTGTGT	900
40	CAAAGAGGCC GAGGGGCAGC AAGGGCAGMC AGGGCACCTG TGACTTCTTA GTACAAGATT	960
	GTCTGTCTTT CAGGACTTCC AAGGCTCCCA AAGACTCCCT AAACCATGCA GCTCATGTGTC	1020
45	ACACCAATTC CTGCTTTAAT TAATGGATCT GAGCAAATCT TCCTCTAGCT TCAGGAGGGT	1080
	GGGGAGGGAG TGATTGCTGT CATGGGGCCA GACTTCCAGG CTGATTTGCC AAATGCCAAA	1140
	ATGAAACCTA GCAAAGAACT TACGGCAACA AACGAGGACA TTAAAAGAGC GAGCACCTCA	1200
50	GTGTCTCTGG GGACATGGTT AAGGAGCTTC CACTCAGCCC ACCATAGTGA GTGGGCCGCC	1260
	ATAAGCCATC ACTGGAATC CAACCCAGA GTTCCAGGAG TGATCTCTGA GTGACTCAAC	1320
55	AAAGACAGGA CACATGGGGT ACAAAGACAA GGCTTGACTG CTTCAAAGCT TCCCTGGACC	1380
	TGAAGCCAGA CAGGGCAGAG GCGTCCGCTG ACAAATCACT CCCATGATGA GACCCCTGGAG	1440
	GACTCCAAAT CCTCGCTGTG AACAGGACTG GACGGTTCG CACAAACAAA CGCTGCCACC	1500
60	CTCCACTTCC CAACCCAGAA CTTGGAAAGA CATTAGCACA ACTTACGCAT TGGGGAATTG	1560

	TGTGTATTTT CTAGCACTTG TGTATTGGAA AACCTGTATG GCAGTGATTT ATTCATATAT	1620
5	TCCTGTCCAA AGCCCACTG AAAACAGAGG CAGAGACATG TACTCTGGTG TGATCTCTTG	1680
	TCCTCAGTGT CTCCTCTGGG CTCCTGTCCC TCTTGCTTTA TAGCTAGCTG CCCGGGGACC	1740
	AAGGTACAGG TGAAAGCAAG GTAGCAGCTT GCGGGAGGAG GCCTGTCTGG CTTACCAGTC	1800
10	TATACACTGT GGCCTCAACC TCCCAGACAG GGCAGAGAAC TGTGGGCAGC TCGTTTGCTT	1860
	TCTAGGCTGG CTGGAGAGGT GGGAGCTCAT TGATAGACTC ATGATGGAAA CTATTTTGA	1920
15	AACAGGCTTC CTCCTTCAGG AGAGATCATG CGGACTAAAC TGTAGCAATT CCAGTGCACC	1980
	TGGCAGTGAT CCTTTCTCTT GCAAAGTACT GTCTCTTTGG TTCCAGTAAG TTGGACCACC	2040
	ACATGACATY ATTTTCCCTG GAACCTGGTC ACTGACTAAC ACAGACAATT GGGACTCCAG	2100
20	AGCCTCAAGA GCCAGGAGAG GGCACAGTAC ATACAGAGGG AGTCAAATGG GATCTCATTT	2160
	TGAGTCTGTC CTTCCGCACA CTCAGAACGG CANCCCCAAG GCCCGGAGTG TCCAGGGCTT	2220
25	CTGGCCTGAG GTGAATCTGC CAGGCCCAAG AAGGCACAAA GGTAGGAGCA CAGAGAGCCC	2280
	CATTCCACA GCGGKCGGC CCAGCAGCAC CAGTGAAGC TCAGCTGTCC TCCAGCTGCT	2340
	CTCGGCAGAC AGTTCAGTGC ACAGTTTATG CCCTAGCTGA AAAAGATCTC CCGACGTAT	2400
30	TTCAGCACAT CCTCTTCCTC CTCCTCCTCA GGGCTCCTGC TACAGGCAGA GCTGGAACCC	2460
	CCCGGCTCT GGAAGGGCT GAGGCTGGA GYCACTGCCT GTC	2503

35

(2) INFORMATION FOR SEQ ID NO: 96:

- 40 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 2801 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

- 45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 96:

	CTGGAAGCC GAGGGTAGCC GAGCGGGCG GCGCTCTGG AGCGCGGGT GCTCGGGCTG	60
50	CCGTCCGCTC CGCCAGAAGC ACCGAGCAGC CGAGCCGGG CCCGCCGCC TCCTCCTCCA	120
	TGAGGCCCGA GTGAGGCGCG GCGCTATAG CCGACCCGCG GCGCCTTCCC CCCGCGTCT	180
	ATCGCGAGCG CACGACMAGC GGCCCTGGA GGAGGAGCG GAGGAGGAG AGCATGTCCG	240
55	ACGGTTTCGA TCGGCCCCCA GTGCTGGTC GGGCCGGAR CCGGGGCTG GGCCGCGGAG	300
	GGGGCGGGC TRAGGCGGCG GGTTTYCCGA AMGGARCGGR GCCTGCTGAG CGGRCGCGGC	360
60	ACCAGCCGCC GCAACCCAAA GCGCGGGCT TYCTGCARCC AMCGCCGCTG CGCCARCCCA	420

	GGACGACCCC GCCGCCAGGG GCCCAGTGCG AGGTCCCCGC CAGCCCCCAG CGGCCCTTCCC	480
	GGCCCCGGGC GCTCCCAGAG CAAACGAGGC CCCTGAGAGC TCCACCTAGT TCACAGGATA	540
5	AAATCCCACA GCAGAACTCG GAGTCAGCAA TGGCTAAGCC CCAGGTGGTT GTAGCTCCTG	600
	TATTAATGTC TAAGCTGTCT GTGAATGCCC CTGAATTTTA CCCTTCAGGT TATTCTTCCA	660
10	GTTACACAGA ATCCTATGAG GATGGTTGTG AGGATTATCC TACTCTATCA GAATATGTTT	720
	AGGATTTTTT GAATCATCTT ACAGAGCAGC CTGGCAGTTT TGAAACTGAA ATTGAACAGT	780
	TTGCAGAGAC CCTGAATGGT TGTGTTACAA CAGATGATGC TTTGCAAGAA CTTGTGGAAC	840
15	TCATCTATCA ACAGGCCACA TCTATCCCAA ATTTCTCTTA TATGGGAGCT CGCCTGTGTA	900
	ATTACCTGTC CCATCATCTG ACAATTAGCC CACAGAGTGG CAACTTCCGC CAATTGCTAC	960
20	TTCAAAGATG TCGGACTGAA TATGAAGTTA AAGATCAAGC TGCAAAAGGG GATGAAGTTA	1020
	CTCGAAAACG AITTCATGCA TTTGTACTCT TTCTGGGAGA ACTTTATCTT AACCTGGAGA	1080
	TCAAGGGAAC AAATGGACAG GTTACAAGAG CAGATATTCT TCAGGTTGGT CTTTCGAGAAT	1140
25	TGCTGAATGC CCTGTTTTCT AATCCTATGG ATGACAATTT AATTTGTGCA GTAAAATTGT	1200
	TAAAGTTGAC AGGATCAGTT TTGGAAGATG CTTGGAAGGA AAAAGGAAAG ATGGATATGG	1260
30	AAGAAATTAT TCAGAGAATT GAAAACGTTG TCCTAGATGC AAAGTGCAGT AGAGATGTAA	1320
	AACAGATGCT CTTGAAGCTT GTAGAATCC GGTCAAGTAA CTGGGGCAGA GTCCATGCAA	1380
	CTTCAACATA TAGAGAAGCA ACACCAGAAA ATGATCCTAA CTACTTTATG AATGAACCAA	1440
35	CATTTTATAC ATCTGATGGT GTTCCTTTCA CTGCAGCTGA TCCAGATTAC CAAGAGAAAT	1500
	ACCAAGAAAT ACTTGAAAGA GAGGACTTTT TTCCAGATTA TGAAGAAAAT GGAACAGATT	1560
40	TATCCGGGGC TGGTGATCCA TACTTGGATG ATATTGATGA TGAGATGGAC CCAGAGATAG	1620
	AAGAAGCTTA TGAAAAGTTT TGTTTGGAAT CAGAGCGTAA GCGAAAACAG TAAAGTTAAA	1680
	TTTCAGCATA TCAGTTTTAT AAAGCAGTTT AGGTATGGTG ATTTAGCAGA ACACAAGAGA	1740
45	GCAAGAAAAT GTGTCACATC TATACCAAAT TRAGGATGTT GAGTTATGTT ACTAATGTAT	1800
	GCAACTTTAA TTTTGTPTAA CACTATCTGC CAAAATAAAC TTTATTCCCT ATAACITAAA	1860
50	ATGTGTATAT ATATATAATA GTTTATTATG TACAGTTAAT TCTACTGTTT TGGCTGCAAT	1920
	AAAATCGATT TTGAAATAAA TGAAATGTTG AAAATPTTGC TAGTTGGTTA GATGCTTATC	1980
	CTTTAAATTC TACTTTTCTT GAGGGGAAAA AGTCTTCGTC TGGAATACA TATTACTGCA	2040
55	AAAATGTAGC ATCCTTTTTT AGGTAGGAGT ATTATAGCTT YCATTTTAGT TKGACATTTA	2100
	GTGTCCCAAT GAATTGAATT TCAAATATGA ATCATAATCT TGAAAATCTT TAGCACTAAA	2160
60	GTCTTGGGAA TATATCAACA ACTGATTTAC ATATGCAGAT GCTATTTGNA TACCAAGGGC	2220

TTTTAAATG TCATGGGGG GAAAAACCCA ACTTGGTGA ACTCCAGCT AAACAACCAA 2280
 GACTTCACTG GAAGATTAT TCCAATTCTA GGAATTGTC TTTTATTTT TTATTTTTC 2340
 5 AACTGRCTAA CTTCATTACC TTAAAGCCTA GAACATTATT CTGCTTTATT TATATGGCTT 2400
 TCTCACTTTT ATTTGTAGC AKGGGTGCA TCGACTTTT TACTAGAGAA TTTTACTAGA 2460
 TATTTGTCAT TCAAGTTTC ATCTGCTTTA TAATTGATAC ACCTGAGGG TCACTTTTCT 2520
 10 AATACTTTTA CTATAATGTG GTACCACCTC AGCCCTAATA AATAATATTT TTACCTAATG 2580
 TCAATCTTTT TTCCAGCTAA CTAATAACTG TGTACAAAAG GATTGCTTGT AAATATGCAT 2640
 15 GTAAATAGTT CTGTTAATAA CCCACTGTTT TACATTGGT ACATCTGTGT CTGCTAATAC 2700
 AGTTAGCTTT CTCACCTTTC TGCTGTGTTG TTCAGTCTGA ATTAAATTA GACTTTGAAA 2760
 ATAAAGCTTA AAAAAAAAAA AAAAAAAAAA AAAAAGCTCGA G 2801
 20

(2) INFORMATION FOR SEQ ID NO: 97:

25

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1631 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 97:

35 ATGGAGCCAA AGACAATCAC TGATGCTTTG GCTTCTAGTA TAATTAAGAG TGTGCTGCCT 60
 AATTTTCTTC CATACAATGT CATGCTCTAC AGTGATGCTC CAGTGAGTGA ACTGTCCCTC 120
 GAGCTGCTTC TGCTTCAGGT TGTCTTGCCA GCATTACTCG AACAGGGACA CACGAGGCAG 180
 40 TGGCTGAAGG GGCTGGTGGC AGCGTGGACT GTGACCGCCG GATACTTGCT GGATCTTCAT 240
 TCTTATTTAT TGGGAGACCA GGAAGAAAAT GAAAACAGTG CAAATCAACA AGTTAACAAT 300
 AATCAGCATG CTCGAAATAA CAACGCTATT CCTGTGGTGG GAGAAGGCCT TCATGCAGCC 360
 45 CACCAAGCCA TACTCCAGCA GGGAGGGCCT GTTGGYTTTC AGCYTTACCG CCGACCTTTA 420
 AATTTTCCAC TCAGGATATT TCTGTTGATT GTCTTCATGT GTATAACATT ACTGATTGCC 480
 50 AGCCTCATCT GCCTTACTTT ACCAGTATTT GCTGGCCGTT GGTAAATGTC GTTTTGGACG 540
 GGGACTGCCA AAATCCATGA GCTCTACACA GCTGCTTGTC GTCTCTATGT TTGCTGGCTA 600
 ACCATAAGGG CTGTGACGGT GATGGTGGCA TGGATGCCCT AGGGACGCAG AGTGATCTTC 660
 55 CAGAAGGTTA AAGAGTGGTC TCTCATGATC ATGAAGACTT TGATAGTTGC GGTGCTGTTG 720
 GCTGGAGTTG TCCCTCTCCT TCTGGGGCTC CTGTTTGAGC TGGTCATTGT GGCTCCCTCG 780
 60 AGGGTTCCTT TGGATCAGAC TCCTCTTTT TATCCATGGC AGGACTGGGC ACTTGGAGTC 840

CTGCATGCCA AAATCATTGC AGCTATAACA TTGATGGGTC CTCAGTGGTG GTTGAAAAC 900
 5 GTAATTGAAC AGGTTTACGC AAATGGCATC CGGAACATTG ACCTTCACTA TATTGTTCGT 960
 AAAGTGGCAG CTCCCGTGAT CTCTGTGCTG TTGCTTTCCC TGTGTGTACC TTATGTCATA 1020
 GCTTCTGGTG TTGTTCTTTT ACTAGGTGTT ACTGCGGAAA TGCAAAACTT AGTCCATCGG 1080
 10 CGGATTTATC CATTTTACT GATGGTCGTG GTATTGATGG CAATTTTGTG CTTCCAAGTC 1140
 CGCCAGTTTA AGCGCCTTTA TGAACATATT AAAAATGACA AGTACCTTGT GGGTCAACGA 1200
 CTCGTGAAC ACGAACGGAA ATCTGGCAAA CAAGGCTCAT CTCCACCACC TCCACAGTCA 1260
 15 TCCCAAGAAT AAAGTAGTTG TCTCAACAAC TTGACCTTCC CCTTTACATG TCCTTTTTTG 1320
 TGGACTTCTC TCTTTGGAGA TTTTCCCAG TGATCTCTCA GCGTTGTTTT TAAGTTAAAT 1380
 20 GTATTTGACT TGTGTTCTCA GCATTCAGAG AGCAGCGGTG TAAGATTCTG CTGTTCTCCC 1440
 TGGATCTTCT GACATTACTG CTGTCGAGA TTTGTATATG TGTAATAACA AGTTCTTGA 1500
 TACCCATAAAA CCTTGGATTA AACAGAATGT GCATTGTACA TCTTTAAACA AAATGTATAT 1560
 25 TAATTTATTA AATCTAGTTG TCACTTTAAA AAAAAAAAAA AAAAAACTCG AGGGGGGCCC 1620
 GGTACCCAAA T 1631

30

(2) INFORMATION FOR SEQ ID NO: 98:

35 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 504 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 98:

CCGAGCTGGG CGAGAAGTAG GGGAGGGCAC GAGCCGCCGC GGTGGCGGTT GCTATCGCTT 60
 45 CGCAGAACCT ACTCAGGCAG CCAGCTGAGA AGAGTTGAGG GAAAGTGCTG CTGCTGGGTC 120
 TGCAGACGCG ATGGATAACG TGCAGCCGAA AATAAACAT CGCCCTTCT GCTTCAGTGT 180
 GAAAGGCCAC GTGAAGATGC TCGGCTGGA TATTATCAAC TCACTGGTAA CAACAGTATT 240
 50 CATGCTCATC GTATCTGTGT TGGCACTGAT ACCAGAAACC ACAACATTGA CAGTTGGTGG 300
 AGGGGTGTTT GCACCTGTGA CAGCAGTATG CTGTCCTGCC GACGGGGCCC TTATTTACCG 360
 55 GAAGCTTCTG TTCAATCCCA GCGGTCCTTA CCAGAAAAAG CCTGTGCATG AAAAAAAGA 420
 AGTTTTGTAA TTTTATATTA CTTTTAGTT TGATACTAAG TATTAAACAT ATTTCTGTAT 480
 TCTTCCAAAA AAAAAAAAAA AAAA 504
 60

(2) INFORMATION FOR SEQ ID NO: 99:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1416 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 99:

5	GGCACGAGGG AGGGAGCCCT CTCGGTGGG TGACTCTTGT GTGCCCTTTA GACAGGCTGG	60
15	CCTGCCGGTT CCACAGGTA CAGTTAGGAC TTGAGTCTTT CTTTTCCTGT TTTGAGTTGG	120
	TGAGTGAGTG ATAGGGTAAC ATGGGCCTTC AGGATGACCC CTTGGAAGTG TGCCGAGTTC	180
20	CTTAAATCTC AGCTGGGATC CTGGACCTGG GAGGCCCTCG TGAGGGCCAG CTCCTGAAAA	240
	ACCTGGGAGT TGATGCCGGA GCTGTGGAAG AACTCTGCTC GAGGGCAGGG TGCCCTGGAA	300
25	CACTGGTAGT TCTGGGGCTG GGAGGGAGAG GGGCTCCGGC TTTCTCTGAA ATGAACACTG	360
	CTCTTCAGCA GTTCAAGTAC TTGTTCTCAA AACATTTTCT AATTGATTGG TAGGTTTTCA	420
	TAAGCATTGT TTCTTTAAGG CATGGAAAGG GAAGAATGCT CAAGCAAGTC ATGTTTGTTT	480
30	TCAGTGGGAT GGGCCCCGGT TCTCACTGCT GGGGGCTTCC CCTTCATGTG GCACCTTTGT	540
	GCAGGGGCCA CCAGGCAGAC TCTTCCCACC TTCTCCCACT GAAGCACCAA GGGGCTTGGA	600
35	ACCGTAATTT GGCTAATCAG AGGCATTTTT TTTGTCTAG TATCTTTCAC ACTTGTCCAA	660
	CCGTCTTATP TTTTAAAAAG TTCTGTTGCT TGTATTAACA CGAACTAGA GAGAAATAGT	720
	TTCTGAAGCC AGTTTATGTG GAAGATCCCC AAGGGGAGGT TCGGTAGAGA AAAATAGTAA	780
40	GCTGGTTTAG AACTGACGA GGGCAAACAG CCAGGACGCA TTGGAGAGGA ATTTGCCAAA	840
	GATCTACCCT GAGATAACGC CTGTCCAGTG TCTTCACCAC GTGAATAACC AGCGCTCCAA	900
45	AGTGTTTTTC TGCTTTGAAA AAAAAAATTC CACAAGCTTT TAAAGGTGCA TTTAAGAATC	960
	CATGTGACTT TAGAATGGAA CTGCCGGCCC TGGCAACTGT CACGTGTGCT AGAAGGTTCG	1020
	ATGCCCTCTG AATGCATGTG ATACTCATCT CCATTTTGTT TCCTTGATTG CATTTTGTGT	1080
50	CTTTTAGCAG ATCTGTCCCT GTGGGTGGTG TCTAAGAAGT CGGACACCTT GGTTTTGTGT	1140
	TTAGATTGAG CTGGGCAGCT GCAATCAGCT TCTTTATATG CAAATTAGGC ACGACCCATC	1200
55	TGTGGTTTCT GGTGGTGGC TAATGAAGTG AGGGGAGGGA GGGATGTAC CCCAAAAGTA	1260
	GGCCCTCCCA TTGGCTTTGG CCAGGCCAGA CACTTCACAT CGTTTACATG GTTCTGTGTA	1320
	ATTTTAAAGT TTATGTGTAT AAAGCGAAGC TGTTCCTGTG AACTGTATA TTTTGTAAAT	1380
60	AAATATATTG CTACTTGAAA AAAAAAAAAA AAAAAA	1416

5 (2) INFORMATION FOR SEQ ID NO: 100:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 2847 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 100:

15 GGCTAGGACA ATTTTGGTGC TTTACCTATC TCTGCAAAGA CTGGAGAATT TGGCATACCA 60
 TTAATTACAA CCACCAATCA TATCCAACAA AAGTACCCTA AAAGAAGGAC CAGTGGCCAC 120
 TCTCGAAAAA ATTTAAGTAT CAGAAGATTA AAAAGATTTT AGGATTTGGA AGCTTGTATT 180
 20 GTCTTTCCCC AATAATCATT GTTTGATCTC CAAATAGTAG CCTTATATTA GCAATRGACA 240
 GATCATGGT TCTCCATATC TGATCATATG TTACTACTTT GGAATCAGTA TTTGGGCAAA 300
 25 TTCAAGCATT TATGCAGTGG ATATAAATGG AAATATAAAA ATATTTGCCA ACCTGTCTCA 360
 GTAACCTATC ATATCTCTGT GNATCCTCAA GGAAAGCACT TTTGCTTTTA CTTAGAAAGC 420
 GTTTCAGATT TGCTTTATAG ACTCCTGCTG TCTTCAGTAC CTGATAAAAC TTTAACCAGG 480
 30 GAAGCATTAA ACACAGTGCA GCAGCTTTTG CCCAGGCTTC TAAGTTCCTG CCGGCAGCAT 540
 TTATCAATGT AAGAACTAGG ATGCTTCCTG CAGTGGCACT ACCCTCCCCT AGAGCTGGAG 600
 35 CATGCTGCTT GGCCTTAAGC CCCAGCATGA TGAGGCTTCC CTCCTGCCAG GTCAGTAAAA 660
 GTTAGAGAGC TCAGAATTGG GTCTTGCTTG GGTGCAGGTG GCAGGGTTTG CTGAAACCCC 720
 TAAAGAGAAG TCACCAAGGG AGGCAGGTAA TGAATGTTTC CAGAATCAGT CKGATACTCA 780
 40 TAGCAATTTT TGGCTATCTT TCAAATGTTG AATTTCTGGA TGCTGAGAGG GACTTTGATT 840
 TGATATCATT AAATCCAGGA CAGTCCCAAG AAGTGCTTGG AGTCTCGGCT CTGACAGCCC 900
 45 AAGAAGGGAA ATAACTTGTA TTAAGGAACA ACTATGAGCC AGGCCCTGAG CTGTCTCTTA 960
 GATAATAAAA CAGATGGGGA GTGGAAGAGT CATTTGCTTC AAGTTATACA GCTAGGAAAT 1020
 ACTCAAGCCA AATCTTGAAC GCAGCTCCCC CTAATTCGTG GGACAGGCAC TTTGTACCAC 1080
 50 ACACCATGGT CCACCTAAAA ACAGAAGGAT AAAAAGACTT CAGGTTTTC CACTGTGTGC 1140
 TGACCATCCC AATTTATGAA TCTTCTTCAA AATGACATTT CACAGTTATA GTTAGGGCTC 1200
 55 AGAAATGGCA TTGAGGTAGC CTTATTTCTC CCCTTTAGCA GATGCTTTAA GTACACATTG 1260
 CTGACTTGAG CCCACCCCA GGAGTTAGGA GAACATTTCC TTTTTCATGC CATCTTCCAT 1320
 60 AAATAAGGTG TTTCTTGGCC TTCAAAGATA TAGAACTTTG CAGCAGTAGT AAAAGTGAAG 1380

	GGTGTTCCTGC TCTCTACTCA ACITTTATTTG AAAATGTCCTG CAGCTTCACT CCTGTAGAAA	1440
	AGGAAATCTT CATATTTTAG TAAACTTAGC CGCCAGTGTA CTCTGTGAGG ATGTGGCAAT	1500
5	TCAAAGTCCA GTGAATCTGG CTCTCTTACT GATTCTCTGGT TTTAGTGTGT GTGTCGGGGG	1560
	AGTGTGTACC TATATATAAA GGACAAGTGT GATATGTGTG TATATGTATA TACATACATA	1620
10	CATGTCCACA CACACACACA CAATATTTGA GAGCTAAGGA AAACCTCAAAG CAGCCCCCTTC	1680
	ATTATCTTGC GTACTACTTC AAAGATTTCT GTCAGCCCTA ATTACAAGTG TCACCATATA	1740
	GTGGGGCTT AGGTACTTGC TTACAGGAAG AGCAATTCCT TAGCAAAGGT CATTAGCTCC	1800
15	TAAGGCACTG AGTCAAAGTG ACAGCCCTGA AGGAAATGTC ACTCCAGCCC TCCTCCAGGA	1860
	TGTCTAATAA GATGGGAAAC TTGGATGCCC AGCCATTTTG GTGACCTGAG AGTCTAACTA	1920
20	CTCCAGTTAG ACCTAAGGCG ACAATGTCAG AATTCATGAC CTTGTAGTTG TGGCAGGGTC	1980
	TAGGAAGTCC TCTCTCCCA AGTAGAAAAT ATTCTCTTGC CATTCCTGAA ATTCCACATT	2040
	CATATAATGG CTGTGCAATA CATGCTTCTC AATAAGAAAA TTAAGTGCAT GTTTACTGTG	2100
25	TGCTGATCAC ATCAGATTTT TATGTTTAA AAAATCTCAT TATGGNTTGA GTCCAGCCCA	2160
	GCTCTAAGAG AAAAAGAAGG CCCATATGGG AGACTTCAGT CTCATTATTA TTGCCTTTAT	2220
30	CCAGCAGTGC TTATRAAGCC CCCTACCCCTG TCCCATTCOA GAAACCATAA GACTCAGGCA	2280
	GTCTCTGATT CTGGAGGCCT GCCTGGTAAG ATAAGATAGT ATAATTTGGA ACTGAGAACA	2340
	TACCAGAAAC AGCAGAACGA GGGCCAGAGC AGAAAAATGA AAATAAGTGG AGACACTTAT	2400
35	GGATACATTG GTGCAAAAA AGCCACGGGS CCCATACTGG GCTTGATATG ACTTTGAGGG	2460
	GACAGCAGAT TAATACTTAA TGAGGGTTAA ACCTGACCAG TCTTTCTACA GTGACAGGCC	2520
40	ACACTGCATG AATGGGGAGA ACCAATGAAT CCATTGTCTT CTGCCTATTT TCCTGTGCAC	2580
	AGTCACATTC CCTCCTTAGG AATCTTCCCC TTCCACCCTT TACATTAAAC AAGGGAACAC	2640
	TGAATCTTTC AAGGGAATTA CACGTTTGGG TTAATGTTTC AGTATATCAT TTTCATACTG	2700
45	TAAATTATTT TGTAAGAGAG ATTTACTGCT ATCCCAGGAT GTTCGGACTT GGTGCCCTG	2760
	TGCATTGGA AATCAATAAA CTATTACTGG AAATGCCAAA AAAAAAAAAA AAAAAAAAAAN	2820
50	NAAAAAATC GAGGGGGGCC CGTACCC	2847

55 (2) INFORMATION FOR SEQ ID NO: 101:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1394 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

60

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 101:

5	GAGATTGGTG GAGGAGAGTA AATAATCTAG AGGCAAGAGT TCAGTGAGGG CCAAGGGGGA	60
	CCCCCAGAAA AAGGTATGGA GCTAACTCAT CTCCTTTACA AGGGGTGGCC ATGACTTACT	120
	GTTCACAACT ACTCAGTGTA TATTTAATGT TGATTGTTGA ATTTTAGTTA CGAGAGGGAA	180
10	GAACAATTTT ACTTCTGTCC TTATTTCACT TGCTGAAAAG CTGTGGGACA AAATGTATGG	240
	AATAGACAAG GCCACTTTCT TTGTGATTTC TGCTTTTCAT GCATATTATT TTATTTACCC	300
15	ATAATTTCCA AGAGGTTTGG CGTTCGCTC TCCTGCTTTT TTCTTTTCATC CACCCCTTTT	360
	CTTTTTTTGG AAGGGGGTTA TATATGAGAG TTCATTGAAG AAGTCCAGTG AGGCTGAACT	420
	AAAGGGGCAA GATAGGGCAG TTAACATAAG AGCACTTTAT TTCTTTGAAG CCTTCTAAG	480
20	AAAGAAATGG GGGTGCAGT GGCTTGAATC TCCCATGATG TTGGAGGGCA CTTAGTGGGG	540
	TTGAAGTATG ACATAATATT TCCCATGGG GAAAGGAGAA TTCTCTTAG AGGTGGCAA	600
	AATGCCTTTG CCCAGTGTCC CTATTTTAGG CATCTTTCC TTCTTTATTC CTTCAGTCA	660
25	GGGTGTGTCC TATACAAAAC TTCCCATCAG TTCTCCTCAA TATTCOCAT TTGTAAATGA	720
	TCACTTCTCT TTTCTAAACC CTTTCTCTGT TCAGATCCAT ACAGGATTTG CAAGGGTAGG	780
30	ATCATACATG CAAATGCCCC TTGTTTCATCT GTGTCTTCTG CAACTAGTC TCATGAAGAA	840
	TTCTGGCGTG CAGCAGGGTA GCTGAAGTTT GGGTCTGGGA CTGGAGATTG GCCATTAGGC	900
35	NTCNCTGAGA TTCCAGCTCC CTTCACCAA GCCCAGTCTT GCTACGTGGC ACAGGGCAAA	960
	CCTGACTCCC TTTGGGCCCT AGTTTCCCTT CCCCTTCATG AAATGAAAAG AATACTACTT	1020
	TTTCTTGTG GTCTAGCATT GCTGGACACA AAGTGTAGTC ATTATGTTG TATGGGTGA	1080
40	TGTGTGCAAA ACTGCAGAAG CTCCTGCCT ATAAGAGGAA ATAAGAGAGA AAGTGGAGGA	1140
	GAGGACAAA AGGAGTAATT ATTTGGTATA GATCCACCCA TCCCAACCTT TCTCTCCTCA	1200
45	GTCCCTGCTC CTCATGTTTC TGGTTTGGTG AGTCTTTGT GCCACCACCC ATAATGCTTT	1260
	GCATGCTGC ATCCTGGGAA GGGGTATAT GGTCTCACA GTGTGTGCA TTGTTTTTTT	1320
	GCATGCTTTC TTAATAAAAA AAAAAAAAAA ATGTTTANAG TTTTATCTTA AAAAAAAAAA	1380
50	AAAAAAAAA ACCC	1394

55 (2) INFORMATION FOR SEQ ID NO: 102:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 794 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

60

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 102:

5	GGMRCGAGGC GGAGTAAAGG GACTTGAGCG AGCCAGTTGC CGGATTATTC TATTTCCCTT	60
	CCCTCTCTCC CGCCCGTAT CTCTTTTCAC CCTTCTCCCA CCTCGCTCG CGTACCATGG	120
	CGGAGCGTCG GCGGCCACTC AGTCCCATTC CATCTCCTCG TCGTCCTTCG GAGCCGAGCC	180
10	GTCCGCGCCC GCGGCGGCGG GGAGCCCAGG AGCCTGCCCC GCCCTGGGGA CGAAGAGCTG	240
	CAGCTCCTCC TGTGCGGTGC ACGATCTGAT TTTCTGGAGA GATGTGAAGA AGACTGGGTT	300
15	TGTCTTTTGA CACGCTGATC ATGCTGCTTT CCCTGGCAGC TTTCAGTGTC ATCARTGTGG	360
	GTTTCTTAMC TCATCCTGGC TCTTCTCTCT GTCACCATCA RCTTCAGGAT CTACAAGTCC	420
	GTCATCCAAG CTGTWCAGAA RTCAGAAARA GCCCATCCAW TCCAAAGCCT ACCTGGACGT	480
20	AGACATTACT CTGTCTCAG AAGCTTTCCA TAATTACATG AATGCTGCCA TGGTGACAT	540
	CAACAGGGCC CTGAAACTCA TTATTCGTCT CTTTCTGGTA GAAGATCTGG TTGACTCCTT	600
25	GAAGCTGGCT GTCTTCATGT GGCTGATGAC CTATGTTGGT GCTGTTTTTA ACGGAATCAC	660
	CCTTCTAATT CTGTCTGAAC TGCTCATTTT CAGTGTCCCG ATTGTCTATG AGAAGTACAA	720
	GACCCAGATT GATCACTATG TTGGCATCGC CCGAGATCAG ACCAAGTCAA TTGTTGAAAA	780
30	GATCCCAAGC AAAA	794

35

(2) INFORMATION FOR SEQ ID NO: 103:

(i) SEQUENCE CHARACTERISTICS:

40

- (A) LENGTH: 1544 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 103:

45

45	TTTGCTTGCT AGTCTGAACC AAAGAGTTGT TTGGGCATTT GCTGTGTTGG CCATTTCTGG	60
	AGCAAGAGGG TCTTCTTCTT CCTTCCCCCA GCCAGCCAGC TGTCTGGGG CCAGGCTTTC	120
50	CTGGGTGGAA AGAAGTATAC CTTTCCCTGG GGCCCTAGGA TAGCAAAGTG AGCCATAGTG	180
	GGCCAGGCTG CCTTCCATGC TGGGCCCCAG CCCAGGTCTG CACTCGCCTG GATCACCTTC	240
	TTTGAGCCTT AGCCATCTCC TGTACGGTAG GAATGAACTT GCCAGCCTTC AGGYTCGTTT	300
55	AGCTATGACC ATCTGTGCGG TCAGGTACA CTCAGCTCTC CTCCCCAACT CCAGCAGCCT	360
	TTAAGAAGTG TCCCTTTTGGC GCCCCCTGGA GGCAGAGCAC TGAGCTGGAC CCTGGGTAGA	420
60	CTCCACAGG GAGGACGGAG CTGGCCTCAG GAGTGGGACA CCCAGACTTG GCAGGGCCTT	480

CAAGAGGCCT GTGTGGGGGC CCCAGGAATC CTTAGCTGAA GCGGGGAGAC TCACTCTCCA 540
 TCTCAGGAAA TTCTAGCCCT TGCCCTCAGG GAGCCACGGT TGAGGGTGAG GCCCAACACC 600
 5 TGCCCTTAGGG CCCTGGGTGG GCAAGTCTGG GCCCTGGGGT AGGGAGGGAG ACTCAGGCCC 660
 ACACCTGGGT ATTTTCTAAT TTCAGACAAA CACACACTCA GCGCGCACTC ACTGATTCTT 720
 10 ACACATGCCC AAGATTTTAC ACATGTGACC AGGGGCCACC AAAGTCCCTG TGACCTTTGT 780
 GACTAGGATC CTAATTTCTC TATTTTCTCC TGGGTGCCTG GGTCTGTGTC ACCTGGGGCA 840
 GTGTGGATAA TGTTTAGTTC TGTGACACTG TTTTGTGGG GTGGCACCTG GTTCTCCGAT 900
 15 GCCTGGGCTG GTGTCAAGCC CAGGACTGTA GTGCTGGGAG CAGTAAAGCT CAGCTCTGTG 960
 TAATGAGTGA TGCTATGGCT TGCTCGTGTC TTATGATCCA ATCCTTTTCT ACATCAGCCC 1020
 20 TTGTTTGTGTT TTATGGCTAG TCTTATCTGG CCTGGTTATT TCCTTGCGGG GAGGAGAGGG 1080
 TTGCTAATC TGCTCCCAGC CCAACCTATT ACCACCCAC CTCGCTGGGA CCTACTGCTC 1140
 GGGAGGCAGC AGACAGGGAG CCACCAGCAG TGGCTTCCTG GCCCTGTGCT GGGGGTGGG 1200
 25 GGAAGCTGGG GGCACATGTG GCCCTTGCCT TCTGAGCAGC TCCAGTGCC AGGGCTTTGA 1260
 GACTTTCCCA CATGATAAAA GAAAAGGGAG GTACAGAAGT TCCAATTCCC TTTTATTTTT 1320
 30 GCTGGTTGGT ATCTGTAAAT GTTAATAAA TATCTGAGCA TGTATCTATC AACGCCAAGA 1380
 ATTTCAAAGT CTCCTTCAAC AATATGAGGC TTTTAGGATG TTTATATTCC TTCATCCCTC 1440
 TTGTTTCCCA GGTTTTGCAG GGAAAAAAG TCTGGAATTA TAGATACAGC TTATTATTAA 1500
 35 ATTTGTCTT GCATAAAAAA AAAAAA AAAACNNGGG GGGG 1544

40

(2) INFORMATION FOR SEQ ID NO: 104:

(i) SEQUENCE CHARACTERISTICS:

45

- (A) LENGTH: 871 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 104:

50

ACCCACGCGT CCGNCTTGTC CACCCGGGGG CGTGGGAGTG AGGTACCAGA TTCAGCCCAT 60
 TTGGCCCCGA CGCCTCTGTT CTCGGAATCC GGGTGCTGCG GATTGAGGTC CCGGTTCTTA 120
 55 AGGTGGGTG CTGTCCACCC GGGGGCGTGG GAGTGAGGTA CCAGATTCAG CCCATTTGGC 180
 CCCGACGCCT CTGTTCTCGG AATCCGGGTG CTGCGGATG AGGTCCCGGT TCCTAACGGA 240
 CTGCAAGATG GAGGAAGCGG GGAACCTAGG AGGCCTGATT AAGATGGTCC ATCTACTGGT 300
 60

CTTGTCAGGT GCCTGGGGCA TGCAAATGTG GGTGACCTTC GTCTCAGGCT TTCTGCTTT 360
 TCCGAAGCCT TCCCCGACAT ACCTTCGGAC TAGTGCAGAG CAAACTCTTC CCCTTCTACT 420
 5 TCCACATCTC CATGGGCTGT GCCTTCATCA ACCTCTGCAT CTTGGCTTCA CAGCATGCTT 480
 GGGCTCAGCT CACATTCTGG GAGGCCAGCC AGCTTTACCT GCTGTTCTTG AGCCTTACGC 540
 TGGCCACTGT CAACGCCCGC TGGCTGGAAC CCCGCACCAC AGCTGCCATG TGGGCCCTGC 600
 10 AAACCGTGGG AGAAGGAGCG AGGCCTGGGT GGGGAGGTAC CAGGCAGCCA ACAGGTTCCT 660
 GATCCTTAAC GCCAGTTCG AGAGAAGGAC CCCAAGTACA GTGCTCTCCG CCAGAATTTT 720
 15 TTCCGCTACC ATGGGCTGTC CTCCTTTTGC AATCTGGGCT GCGTCTGAG CAATGGGCTC 780
 TGTCTCGCTG GCCTTGCCCT GGAAATAAGG AGCCTCTAGC ATGGGCCCTG CATGCTAATA 840
 AATGCTTCTT CAGAAAAAAA AAAAAAAAAA A 871
 20

25 (2) INFORMATION FOR SEQ ID NO: 105:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 404 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 30 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 105:

GGCACGAGTT ATAGCATGGC ATTCATACTT TTGTTTTATT GCCTCATGAC TTTTITGAGT 60
 35 TTAGAACAAA ACAGTGCAAC CGTAGAGCCT TCTTCCCATG AAATTTTGCA TCTGCTCCAA 120
 AACTGCTTTG AGTACTCAG AACTTCAACC TCCCAATGCA CTGAAGGCAT TCCTTGTCAA 180
 40 AGATACCAGA ATGGGTTACA CATTTAACCT GGCAACATT GAAGAACTCT TAATGTTTTT 240
 TTTTAAATAA GAATGACGCC CCACTTTGGG GACTAAAATT GTGCTATTGC CGAGAAGCAG 300
 TCTAAAATTT ATTTTTTTAA AAAGAGAAAC TGCCCCATTA TTTTGGTGGG GTTGGTTTTT 360
 45 AATTTNTAAT NTGAAAAATT TTTTGGGGT TTTTGGGGCC ATGG 404

50 (2) INFORMATION FOR SEQ ID NO: 106:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1542 base pairs
 55 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 106:

60

	GTGACACAGG TGGAGCCGCC GGGGCAGGAG TCTCAAAGAG CCAGGCTCCA GGAGAGGAAG	60
	GGCTCTRCGA GAGGAGAGAG GAGAGCGCTG GAGAGGAGAG GCTGGAGAGT CCTTAGCCAG	120
5	GATGGAGGCT GTTGTGAAC TGTACCAAGA GGTGATGAAG CACGCAGATC CCCGGATCCA	180
	GGGCTACCCT CTGATGGGGT CCCCCTTGCT AATGACCTCC ATTCTCCTGA CCTACGTGTA	240
10	CTTCGTCTTC TCACTTGGGC CTCGCATCAT GGCTAATCGG AAGCCCTTCC AGCTCCGTGG	300
	CTTCATGATT GTCTACAAC TCTCACTGGT GGCACCTCTCC CTCTACATTG TCTATGAGTT	360
	CCTGATGTCG GGCTGGCTGA GCACCTATAC CTGGCGCTGT GACCCTGTGG ACTATTCCAA	420
15	CAGCCCTGAG GCACTTAGGA TGGTTCGGGT GGCCTGGCTC TTCCTCTTCT CCAAGTTCAT	480
	TGAGCTGATG GACACAGTGA TCTTTATTCT CCGAAAGAAA GACGGGCAGG TGACCTTCCT	540
20	ACATGTCTTC CATCACTCTG TGCTTCCTTG GAGCTGGTGG TGGGGGGTAA AGATTGCCCC	600
	GGGAGGAATG GGCTCTTTCC ATGCCATGAT AACTCTTCC GTGCATGTCA TAATGTACCT	660
	GTACTACGGA TTATCTGCCT TTGGCCCTGT GGCACAACCC TACCTTTGGT GGAAAAAGCA	720
25	CATGACAGCC ATTCAGCTGA TCCAGTTTGT CCTGGTCTCA CTGCACATCT CCCAGTACTA	780
	CTTTATGTCC AGCTGTAAC ACCAGTACCC AGTCATTATT CACCTCATCT GGATGTATGG	840
30	CACCATCTTC TTCATGCTGT TCTCCAACTT CTGGTATCAC TCTTATACCA AGGGCAAGCG	900
	GCTGCCCGT GCACCTCAGC AAAATGGAGC TCCAGGTATT GCCAAGGTCA AGGCCAACTG	960
	AGAAGCATGG CCTAGATAGG CGCCACCTA AGTGCCTCAG GACTGCACCT TAGGGCAGTG	1020
35	TCCGTCAAGT CCCTCTCCAC CTACACCTGT GACCAAGGCT TATGTGGTCA GGACTGAGCA	1080
	GGGGAAGTGC CCTCCCTTCC CCACAGCTGC TCTACAGGGA CCACGGCTTT GGTTCCTCAC	1140
40	CCACTTCCCC CGGGCAGCTC CAGGGATGTG GCCTCATTGC TGTCTGCCAC TCCAGAGCTG	1200
	GGGGCTAAAA GGGCTGTACA GTTATTTCCC CCTCCCTGCC TTAAAACTTG GGAGAGGAGC	1260
	ACTCAGGGCT GGCCCCACAA AGGGTCTCGT GGCCTTTTTC CTCACACAGA AGAGGTCAGC	1320
45	AATAATGTCA CTGTGGACCC AGTCTCACTC CTCCACCCCA CACACTGAAG CAGTAGCTTC	1380
	TGGGCCAAAG GTCAGGGTGG GCGGGGCGCT GGAATACAG CCTGTGGAGG CTGCTTACTC	1440
50	AACTTGTGTC TTAATTAAAA GTGACAGAGG AAACCANAAA AAAAAAATAA AAAAACTCGA	1500
	GGGGGGCCCG TACCCAAATC GCCGGTATGA TCGTAAACAA TC	1542

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(2) INFORMATION FOR SEQ ID NO: 107:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2327 base pairs

(B) TYPE: nucleic acid

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(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 107:

5	GGTAGCTCAN TGCAGTGAAA TAGTCTTACT GGAAACAAAG CCCTTTATCA AGAATAATTA	60
	ACTCTTCCTT TTTCTTTTTC GAGAGGTGCT TTGTTTCTGA TCGGACCATT TCACTGCAGC	120
10	AAGCAACACA GTATTCTTRAG CAGAAGATCG GGACTTGAGG CCATGTTGCG GAGGGCCAGT	180
	RACATTATCT GGA CTCTGGA GTGTGAGGAA TATGGACTCC ACTCTTCACT ATATTACAR	240
	CGATTTCAGAC TTGAGCAACA ATAGCAGTTT TAGCCCTGAT GAGGAAAGGA GAACTAAAGT	300
15	ACAAGATGTT GTACCTCAGG CGTGTGTAGA TCAGTATTTA TCTATGACTG ACCCTTCTCG	360
	TGCACAGACG GTTGACACTG AAATTGCTAA GCACTGTGCA TATAGCCTCC CTGGTGTGGC	420
20	CTTGACACTC GGAAGACAGA ATTGGCACTG CCTGAGAGAG ACGTATGRGA CTYTGGCCTC	480
	AGACATGCAG TGGAAAGTTC GACGGAACTC TAGCATTCTC CATCCACGRG CTGTCAGTTA	540
	TTCTTGAGAG TCAATTGACA GCTGCAGATC TGGTTCCAAT TTTTAATGGA TTTTAAAAG	600
25	ACCTCGATGA AGTCAGGATA GGTGTTCTTA AACACTTGCA TGATTTTCTG AAGCTTCTTC	660
	ATATTGACAA AAGAAGAGAA TATCTTTATC AACTTCAGGA GTTTTGGTG ACAGATAATA	720
30	GTAGAAATG GCGGTTTCGA GCTGAAGTGG CTGAACAGCT GATTTTACTT CTAGAGTTAT	780
	ATAGTCCAG AGATGTTTAT GACTATTTAC GTCCCATGTC TCTGAATCTG TGTGCAGACA	840
	AAGTTTCTTC TGTTCGTTGG ATTTCCTACA AGTTGGTCAG CGAGATGGTG AAGAAGCTGC	900
35	ACGCGGAAC ACCACCAACG TTCGGAGTGG ACCTCATCAA TGAGCTTGTG GAGAACTTTG	960
	GCAGATGTCC CAAGTGGTCT GGTGCGCAAG CCTTTGTCTT TGTCTGCCAG ACTGTCTATG	1020
40	AGGATGACTG CCTTCCCATG GACCAGTTTG CTGTGCATCT CATGCCGCAT CTGCTAACCT	1080
	TAGCAATGA CAGGGTTCCT AACGTGCGAG TGCTGCTTGC AAAGACATTA AGACAACTC	1140
	TACTAGAAAA AGACTATTTT TTGGCCTCTG CCAGCTGCCA CCAGGAGGCT GTGGAGCAGA	1200
45	CCATCATGGC TCTTCAGATG GACCGTGACA GCGATGTCAA GTATTTTGCA AGCATCCACC	1260
	CTGCCAGTAC CAAAATCTCC GAAGATGCCA TGAGCACAGC GTCTCAACC TACTAGAAAG	1320
50	CTTGAATCTC GGTGTCTTTC CTGCTTCCAT GAGAGCCGAG GTTCAGTGGG CATTCGCCAC	1380
	GCATGTGACC TGGGATAGCT TTCGGGGGAG GAGAGACCTT CCTCTCCTGC GGACTTCATT	1440
	GCAGGTGCAA GTTGCTTACA CCAATACCA GGGATTTCAA GAGTCAAGAG AAAGTACAGT	1500
55	AAACACTATT ATCTTATCTT GACTTTAAG KKWAWKMMWW KCTCAGMSRA TTATAMITSW	1560
	CWMMRARGSM WYMAAWSCTK SWGCTCYWCC KSRSTGRMKG MMRCTCTAGA AYTRGYRGAK	1620
60	CMYYYKSGCT KMWGGAAKKS GGCASGAGCC AGAGACCTGC ATTGCTTTCT CCTGGTTTTA	1680

5 TTTAACAATC GACAAATGAA ATTCTTACAG CCTGAAGGCA GACGTGTGCC CAGATGTGAA 1740
 AGAGACCTTC AGTATCAGCC CTAACCTTTC TCTCCCAGGA AGGACTTGCT GGGCTCTGTG 1800
 GCCAGCTGTC CAGCCCAGCC CTGTGTGTGA ATCGTTTGTG ACGTGTGCAA ATGGGAAAGG 1860
 AGGGGTTTTT ACATCTCCTA AAGGACCTGA TGCCAACACA AGTAGGATTG ACTTAAACTC 1920
 10 TTAAGCGCAG CATATTGCTG TACACATTTA CAGAATGGTT GCTGAGTGTG TGTGTCTGAT 1980
 TTTTTCATGC TGGTCATGAC CTGAAGGAAA TTTATTAGAC GTATAATGTA TGTCTGGTGT 2040
 TTTTAACTTG ATCATGATCA GCTCTGAGGT GCAACTTCTT CACATACTGT ACATACCTGT 2100
 15 GACCACTCTT GGGAGTGCTG CAGTCTTTAA TCATGCTGTT TAAACTGTTG TGGCACAAGT 2160
 TCTCTGTGCC AAATAAAATT TATTAATAAG ATCTATAGAG AGAGATATAT ACACCTTTTGA 2220
 20 TTGTTTCTA GATGTCTACC AATAAATGCA ATTTGTGACC TGTAACAAAA AAACAAAAAA 2280
 ACTCGAGGGG GGGCCGGTAC CCAAATCGCC GATATGATCT AANCATC 2327

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(2) INFORMATION FOR SEQ ID NO: 108:

30 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1062 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 108:

GGCCGCCGAG GCGCAACAGC CGTTCTGTCA GCTCTGGGTC CAACCGGACT AGCGAANATC 60
 TTCTTCATCC TCATCATCGT CTTCTCATC CCGATCTCGG TCCAGGTCCC TCTCCCCCCC 120
 40 ACACAAGAGG TGGCGAAGGT CCAGCTGTAG TTCTCTGGA CGTTCTCGAA GATGCTCTTC 180
 CTCTTCTTCG TCATCATCTT CCTCTTCGTC TTCTTCATCC TCATCATCCA GTTCTCGAAG 240
 45 CCGCTCACGA ATCCCCATCC CCCC GCCGGA GRAAGTGACA GGAGCGGGC GTACAGCTCT 300
 TATCGTTCAC ATGACCATTA CCAAAGGCAA AGAGTGCTAC AAAAGGAGCG TGCAATAGAA 360
 GAAAGAAGGG TGGTCTTCAT TGGAAAGATA CCTGGCCGCA TGA CTGATC AGAGCTGAAA 420
 50 CAGAGGTCTT CCGTTTTTGG AGAGATTGAG GAGTGACCA TCCACTTCCG TGTCCAAGGG 480
 GACAACTACG GCTTCGTCAC TTATCGCTAT GCTGAGGAGG CATTGACAGC CATTGAGAGT 540
 55 GGCCACAAGC TCGGCAGGC AGATGAGCAG CCCTTTGATC TCTGCTTTGG GGGCCGAAGG 600
 SWGTNCTGCA AGAGGAGCTA TTCTGATCTT GACTCCAACC GGAAGACTT TGACCCAGCA 660
 CCTGTAAAGA GCAAATTTGA TTCTCTTGAC TTTGACACAT TGTGAAACA GGGCCAGAAG 720
 60

AACCTCAGGA GGTAACCTTG GGCCCTTCCC TGCTATCCTT TTTCTCCTTT GGAGGTGCCC 780
 AACCTCCTCC ACCCCCTTCC CCTACTCTAG GGGAGAGAGC TGCTAGTGAG ATGACTGTMT 840
 5 TATAAAGAAA TGGAAAAAG TGAAATAAAA AATATGTTGA ATCAGATTTT TTAAAAGGGG 900
 TATTGTMTT TTTATAACAG GTATTGAAAC AAGTTAACTT GCATTCTAT GTAAGATAGG 960
 10 AGGGGCTGAG GGGATCCCCA GTGTTTGGA CATAAGTCAC TATGCAGACT AATAACATC 1020
 AACTAGAGAG NAAAAAAAAA AAAAAAAAAA ATTTAAAAAA CT 1062

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(2) INFORMATION FOR SEQ ID NO: 109:

(i) SEQUENCE CHARACTERISTICS:

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- (A) LENGTH: 2539 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 109:

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GAGAGACTCA CACTTCTTTT CCATTATCAC TGACGATGTA GTGGACATAG CAGGGGAAGA 60
 GCACCTACCT GTGTTGGTGA GGTTTGTGA TGAATCTCAT AACCTAAGAG AGGAATTTAT 120
 30 AGGCTTCTCG CCTTATGAAG CCGATGCAGA AATTTTGGCT GTGAAATTC AACTATGAT 180
 AACTGAGAAG TGGGGATTAA ATATGGAGTA TTGTCGTGGC CAGGCTTACA TTGWCTCTAG 240
 TGGATTTTCT TCCAAATGA AAGTTGTTGC TTCTAGACTT TYAAGMKMRA TWKCCCMK 300
 35 YWAWCKGAAC AMAMKCTGSW CYTCCWSYGC SKTRRMKRYC GYKSTATRRC WARWKSAYM 360
 CCYGKMTGS RRGTAWYTSK TGCAKAGGG AACAATTGAG GAAGTTTGTT CTTTTTCCA 420
 40 TCGATCACCA CAACTGCTTT TAGAACTTGA CAACGTAATT TCTGTTCTTT TTCAGAACAG 480
 TAAAGAAAGG GGTAAAGAAC TGAAGGAAAT CTGCCATTCT CAGTGGACAG GCAGGCATGA 540
 TGCTTTTGAA ATTTTAGTGG AACTCCTGCA AGCACTTGTT TTATGTTTAG ATGGTATAAA 600
 45 TAGTGACACA AATATTAGAT GGAATAACTA TATAGCTGGC CGAGCATTG TACTCTGAGT 660
 GCAGTGTGAG ATTTTGATTT CATGTTACT ATTGTTGTTT TAAAAATGT CCTATCTTTT 720
 50 ACAAGAGCCT TTGGGAAAAA CYCMAGGGG CAAACCTCTG ATGTCTTCTT TGCKKMSRT 780
 ARMTTTTGAY ATRMARYACT RMTKSAYTY AAYGRWGTGA CWSGAWAATA TTRAASTYTA 840
 TACAATKAAT YWTRRYTSM KRMAGMYAAT CCGAAAYTGT GGMAAMYAAA CTTGATATTC 900
 55 AAATGAAACT CCTGGGAAA TTCCGCAGAG CTCACCAGGG TAACTTGGAA TCTCAGCTAA 960
 CCTCTGAGAG TTAATAATAA GAAACCCTAA GTGTCCAAC AGTGGAGCAC ATTATTCAGG 1020
 60 AACTTAAAGA TATATTCTCA GAACAGCACC TCAAAGCTCT TAAATGCTTA TCTCTGGTAC 1080

	CCTCAGTCAT GGGACAACCTC AAATTCAATA CGTCGGAGGA ACACCATGCT GACATGTATA	1140
5	GAAGTGACTT ACCCAATCCT GACACGCTGT CAGCTGAGCT TCATTGTTGG AGAATCAAAT	1200
	GGAAACACAG GGGGAAAGAT ATAGAGCTTC CGTCCACCAT CTATGAAGCC CTCCACCTGC	1260
	CTGACATCAA GTTTTTTCCT AATGTGTATG CATTGCTGAA GGTCTGTGT ATTCTTCCTG	1320
10	TGATGAAGGT TGAGAATGAG CGGTATGAAA ATGGACGAAA GCGTCTTAAA GCATATTGA	1380
	GGAACACTTT GACAGACCAA AGGTCAAGTA ACTTGGCTTT GCTTAACATA AATTTTGATA	1440
15	TAAACACGA CCTGGATTTA ATGGTGGACA CATATATTAA ACTCTATACR AKTAMGTCAG	1500
	MGCTYYCTAC AKAYRAYTCM SWAWMTGTGG AAARYWSSTA MGMSWGCWKK TAMMRRTMCG	1560
	GMWWTYYYMK RKTYGAYMYW YGCGWMCGAG AAAAAGCCGT AAGGTGTATG TAGACCACTT	1620
20	AATCACTAAA TATCTTTGCC TATAGGACTC CATTGAATAC ATTAGCCATT GATAATCTAC	1680
	CTGTTTAAAT GGCCCTGTGT TGAACCTCA AGCTTTGAAG ACCTACCTGT TCTTCCAGAA	1740
25	GAGAACGTTG AAAGTGCCAT GTTTCCTTTT GCGTGATCTC TGTTGATGGC ACTCTGGAAT	1800
	TGTTTCCAGT TTAAKTCATT TTAGACATAG CATTATATTAT CACTGTGGAT CTCTACTTGT	1860
	TGGGTGTTAT GAATTCCTTG AAGAATATAT TTTGAAGAGG TGTGGGAGGA AGGAATACAT	1920
30	TTTATAAAAT GTTGTAGTGA AGCCCAACAAT TGACCTTKGA CTAATAGGAG TTTTAAGTAT	1980
	GTAAAAATC TATACTGGAC AGTTACAAGA AATTACCGGA GAAAAGCTTG TGAGCTCACC	2040
35	AAACAAGGAT TTCAGTGTAG ATTTTGTCTT TCTTGAACCT AAAGAAACAA ATGACAAAGT	2100
	TTGAATGGAA AAGCTGCTG TTGTTCCACA TCTCGTTGCT GTTTACATTC CTTTGTGGAG	2160
	CCTACATCTT CCTAAGCTTT TTAGCAGGTA TATGTTGAAC ACTTCTGTTT CATGGTTGAG	2220
40	ACAGAATCAG AGGCCATGGA TACTGACAAC TGATTGTGCT GTTTTTTTTC TCTGTCTTTT	2280
	TCCATGACTC TTATATACTG CCTCATCTTG ATTTATAAGC AAAACCTGGA AAACCTACAA	2340
45	AATAAGTGT GTGGTTTATC TAGAAAAATA TGGAAAATAT TGCTGTTATT TTTGGTGAAG	2400
	AAAATCAATT TTGTATAGTT TATTTCAATC TAAATAAAAT GTGAATTTTG TTWWATTAAA	2460
	AATTWGSAC AAABTBGHGG GGGDTCCAAA CHTWVTCGHG KAAMTCTCT WAARMATYTK	2520
50	ATAAACMSCT TCACAATTC	2539

55 (2) INFORMATION FOR SEQ ID NO: 110:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1751 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

60

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 110:

5	AGCATGAAGC CGATGGCCGT GGTGGCCAGT ACCGTCCTGG GCCTGGTGCA AAACATGGGT	60
	GCGTTTGGCG GGATCCTGGT GGTGGTCTAC TACGTATTG CCATCATTGG GATCAACTTG	120
	TTTAGAGGCG TCATTGTGGC TCTTCCTGGA AACAGCAGCC TGGCCCTGC CAATGGCTCG	180
10	GCGCCCTGTG GGAGCTTCGA GCAGCTGGAG TACTGGGCCA ACAACTTCGA TGACTTTGCG	240
	GCTGCCCTGG TCACTCTGTG GAACTTGATG GTGGTGAACA ACTGGCAGGT GTTCTTGAT	300
15	GCATATCGGC GCTACTCAGG CCCGTGGTCC AAGATCTATT TTGTATTGTG GTGGCTGGTG	360
	TGCTCTGTCA TCTGGGTCAA CCTGTTCTG GCCCTGATTC TGGAGAACTT CCTTCACAAG	420
	TGGGACCCCC GCAGCCACCT GCAGCCCCCT GCTGGGACCC CAGAGGCCAC CTACCAGATG	480
20	ACTGTGGAGC TCCTGTTTCTG GGATATTCTG GAGGAGCCCG GGGAGGATGA GCTCACAGAG	540
	AGGCTGAGCC AGCACCCGCA CCTGTGGCTG TGCAGGTGAC GTCCGGGCTG CCATCCCAGC	600
25	AGGGGCGGCA GGAGAGAGAG GCTGGCCTAA CACAGGTGCC CATCATGGAA GAGGCGGCCA	660
	TGCTGTGGCC AGCCAGGCAG GAAGAGACCT TTCTCTGAC GGACCACTAA GCTGGGGACA	720
	GGAACCAAGT CCTTTGCGTG TGGCCCAACA ACCATCTACA GAACAGCTGC TGGTGCTTCA	780
30	GGGAGCGGCC GTGCCCTCCG CTTTCTTTTA TAGCTGCTTC AGTGAGAAIT CCCTCGTCGA	840
	CTCCACAGGG ACCTTTTCTG CAAAATGCA AGAAGCAGCG GCCTCCCCCTG TCCCCCTGAG	900
35	CTTCGGTGGT GCCTTTGCTG CCGGCAGCCC TTGGGGACCA CAGGCCTGAC CAGGGCCTGC	960
	ACAGGTTAAC CGTGAGTCTG TCTCATCTAT TCACAGCTGG GAATGATACT AATACCTCCG	1020
	ATTTTAGCCC AGCACCACAG GGTACGTTCC AGTTTTCTC TCTTTCCATA GCTGTAAGGC	1080
40	CCTTTCTGGG AATGGTCTC ATTCTCCTTA ATCTATTATT GGGTCAGTTT TCCTGCATGT	1140
	CCCCAGCCTC CCATCACTGC CACCCACTCC CCACAGAGAT GCCCTGCTCA TCCGACTGGG	1200
45	GCTTTGACTC CCACACTGTG TACCCCTCTT GTGTGGACGC CCGCTGCCA AAACCTTCAG	1260
	CAAACAGCTT TCCAAATGGA AGTTGTCACT GTCAGGCCTT TACAATCAGC AACAGCAAAA	1320
	TCTACATGCT GCTGAGGGTC CTGCCTCATT AAGATGCAAT AAATATGTAA GTACATAAAA	1380
50	ACAGCAATAG AAGAAACGTA ATGCTTTATT CTCAAATATG ATGTCTACAT AGAAAAGCCA	1440
	AAATTATTAA GAATAGTAAG AATTACCCCA GCACTTTGGG AGGCCGAGGC GGGTGGATCA	1500
55	TGAGGTCAGG AGATCGAGAC CATCTGGCT AACAGGGTGA AACCCGCTCT CTAATAAAAA	1560
	TACAAAAAAT TGGCCGGGCG CAGTGGCGGG CGCCTGTGGT CCCAGCTACT GGGGAGGCTG	1620
60	AGGCAGGAGA ATGGCGTGAA CCCGGGAAGC GGAGCTTGCA GTGAGCCGAG ATTGCGCCAC	1680

TGCAGTCCGC AGTCCAGCCT GGGCGACAGA GCGAGACTCC GTCTCAAAA AAAAAAAAAA 1740
AAAAAAAAA A 1751

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(2) INFORMATION FOR SEQ ID NO: 111:

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(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1117 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 111:

AATGTTGTGG TGGTAGCATT TGGGTTAATT CTRATTATAG AGTCTCTTGG AGAGCAATGT 60
20 CCATAAACTA ATCCCAAACA ACATTGCTCTT TTTRATGTTG TAGTGAACAG CAGAGAATTT 120
CAAAGGACCT TGCTAATATC TGTAAGACGG CAGCTACAGC AGGCATCATT GGCTGGGTGT 180
ATGGGGGAAT ACCAGCTTTT ATTCAATGCTA AACACAATA CATGAGCAG AGCCAGGCAG 240
25 AAATTTATCA TAACCGGTTT GATGCTGTGC AATCTGCACA TCGTGTGCC ACACGAGGCT 300
TCATTCTGTTA TGGCTGGCGC TGGGTTGGA GAACTGCACT GTTGTGACT ATATTCAACA 360
30 CAGTGAACAC TAGTCTGAAT GTATACCGAA ATAAAGATGC CTTAAGCCAT TTTGTAATG 420
CAGGAGCTGT CACGGGAAGT CTTTTTAGGA TAAACGTAGG CCTGCGTGGC CTGGTGGCTG 480
GTGGCATAAT TGGAGCCTTG CTGGGCACTC CTGTAGGAGG CCTGCTGATG GCATTTCAGA 540
35 AGTACTCTGG TGAGACTGTT CAGGAAAGAA AACAGAAGGA TCGAAAGGCA CTCCATGAGC 600
TAAAACTGGA AGAGTGGAAA GGCAGACTAC AAGTTACTGA GCACCTCCCT GAGAAAATTG 660
40 AAAGTAGTTT ACAGGAAGAT GAACCTGAGA ATGATGCTAA GAAAATTGAA GCACTGCTAA 720
ACCTTCCTAG AAACCTTCA GTAATAGATA AACAGACAA GGACTGAAAG TGCTCTGAAC 780
TTGAAACTCA CTGGAGAGCT GAAGGGAGCT GCCATGTCCG ATGAATGCCA ACAGACAGGC 840
45 CACTCTTTGG TCAGCCTGCT GACAAATTTA AGTGCTGGTA CCTGTGGTGG CAGTGGCTTG 900
CTCTTGCTTT TTTCTTTTCT TTTTAACTAA GAATGGGGCT GTTGTACTCT CACTTTACTT 960
50 ATCCTTAAAT TTAAATACAT ACTTATGTTT GTATTAATCT ATCAATATAT GCATACATGA 1020
ATATATCCAC CCACCTAGAT TTAAAGCAGT AAATAAACA TTTCGCAAAA GATTAAAGTT 1080
55 GAATTTTACA GTTAAAAAAA AAAAAAAAAA AAAAAA 1117

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(2) INFORMATION FOR SEQ ID NO: 112:

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(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1313 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 112:

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GGCAGAGGTT TTCTTATATT TTAAGTAAAT TTAAAGTGGC TATCAGAATA TTTATTCTTG 60
TTTGAGACTA CCAACATAAC TACGTGTTGA AGGTGCTTCA CAGAGAATAT ATTGCCTTTA 120
ATGTGAAATA ATTTTCACCA ATGTTGCTAA CTTTAATAAA GTATAAAAT TGTAGAATAT 180
TCAGTTAAGT AGTTGGTAAC CCTTTCTAT TTTAGTAAAA CTTAATGCAT GTTTACTTTT 240
TTTTGAAAGA TGCAGACAAT CTCTTTGAAC ATGAATTGGG GGCTCTCAAT ATGGCTGCAT 300
TACTACGAAA AGAAGAAAGA GCAAGTCTTC TTAGTAATCT TGGCCCATGT TGTAAGGCGT 360
TGTGCTTCAG ACGGGAATTCT GCAATTCGAA AGCAGCTTGT TAAAAATGAG AAGGGCACCA 420
TAAACAAGC TTACACGAGT GCTCCAATGG TAGACAATGA ATTACTTCGA TTGAGTCTTC 480
GGTTATTTAA GCGGAAGACT ACTTGCCATG CTCCAGGACA TGAAAAGACT GAAGATAATA 540
AACTTTCACA GTCCAGTATC CAACAGGAAC TGTGTGTGTC TTAAGACCGA AGTTACAATA 600
TGGTATTTTT GGTACTGTCT TCCTTCAGCA GTGCATATTC TTTTGCAAAG TTCTTTGGTT 660
TGACAAGCAT TAGTGACAAA GGCAGAAAAG ATTTATCAGC CATGCTAAAA GAGTGAAGAA 720
TTTTGATCTT TAGAGACACT AGTTTGGCC AACTTAAGAT TTTACGTTAA TTTTACATA 780
GTATTTGACA CTCATGCAAA ATAATGTGAA AACATCTAGA TTTAGTAGTT TATTCTGCGC 840
CTTTTGTTAA AACTGAAGAT TTTGAAAAT GGTGTCACT GCTCTTCCAG CCTATGAATA 900
TTTTTGTAAT ATGGAACCAT GGATTATGT CTGGATCATC CATAAGAAC CAACAATTTT 960
ATTCAAAAAC AATGTGTTCA TCAAAGTAAT TGCTCACATT GTGCAGTACT ATGTTGTACA 1020
GACCACGTGA AAGGAATGC TGGTCTAGCT GGGTGGTAT GTTTATAGGC GAATTTTCAGC 1080
AGAAGGAAGC CAAAATAGTT TTTTCCTTTT GAAAGTTTTT TAAAAATTAT TTCAATGGTC 1140
TTTTTTTAA TTAATATGTG TGCATGTGTA CAATGTATGT TGGGATGTCT TTTGACCCTA 1200
AATGCTTTTT TTGTTATCAG AGATTGTGTA CTATTTTAT TTTTAATAAA TGTATCTTCC 1260
CTTTTMAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAA 1313

(2) INFORMATION FOR SEQ ID NO: 113:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1654 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 113:

5	ACAGGGACAG AATACTTTCT TTCCTTCCTT CAAGTACAAG AAGGCTTTCT CTACCATTTG	60
	CGTCTACACT TTATTTTAAA AGCTATCCTT TTCTAGTAGT ATTTTATCAT GGCAATGGCA	120
10	TGATGACAAC AACAGTCTTT CATTACAGAC TGAAGGGAAG CATGTCCTTA CTTAAAATAG	180
	TTCTGCTACT TTCCCTCCTA TTATAAGGAA ATTTTACAGA TTCTAAAAAT ACCTTAATTT	240
15	TTCTTTGATT TTTATTTTAC CAAGTCACAA ATGTCTTTTT GATGTTTTGA GAATGTTCT	300
	CATAGAATCA CAAATACTGA CATTTCAATTA GATGATTATT TTCCTAGAAT CCCCAAAGAG	360
	CAGTGGCAGT CCATGGCTTG GTTGAAGCTA GAAATTTTCC TGCCCTGGT GACCTGGTAA	420
20	GCCTCCTGCT CGGAACCGTG TGAGTGGGTG AGGAAGATGA GAGATGGTCA GATGGAAGAG	480
	AGRAATACAT GAACTGCTCT GGCCTCTCTG GTTCTGTTCT TGGCCAGAG TTTTGA AAA	540
	GCAGCGGANA TNGACTGACT TCACATGCTC AGCTTTCTCA GCCTTTTGTT TATTTGTTG	600
25	TCCTTAGATT TCCCTGTTGT AAAAGGGCA AGAAAAGTAA CTCATCATCT CTAACACACC	660
	ATGGCAGCTT AGCCAGGTAG TCTTAGTGGT GGTGTTTAGG CATAAGATAT GCTGATCATC	720
30	AGTCTCAGGC CACAGTTTCC TTCACTAATC GTCCAGCTTG AGTGTCTGT TCTCTTCCTG	780
	CCCATTTCTT TGAACCTCCT GCTCTAGCCT TGGCGGAGGG AGAGTGCTAT TTGCTTTTGT	840
35	TCTCCCTCTG TCTTAGGAAA AGCCATCTTT AATATAGTTC TTCACCACTG TTGGGGTTGT	900
	TTTGATGATT TTTTCTCTT CCGAAGAACT CCTGGTTGTT ATGAGATTTT GTATTTTAAT	960
	ACAAATTATT GAATTTTATA AGCTTGTTACA CAATATTTAA TTAGTGTGAA AGGAAACAAA	1020
40	GAATGCAGGA AAAATAATTT AATATCAACC TCAGTTGACA AGGTGCTCAG ATTATTC AAT	1080
	TCGGGATCCT CCTTTTGTTA GGTTTTTGAG ACAACCCTAG ACCTAAACTG TGTCACAGAC	1140
45	TTCTGAATGT TTAGGCAGTG CTAGTAATTT CCTCGTAATG ATTCTGTTAT TACTTTCTTA	1200
	TTCTTTATTC CTCTTCTTC TGAAGATTAA TGAAGTTGAA AATTGAGGTG GATAAATACA	1260
	AAAAGGTAGT GTGATAGTAT AAGTATCTAA GTGCAGATGA AAGTGTGTTA TATACATCCA	1320
50	TTCAAAATTA TGCAAGTTAG TAATTACTCA GGGTTAACTA AATTACTTTA ATATGCTGTT	1380
	GAAYCTACTC TGTTCTCTGG CTAGAAAAAA TTATAAACAG GACTTTGTAG TTTGGGAAGC	1440
55	CAAAATTGATA ATATTCTATG TTCTAAAAGT TGGGCTATAC ATAAATTATT AAGAAATATG	1500
	GATTTTTATT CCCAGGATAT GGTGTTCAAT TTATGATATT ACGCAGGATG ATGTATTGAG	1560
	TAAAATCAGT TTTGTAAATA TGTAAATATG TCATAAATAA ACAATGCTTT GACTTATTTT	1620
60	CAAAAAAAA AAAAAATAAA NTTCGAGGGG GGCC	1654

5 (2) INFORMATION FOR SEQ ID NO: 114:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 1171 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 114:

15 GGCAAACTTT CCCCAANGC TTCGAAACTT GCAAGCCGAA ACCTTGAATC GTTAAAAGTT 60
GGGTTGCGNC GCGGCCCTGG CCCGAAGAAG CGCAATTGGC GTTCCGCGAA CGTTGGCCCT 120
CAACGGCTCG GCAGCCAGCC ATGTCTCGCA CCCAGGACAG CGGCCCTGGG CTACAAGGAC 180
20 CTGGMCCICA TCTTCTGCG CCGACCTGCG CGGGTAAGG GGWAGTTTCA GACTGTGAAG 240
GACGTCGTGC TGGACTGCCT GTTGGACTTC TTACCCGAGG GGGTGAACAA AGAGAAGATC 300
25 ACACCACTCA CGCTCAAGGA AGCTTATGTG CAGAAAATGG TTAAAGTGTG CAATGACTCT 360
GACCGATGGA GTCTTATATC CTTGTCAAAC AACAGTGGCA AAAATGTGGA ACTGAAATTT 420
GTGGATTCCC TCCGAGGCA GTTTGAATTC AGTGTAGATT CTTTCAAAT CAAATTAGAC 480
30 TCTCTTCTGC TCTTTTATGA ATGTTTCAGAG AACCCAATGA CTGAGACATT TCACCCACA 540
ATAATCGGG AGAGCGTCTA TGGCGATTTC CAGGAAGCCT TTGATCACCT TTGTAACAAG 600
35 ATCATTGCCA CCAGGAACCC AGAGGAAATC CGAGGGGAG GCCTGCTTAA GTACTGCAAC 660
CTCTTGGTGA GGGGCTTTAG GCGCCCTCT GATGAAATCA AGACCTTCA AAGGTATATG 720
TGTTCCAGGT TTTTCATCGA CTCTCAGAC ATTGGAGAGC AGCAGAGAAA ACTGGAGTCC 780
40 TATTTGCAGA ACCACTTTGT GGAATTTGGA AGACCGCAAG TATGAGTATC TCATGACCCT 840
TCATGGAGTG GTAAATGAGA GCACAGTGTG CCTGATGGGA CATGAAAGAA GACAGACTTT 900
45 AAACCTTATC ACCATGCTGG CTATCCGGGT GTTAGCTGAC CAAAATGTCA TTCCTAATGT 960
GGCTAATGTC ACTTGCTATT ACCAGCCAGC CCCCTATGTA GCAGATGCCA ACTTTAGCAA 1020
TTACTACATT GCACAGGTTT AGCCAGTATT CACGTGCCAG CAACAGACCT ACTCCACTTG 1080
50 GCTACCCTGC AATTAAGAAT CATTTAAAAA TGTCTGTGG GGAAGCCATT TCAGACAAGA 1140
CAGGAGAGAA AAAAAAAAAA AAAAAAAAAA A 1171

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(2) INFORMATION FOR SEQ ID NO: 115:

60 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 842 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 115:

	GGTCTGCGCC GGAAGTGCAT GAGCTGCCGA TGTGGTGCTT AGTGATTGCG GTTTCGGTCG	60
10	CTCTCCCGTG TTTCCCGGGC TGGGTATTTG CCTCGCACCA TGGCGCCCAA GGGCAAAGTG	120
	GGCAGCAGAG GGAAGAAGCA GATATTTGAA GAGAACAGAG AGACTCTGAA GTTCTACCTG	180
	CGGATCATAC TGGGGGCCAA TGCCATTAC TGCCTTGTA CGTTGGTCTT CTTTACTCA	240
15	TCTGCCTCAT TTTGGGCCTG GTTGGCCCTG GGCTTTAGTC TGGCAGTGTA TGGGGCCAGC	300
	TACCACTCTA TGAGCTCGAT GGCACGAGCA GCGTCTCTG AGGATGGGGC CCTGATGGAT	360
20	GGTGGCATGG ACCTCAACAT GGAGCAGGGC ATGGCAGAGC ACCTTAAGGA TGTGATCCTA	420
	CTGACAGCCA TCGTGCAGGT GCTCAGCTGC TTCTCTCTCT ATGTCTGGTC CTTCTGGCTT	480
	CTGGCTCCAG GCCGGGCCCT TTACCTCCTG TGGGTGAATG TGCTGGGGCC CTGGTTCACT	540
25	GCAGACAGTG GCACCCAGC ACCAGAGCAC AATGAGAAAC GGCAGCGCCG ACAGGAGCGG	600
	CGGCAGATGA AGCGTTATA GCCATGACA TTGTGGCCAC AGGCCACTGG CCCTGGGTGG	660
30	CTCTGTCAGG GTGCACAGCC CCTCATGCCT GGAGCAATGA GGGTCTAGTC CAGGGGCCAA	720
	AAGCAGTCTG AGGTATTGGG TATACTTATA CTCTATAGGG TCGTTGAATA AATGGCTTAG	780
35	AATGTGAAAA AAAAAAAAAA AAAAACTCG AGGGGGGCC GGTACCCAAT TTCNCCTANA	840
	AT	842

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(2) INFORMATION FOR SEQ ID NO: 116:

(i) SEQUENCE CHARACTERISTICS:

45

(A) LENGTH: 1640 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 116:

	GGCAGAGGC GGCGCAGCG GTGGCGCGG CGCCCCCGG CGGGAGCCGT TCCCTTTCCC	60
	GTCGGGGAGC GCGGGGYCGG GGCCAGGGG ACCCGGGCC ACGGAGAGCG GGAAGAGGAT	120
55	GGATTGCCCG GCCCTCCCC CCGATGGAA GAAGGAGGAA GTGATCCGAA AATCTGGGCT	180
	AAGTGCTGGC AAGAGCGATG TCTACTACTT CAGTCCAAGT GGTAAGAAGT TCAGAAGCAA	240
60	GCCTCAGTTG GCAAGGTACC TGGGAAATAC TGTGATCTC AGCAGTTTGT ACTTCAGAAC	300

	TGGAAAGATG ATGCCTAGTA AATTACAGAA GAACAAACAG AGACTGCGAA ACGATCCTCT	360
	CAATCAAAAT AAGGGTAAAC CAGACTTGAA ATACAACATT GCCAATTAGA CAAACAGCAT	420
5	CAATTTTCAA ACAACCGTA ACCCAAAGTC ACAAATCATC CTAGTAATAA AGTGAAATCA	480
	GACCCACAAC GAATGAATGA ACAGCCACGT CAGCTTTTCT GGGAGAAGAG GCTACAAGGA	540
10	CTTTAGTGCA TCAGATGTAA CAGAACAAAT TATAAAAACC ATGGAACCTAC CCAAAGGTCT	600
	TCAAGGAGTT GGTCCAGTAG CAATGATGAG ACCCTTTTAT CTGCTGTTGC CAGTGCTTTG	660
	CACACAAGCT CTGCGCCAAT CACAGGGCAA GTCTCCGCTG CTGTGGAAAA GAACCTGCTG	720
15	TTTGGCTTAA CACATCTCAA CCCCTCTGCA AAGCTTTTAT TGTACAGAT GAAGACTCAG	780
	GAAACAGAAG AGCGAGTACA GCAAGTACGC AAGAAATTGG AAGAAGCACT GATGGCAGAC	840
20	ATCTTGTCGC GAGCTGCTGA TACAGAAGAG ATGGATATTG AAATGGACAG TGGAGATGAA	900
	GCCTAAGAAT ATGATCAGGT AACTTTTCGAC CGACTTTCCC CAAGAGAAAA TTCCTAGGAA	960
	ATTGAACAAA AATGTTTCCA CTGGCTTTTG CCTGTAAGAA AAAAAATGTA CCCGAGCACA	1020
25	TAGAGCTTTT TAATAGCACT AACCAATGCC TTTTATAGATG TATTTTIGAT GTATATATCT	1080
	ATTATTCAAA AAATCATGTT TATTTTGAGT CCTAGGACTT AAAATTAGTC TTTTGTAATA	1140
30	TCAAGCAGGA CCCTAAGATG AAGCTGAGCT TTTGATGCCA GGTGCAATCT ACTGGAAATG	1200
	TAGCACTTAC GTAAACATT TGTTCCTCCC ACAGTTTAA TAAGAACAGA TCAGGAATTC	1260
	TAAATAAATT TCCCAGTTAA AGATTATTGT GACTTCACTG TATATAAACA TATTTTATA	1320
35	CTTTATTGAA AGGGGACACC TGTACATTCT TCCATCGTCA CTGTAAAGAC AAATAAATGA	1380
	TTATATTCCA CAGAAAAAA AAAAAAAAW MWSTYGARRR GSRGCMCRSW AYMMARWCC	1440
40	CCWMRIWRGS MKTCSMTKA YTTACATTCA ACTCTGATCC CGGGGCCTTA GGTTTGACAT	1500
	GGGAGGTGGG AGGAAGATAG CGCATATATT TGCAGTATGA ACTATTGCCT CTGGGACGTT	1560
	GTGAGGAATT GTGCTTTCAC CAGAAATTCT AAGGATTCTT GGCTTAAATA TCACCTAGCC	1620
45	TGTGGTAATT TTTTTCCTCT	1640

50 (2) INFORMATION FOR SEQ ID NO: 117:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 952 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 117:

60 TGAATTTAGN AAACACTTTG GAAAACTCAT AACCTCATCA GAAACTGCCT TTAGCCACAC 60

	TCCTGACCTT CTAGATGAGT AACAAAAAA TGAAATAAGT TCCTGGAAAT TAAGCCATTT	120
5	ATTTTAATTT GCTATTTTTC TCAATGTTCT AGGTATCTTT AAATTTGTTA TTGTGGAATC	180
	ATTTTCCTGC CAGATACCTT TATCAAAAT ATTGGCCTCA TGAGAGCTGA AGTAAGTCAG	240
	CTTTTGGTG AACTTTAGTG GACTTCTGTG AGATTGTAGT TGTACTTTGT ATCTCTAAAT	300
10	CTAAAGATAG TTTTAAAA CTCCCAAAGA AAATCTGCTC TCCTTTCTGA TCTAAAACT	360
	CATCTTTGGG GTAAAGAGTT AAGTGTCCTA AGTTGTCTAC AGTTCATGAG GTCAGAGGGA	420
15	GCTAGCCTGG CACCTGGACT CTGCCATCC ACAGCTGACA GATTCACA GAAGTGATTT	480
	TAAATTCCTC AGTAGACAAT GCTGGGTAAG GGAGGGGTA GGGCTGGGTT ATTAAGATAC	540
	AGGCTGCTGT ATTTTACATT GGTGTGGGG GAAGGGGAGC CTGGAGAAAA CAAAGTCACT	600
20	ATTCCTTTT TTGAACAGG AAAAAAAT ATTTTGTGT CAGTAAAAAT GGTAGAGAAT	660
	TCCAATGTCC CTAGCCACAA GGGACCAGTT CCACTGAGAA GTGAACAGTG GGAACCAAA	720
25	ATTTTCAGAA CATTTGGGGA AGGGAATAAT GGCTTCTCT TAATTGGCAG ATGTTCCAGT	780
	GGGSGGGG GGCTCTGTT TTGTTGGGAT GTGTTATGTT GTATGTACGC ATATATGGAC	840
	CGGAGTCTGC TGAGTTTATA AGGTTCCAAA AATATGGTAA AATCTTGGTT TTTGTTAATT	900
30	TATCTCAATA AAAGCCCACT GGRACCTCAA AAAAAAAGA AAAAAAAGA NN	952

35 (2) INFORMATION FOR SEQ ID NO: 118:

(i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 1256 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 118:

45	GACGTCATAG GTAAACAGGC TCTGTATCCG TGGCAGCGC CGTGGCAGGC TGGCTGGGTA	60
	CCGGCTGTGC CTGACCCAGG AGAAGCTGCC TGTCTACATC AGCCTGGGCT GCAGCGCGCT	120
50	GCCGCCGCGG GGCCGGCAGC TGAACATATGT GCTCTTCAGG GCGGCACCG TGTTCATTC	180
	ATCTTTGTAC CCCCAGCATC TAGCAGTGTT GGATGTAGT AGGCACTCAA GAAATGTGTG	240
	TTGAATGAAC GATGCCTGTG ACAAGCAAGC GGACTTTATT CTTTCCTGAC CCTTGTCTCT	300
55	ATGACACACC TCCTCCTGAC TGCCACTGTC ACTCCTTCAG AGCAGAACTC CTCTAGGGAA	360
	CCTGGATGGG AAACAGCCAT GGCCAAGGAC ATCCTGGGTG AAGCAGGGCT ACACTTTGAT	420
60	GAAGTGAACA AGCTGAGGGT GTTGGACCCA GAGGTTACCC AGCAGACCAT AGAGCTGAAG	480

GAAGAGTGCA AAGACTTTGT GGACAAAATT GGCCAGTTTC AGAAAATAGT TGGTGGTTTA 540
 ATTGAGCTTG TTGATCAACT TGCAAAAGAA GCAGAAAATG AAAAGATGAA GGCCATCGGT 600
 5 GCTCGGAACT TGCTCAAATC TATAGCAAAG CAGAGAGAAG CTCAACAGCA GCAACTTCAA 660
 GCCCTAATAG CAGAAAAGAA AATGCAGCTA GAAAGGTATC GGGTTGAATA TGAAGCTTTG 720
 10 TGTAAAGTAG AAGCAGAACA AAATGAATTT ATTGACCAAT TTATTTTCA GAAATGAACT 780
 GAAAATTTTCG CTTTATAGT AGGAAGGCAA AACAAAAAA AGCCTCTCAA AACCAAAAA 840
 ACCTCTGTAG CATTCCAGCG GCTTGACCAA TGACCTATGT CACAAGAGGT GGCGTGTAA 900
 15 GAATGCAGCC CCTGAAGAC AGCACTACAA GTCTGGGGGA GCCAGTTTCA ACATCAGTGC 960
 ACAGCTGCTG CTGGTGGCCC TGCAGTGAC GTTCTCACCT CTTATGCTTA GTTGGAAC 1020
 AGCAGTTTGT AAACCTTTCAT CCTTTTTC GTAAATTCAC AAAGCTTTGG AAGGAGAAGC 1080
 20 AATAAATTTT TGTTTTCAA TGCTTGATG TACCTTTTCT CCTGTGCTC TTGAAATATG 1140
 TTTAACTCCT CATGAGAGAA CCCTGGATTG TCTATCCCCT AGTCCACAAA ACAAAACCAGG 1200
 25 CAGTGGTCAG CAGCTACCTT TNATTTGGAT CACACACGTG AGTCAGACAG TACCAC 1256

30 (2) INFORMATION FOR SEQ ID NO: 119:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1143 base pairs

(B) TYPE: nucleic acid

35 (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 119:

40 GGCCGTAGCA GCCGGGCTGG TCCTGCTGCG AGCCGGCGGC CCGAGTGGG GCGCGGCAT 60
 GTACCTTCCA CATTGAGTAT TCAGAAAGAA GTGATCTGAA CTCTGACCAT TCTTTATGGA 120
 TACATTAAGT CAAATATAAG AGTCTGACTA CTTGACACAC TGGCTCGAGC AAACATGAAC 180
 45 GTTGGAGTTG CCCACAGTGA AGTGAATCCA AATACCCGTG TCATGAACAG CCGGGGTATG 240
 TGGCTGACAT ATGCATTGGG AGTTGGCTTG CTTCATATTT TCTTACTCAG CATTCCTTC 300
 50 TTCAGTGTC CTGTTGCTTG GACTTTAACA AATATTATAC ATAATCTGGG GATGTACGTA 360
 TTTTTCATG CAGTGAAAGG AACACCTTTC GAACTCCTG ACCAGGGTAA AGCAAGGCTC 420
 CTAATCATT GGAACAACCT GGACTATGGA GTACAGTTTA CATCTTCACG GAAGTTTTTC 480
 55 ACAATTTCTC CAATAATTCT ATATTTCTG GCAAGTTTCT ATACGAAGTA TGATCCAAC 540
 CACTTCATCC TAAACACAGC TTCTCTCTG AGTGACTAA TTCCAAAAT GCCACAAC 600
 60 CATGGTGTTG GGATCTTTGG AATTAATAAG TATTGAAATG TTTTGAAACT GAAAAAAT 660

	TTTACAGCTA CTGAATTTCT TATAAGGAAG GAGTGGTTAG TAAACTGCAC TGTTCCTSTG	720
5	ATAATGTGAA ATGAGAAGTA TTTACATTGG AGGGCCAATG GCTGGTCCTT CAAGTGCTGT	780
	TTTGAAGTGC AGATTTCAT TAAATGATGC CTCTGTTTAA TACACCTGGT ACATTTCTGA	840
	AGAGGGGCTT TATAAGCAGG CTGGGCAGGC CCAGCTTATA AGTTAAAGGG CATCACAGTG	900
10	AGGGTGTAGT AGATAAATTC AAGGAAATAA GAGATTTGTA AGAACTAGG ACCAGCTTAA	960
	CTTATAATGA ATGGGCATTG TGTTAAGAAA AGAACATTTC CAGTCATTCA GCTGTGGTTA	1020
15	TTTAAAGCAG ACTTACATGT AAACCGAAT CCTCTCTATA CAAGTTTATT AAAGATTATT	1080
	TTTATTACCG TAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA	1140
	GAN	1143

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(2) INFORMATION FOR SEQ ID NO: 120:

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- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1782 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 120:

	CAGGCCCCGG CCCCCACCC ACGTCTGCGT TGCTGCCCCG CCTGGGCCRG GCCCCAAAGG	60
35	CAAGGACAAA GCAGCTGTCA GGAACCTCC GCCGAGTCG AATTTACGTG CAGCTGCCGG	120
	CAACCACAGG TTCCAAGATG GTTTGCGGGG GCTTCGCGTG TTCCAAGAAC TGCCTGTGCG	180
40	CCCTCAACCT GCTTTACACC TTGGTTAGTC TGCTGCTAAT TGGAATTGCT GCGTGGGGCA	240
	TTGGCTTCGG GCTGATTTCC AGTCTCCGAG TGGTCGGCGT GGTCAATTGCA GTGGGCATCT	300
	TCTGTTCCT GATGCTTTA GTGGTCTGA TTGGAGCTGT AAAACATCAT CAGGTGTTC	360
45	TATTTTMTTA TATGATTATT CTGTTACTTG TATTTATTGT TCAGTTTCT GTATCTTGCG	420
	CTTGTTTAGC CCTGAACCAG GAGCAACAGG GTCAGCTTCT GGAGTTGGT TGGAACAATA	480
50	CGCAAGTGC TCGAAATGAC ATCCAGAGAA ATCTAACTG CTGTGGGTC CGAAGTGTTA	540
	ACCCAAATGA CACCTGTCTG GCTAGCTGTG TTTAAAGTGA CCACTCGTGC TCGCCATGTG	600
	CTCCAATCAT AGGAGAATAT GCTGGAGAGG TTTTGAGATT TGTGTTGGC ATTGGCCTGT	660
55	TCTTCAGTTT TACAGAGATC CTGGGTGTTT GGCTGACCTA CAGATACAGG AACCAGAAAG	720
	ACCCCCGCGC RAATCCTAGT GCATTCTTTT GATGAGAAAA CAAGGAAGAT TTCCTTTGCT	780
60	ATTATGATCT TGTTCACTTT CTGTAATTTT CTGTTAAGCT CCATTGCCA GTTTAAGGAA	840

GGAAACACTA TCTGGAAAAG TACCTTATTG ATAGTGAAT TATATATTTT TACTCTATGT 900
 TTCTCTACAT GTTTTTTTCT TTCCGTGCT GAAAAATATT TGAAACTTGT GGTCTCTGAA 960
 5 GCTCGGTGGC ACCTGGGAAT TTACTGTATT CATGTGCGG CACTGTCCAC TGTGGCCTTT 1020
 CTTAGCATTT TTACCTGCAG AAAAAGTTTG TATGGTACCA CTGTGTTGGT TATATGGTGA 1080
 ATCTGAACGT ACATCTCACT GGTATAATTA TATGTAGCAC TGTGCTGTGT AGATAGTTCC 1140
 10 TACTGGAAAA AGAGTGGRAA TTTATTAAAA TCAGAAAGTA TGAGATCCTG TTATGTTAAG 1200
 GGAAATCCAA ATTCCCAATT TTTTGTGGTC TTTTAGGAA AGATGTGTG TGGTAAAAAG 1260
 15 TGTTAGTATA AAAATGATAA TTWACTKGTA GTCTTTTATG ATWACACCAA TGTATTCTAG 1320
 AAATAGTTAT GYCYTAGGAA ATTGTGGTTT AATTTTGTAC TTTTACAGGT AAGTGCAAAG 1380
 GAGAAGTGGT TTCATGAAAT GTTCTAATGT ATAATAACAT TTACCTTCAG CCTCCATCAG 1440
 20 AATGGAACGA GTTTTGAGTA ATCAGGAAGT ATATCTATAT GATCTTGATA TTGTTTTATA 1500
 ATAATTTGAA GTCTAAAAGA CTGCATTTTT AAACAAGTTA GTATTAAATGC GTTGGCCAC 1560
 25 GTAGCAAAAA GATATTTGAT TATCTTAAAA ATTGTTAAAT ACCGTTTCA TGAAAGTTCT 1620
 CAGTATGTA ACAGCAACIT GTYAAACCTA AGCATATTTG AATATGATCT CCCATAATTT 1680
 GAAATTGAAA TCGTATTGTG TGGCTCTGTA TATTCTGTTA AAAAATTAAA GGACAGAAAC 1740
 30 CTTCCTTTGT GTATGCATGT TTGAATTAAA AGAAAGTAAT GG 1782

35

(2) INFORMATION FOR SEQ ID NO: 121:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 610 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 121:

45

GTTGGCTGCA GATTTGTGGT GGTTCCTGAG CCGTCTGTCC TGCGCCAAGA TGCTTCAAAG 60
 TATTATTAAA AACATATGGA TCCCATGAA GCCCTACTAC ACCAAAGTTT ACCAGGAGAT 120
 50 TTGGATAGGA ATGGGGCTGA TGGGCTTCAT CGTTTATAAA ATCCGGGCTG CTGATAAAAG 180
 AAGTAAGGCT TTGAAAGCTT CAGCGCTGC TCCTGGTCAT CACAACCAGA TTTACTTGGA 240
 GTACATGTA AAGAAAACGT CAGTCTGCCT GTAAATTTC AAGAGCCGTG TTAGATGGGG 300
 55 AGCGTGGAAC GTCACGTAC ACTGTATATA GTACCGTTTA CTTCATGGCA TGAATAAATG 360
 GATCTGTGAG ATGCACTGCT ACCTGGTACT GCTTTCAGTG TGTCCCCCT CAGCCCTCCG 420
 60 GCGTGTCAAG CATACTCTGA GTAGATAATT TGTATGCAG CGCATGCAAT CAGAATCTCA 480

CTGAGCCACC CATCATTTGT AAATAATTAC CTCAGTTGTA CAGGACTTGG TGATCAGGAT 540
 5 CCAGGCACTC ACTTGTATTC TACTGCTCAA TAAACGTTTA TTAAACTTGA AAAAAAAAAA 600
 AAAAAAAAAA 610

10

(2) INFORMATION FOR SEQ ID NO: 122:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 526 base pairs
 15 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 122:

GGTACGCCTG CAGGTACCGG TCCGGAATTC CGGGTCGCCC ACGGTCNGG CCACGCGTCC 60
 ACCCAGCGGT CCGSCCAGCG GTCGGAGCCG AGCCGGACTG GTCAGGATGA TCACGGACGT 120
 25 GCAGCTCGCC ATCTTCGCCA ACATGCTGGG CGTGTGCTC TTCTTGCTTG TCGTCTCTA 180
 TCACTACGTG GCCGTCAACA ATCCAAGAA GCAGGAATGA AAGTGGCGCT TTCTCCGCCC 240
 CAGGGTTCCA GGACATAGTC TGAGGCAAGA TGGAGGTAT GAGGGGCCTT CACACTTCAC 300
 30 TTCATCCCTT CTACCCATCA CAACATACAA AGCAACTACA CCTGGATTTT TCCAAACAAC 360
 TTTTATTTCC TCAGAGTCTT CCTTAATCCT ATGGAACAAG AAGCTGCCAC TGAATAGGGC 420
 35 CCAGTATAGG GGCTTGCTTT TCTACTCCCT CCCCCAATA TAAAATATA GACTTTTTAA 480
 AAAAAAAAAA AAAAANTTCG NGGGGGGSCC GGTACCCATC CCCCTA 526

40

(2) INFORMATION FOR SEQ ID NO: 123:

(i) SEQUENCE CHARACTERISTICS:
 45 (A) LENGTH: 2081 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 123:

TGTACCGGTC CGGAAATTCC CGGGTCGACC CACGTCGTCS GGGGAACATG GCGGCTKCGG 60
 AGCCGGCGGT CCTTGCCTC CCCAACAGCG GCGCCGGGGG CGCGGGGGCG CCGTCGGGCA 120
 55 CAGTCCCGGT GCTCTTCTGT TTCTCAGTCT TCGCGGACC CTCGTCGGTG CCACACGGGG 180
 CGGGCTACGA GCTGCTCATC CAGAAGTTCC TCAGCCTGTA CGGCGACCAG ATCGACATGC 240
 60 ACCGCAAATT CGTGGTGAG CTGTTGCGCG AGGAGTGGGG CCAGTACGTG GACTTGCCCA 300

	AGGGCTTCGC GGTRAGCGAG CGCTGCAAGG TCGCCCTCGT GCCGYTGCAG ATCCAGCTCA	360
5	CTACCCTGGG AAATCTTACA CCTTCAAGCA CTGTGTTTTT CTGCTGTGAT ATGCAGGAAA	420
	GGTTCAGACC AGCCATCAAG TATTTTGGGG ATATTATTAG CGTGGGACAG AGATTGTTGC	480
	AAGGGCCCG GATTTTAGGA ATTCTGTGA TTGTAACAGA ACAATACCCT AAAGGTCTTG	540
10	GGAGCACGGT TCAAGAAATT GATTTAACAG GTGTAAACT GGTACTTCCA AAGACCAAGT	600
	TTTCAATGGT ATTACCAGAA GTAGAAGCG CATTAGCAGA GATTCCCGGA GTCAGGAGTG	660
15	TTGTATTATT TGGAGTAGAA ACTCATGTGT GCATCCAACA AACTGCCCTG GAGCTAGTTG	720
	GCCGAGGAGT CGAGGTTTAC ATTGTTGCTG ATGCCACCTC ATCAAGAAGC ATGATGGACA	780
	GGATGTTTGC CCTCGAGCGT CTCGCTCRAR CCGGGATCAT AGTGACCACG AGTGAGGCTG	840
20	TTCTGCTTCA GCTGGTAGCT GATAAGGACC ATCCAAAATT CAAGGAAATT CAGAATCTAA	900
	TTAAGGCGAG TGCTCCAGAG TCGGGTCTGC TTTCCAAAGT ATAGGACATT TGAAGAACTG	960
25	GTATGCTACT CACTGGTGAA GGACAGTCAG GTGAAGGACT GTAAGCCAC ACAAGCTCTT	1020
	CTTATCTCTA CTAGAATTAA AATGTTAAGT CAAAACCGC TCCTTTTTTG CGCCTCCTAG	1080
	TGAAACTTAA CCAGCTAGAC CATTTGAGTA CCAGCATTTA GTTACAAACG TCAAAGGCTT	1140
30	CCGGTGCTGC TTACCTTCCT TTTTGTGTA TGTGCTTTTA TTTATTAAAA AAAATTACAA	1200
	TGAAGATGCC TGTTTTGTCT CTA CTGTGTGA CTCTGATCGT ATCTTTCCAA AGTGCAGACT	1260
35	CTTGTAAGT TTTCTTAAAT TGTTCACITT AAAGAAAATG ACGTACCAAC AATGATTTGG	1320
	CTTTTATATT ACTGTAAGAT GTTATAATGT TAATGTGGAT GTAGTGCTTT TACTTTACAG	1380
	ATTGATTGGA ATAAGATTAT TGCATATGAA TTTACCCACA GGACTCTGAA TCATGTTACC	1440
40	CACTCCCCTC ACAATGTTGT CCACTTAGTG AGTTGCATTG ATCTATCCGT ACCAAATGAT	1500
	GTTGAATAAT TACATATCTT TCTTGACTAT ACTGATTTCT TATTTTGGTC ACTATTACTA	1560
45	AATCTCTGTT AATATTCTCT CTTTAACTG AAAAGGGATG GGATAGAAGG GTTTGCAATG	1620
	CCATATTATT GGTGGAGGGC TGTTTAAACA TCTTTGAAGT ATGGCTTGCT GAATATCTTT	1680
	ACCAACATCT TGAATATATA TTCTAGTGTC CACAAGATTT AGCAAAAAGA TAAAGCTTGG	1740
50	GTGGAATATC ATTTTAAAAT GTTCATGTTT TGTTCATAT TTTCTTCACC TACTCTCCAA	1800
	ATATGTGAAT GCAAAAAGTC TCAGTAATGA TTTGGTAGTA TTAATTTTGT GGTCAATGTT	1860
55	TCTCTTCGAT AAATTTATTT TCATTAAATA CTTRITAGAG GGTTTGAAA TGTTTTCAA	1920
	ATATGTGAAA TGTGAAACTG CTGTCTTTTA TATTAAAGTA ATTAAAGAAA ATGTATTGTG	1980
	ATTGAAATTA TTTTGNCCTC CACAAGATGG CTCTATGAGT ATTCTTCCAG GGATTCTAAT	2040
60	ATTTATTTAA GGTNATAAAA TCTTGACATT TATAATCTTT C	2081

5 (2) INFORMATION FOR SEQ ID NO: 124:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 1717 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 124:

15 CCCC GGCGGA GCTGGACCCG CGGTGGGCTA GGGGCAGGGC CGGAGCCGCG GCGGCGGAGC 60
TGTGGATCCT TCATGATGAG AGATTGGGG ACACTTCTCT CTCTGTGTG TAGTTGATAG 120
TTTGGTGGTG AAGAGATGGC TGACAGTGTC AAAACCTTTC TCCAGGACCT TGCCAGAGGA 180
20 ATCAAAGACT CCATCTGGGG TATTGTACC ATCTCAAAGC TAGATGCTCG AATCCAGCAA 240
AAGAGAGAGG AGCAGCGTCG AAGAAGGGCA AGTAGTGTCT TGGCACAGAG AAGAGCCCAG 300
25 AGTATAGAGC GGAAGCAAGA GAGTGAGCCA CGTATTGTTA GTAGAAATTTT CCAGTGTGTG 360
GCTTGAATG GTGGAGTGT TGGTTCAGT CTCTCTTGT TTTATCGAGT ATTTATTCCT 420
GTGCTTCAGT CGGTAACAGC CGAATTATC GGTGACCCAT CACTACATGG AGATGTTTGG 480
30 TCGTGGCTGG AATTCTTCCT CACGTCAATT TTCAGTGCTC TTTGGGTGCT CCCCTGTGTT 540
GTGCTTAGCA AAGTGGTGAA TGCCATTGCG TTTCAGGATA TAGCTGACCT GGCAATTGAG 600
35 GTATCAGGGA GGAAGCCTCA CCCATTCCCT AGTGTGAGCA AAATAATTGC TGACATGCTC 660
TTCAACCTTT TGCTGCAGGC TCTTTTCCTC ATTCAAGGAA TGTGTGTGAG TCTCTTTCCC 720
ATCCATCTTG TCGGTGAGCT GGTAGTCTC CTGCATATGT CCCTTCTCTA CTCACGTGAC 780
40 TGCTTTGAAT ATCGTTGGTT CAATAAAGGA ATTGAAATGC ACCAGCGGTT GTCTAACATA 840
GAAAGGAATT GGCCTTACTA CTTTGGGTTT GGTTTGCCCT TGGCTTTTCT CACAGCAATG 900
45 CAGTCTCAT ATATTATCAG TGGCTGCCTT TTCTCTATCC TCTTTCCCTT ATTCATTATC 960
AGCGCCAATG AAGCAAAGAC CCCTGGCAAA GCRTATCTCT TCCAGTTGCG CCTCTTCTCC 1020
TTGGTGGTCT TCTTAAGCAA CAGACTCTTC CACAAGACAG TCTACCTGCA GTCGGCCCTG 1080
50 AGCAGCTCTA CTCTGCAGA GAAGTTCCTT TCACCGCATC CGTCGCCTGC CAAACTGAAG 1140
GCTACTGCAG GTCAGTGAGT TGCCTGCCAT CCAAAGGGGA TGGGCGGGAT TGGAAGAAGC 1200
55 TGTGGCAGCT CTTTTCCTG TTACCTCCC GCCTGCCAGG GAAGGCAGGA CCCGCTCTGC 1260
CAAGGCCCT CTGCGTATTC CCTTCTCTCT GAGGAATTGA AATTTTGTG TCTGGTGCAC 1320
GTAAGGCAGA ATGTTCCCTG ACACCACTGT GTGGATTTTT AACATCACCG TGAGTCTGAA 1380
60

AGGACCACAG GTTTTCTGTC AGCTATTTTC TAGCATTTGC CAGTCCCTGT GCCTGGACTG 1440
ATTTGGAACAC TTTGTTTTTC TCCCTGTGCC ATTTACCCCT CCACCTTTCC ATCCTGCCTT 1500
5 CTACCACCCT TGGATGAATG GATTTTGTA TTTAGCTGT TGTATTTTGT GAATTTGTTA 1560
ATTTTGTGT TTTCTGTGA AACACATACA TTGGATATGG GAGGTAAAGG AGTGTCCCAG 1620
TTGCTCCTGG TCACTCCCTT TATAGCCATT ACTGTCTGT TTTGTGAAC TCAGGTTAGG 1680
10 TTTTGGTCTC TCTTGCTCCA CTGCAAAAAA AAAAAA 1717

15

(2) INFORMATION FOR SEQ ID NO: 125:

(i) SEQUENCE CHARACTERISTICS:
20 (A) LENGTH: 804 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 125:

CCACGCGTCC GGTCACTATG TAGTGGAGGG GCAGACACCC TCCCGCAAAT TCTGGAAGGT 60
TCTTAGTCTC GACTAGGGCA GTAGCCCCAG GACTCCTAGT CGCCGGCTTC AGGTCACTGC 120
30 CGGCTGAACG GAGCTGCCGT CGCCATGTTT GGCTGCTTGG TGGCGGGGAG GCTGGTGCAA 180
ACAGCTGCAC AGCAAGTGGC AGAGGATAAA TTTGTTTTTG ACTTACCTGA TTATGAAAGT 240
ATCAACCATG TTGTGGTTTT TATGCTGGGA ACAATCCCAT TTCCTGAGGG AATGGGAGGA 300
35 TCTGTCTACT TTTCTTATCC TGATTCAAAT GGAATGCCAG TATGGCAACT CCTAGGATTT 360
GTCACGAATG GGAAGCCAAG TGCCATCTTC AAAATTTTCTG GTCTTAAATC TGGAGAAGGA 420
40 AGCCAACATC CTTTGGAGC CATGAATATT GTCCGAACTC CATCTGTTGC TCAGATTGGA 480
ATTTCACTGG AATTATTAGA CAGTATGGCT CAGCAGACTC CTGTAGGTAA TGCTGCTGTA 540
TCCTCAGTTG ACTCATTCAC TCAGTTCACA CAAAAGATGT TGGACAATTT CTACAATTTT 600
45 GCTTCATCAT TTGCTGTCTC TCAGGCCAG ATGACACCAA GCCCATCTGA AATGTTTCATT 660
CCGGCAAATG TGGTCTGAA ATGGTATGAA AACTTTTCAA GACGACTAGC ACAGAACCCT 720
50 NTNTTTTGGN AAACATAATT TGAATAAAAT AATTTTTAAT GGATTNTGNA AAAAAAAAAA 780
AAAAAAAAA AAAAAAAAAA AAAA 804

55

(2) INFORMATION FOR SEQ ID NO: 126:

(i) SEQUENCE CHARACTERISTICS:
60 (A) LENGTH: 431 base pairs

(B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 126:

	GGCACAGCCC AGGGCCTTGA AGCCAGCTGG CCCTGGAGAG GGGCTGCTGT GCCAGCTTGG	60
	GGAGGGTCTG GGATGGGGCT GCCCTGATG GCCCTGATGT GGAGTACCTT GCCAGCATCT	120
10	GCTGGGGTGA ACTTTATTTT AGCCCTTCCC TTGTGCTCT TATGGAAGAA CAGAGGAGGG	180
	GTGGGCAGGT CAGTGATGTC AGCAGTGGAG TGATTCCCAG CACAGCGGCT TCTGGGAAGA	240
15	GGGCATGGAG GCATTTCTTT CAGGGAAATG GTCCATNATT TCAGCCAGAA GGCATTGCAT	300
	TAAGTTAAGT CCNGGACTTT TGTTGGCCAG CTCTGTGTTA TTAAGGGCCC TTGGCGAAGA	360
	CTTCAAGGAG GGGGCAAAAN GACCTTTAAG TTTTTAGGTT TAACACAGGG AACCCNCAAA	420
20	GGGTATATTT G	431

25

(2) INFORMATION FOR SEQ ID NO: 127:

(i) SEQUENCE CHARACTERISTICS:

	(A) LENGTH: 3752 base pairs
30	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
	(D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 127:

35	NGGCACGAGG AGAGTCACCT GGACTCAGAA CTAGAGATAT CCAATGACCC AGACAAAATT	60
	AAACTTCAGC TTTCTAAGCA TAAGGAGTTT CAGAAGACTC TTGGTGGCAA GCAGCCTGTG	120
40	TATGATACCA CAATTAGAAC TGGCAGAGCA CTGAAAGAAA AGACTTTGCT TCCCGAAGAT	180
	ASTCAGAAAC TTGACAAATT CCTAGGAGAA GTCAGAGACA AATGGGATAC TGTTTGTTGGC	240
45	AAGTCTGTGG AGCGGCAGCA CAAGTTGGAG GAAGCCCTGC TCTTTTCGGG TCAGTTCATG	300
	GATGCTTTGC AGGCATTGGT TGACTGGTTA TACAAGGTGG AGCCACAGCT GGCTGAGGAC	360
	CAGCCCGTGC ACGGGGACC TTGACCTCGT CATGAACCTC ATGGATGCAC ACAAGGTTTT	420
50	CCAGAAGGAA CTGGNGAAAG CGAACAGGAA CCGTTCAGGT CCTGAAGCGG TCAGGCCGAG	480
	AGCTGATTGA GAATAGTCGA GATGACACCA CTTGGGTAAA AGGACAGCTC CAGGAACTGA	540
	GCACTCGCTG GGACACTGTC TGTAACCTCT CTGTTTCCAA ACAAAGCCGG CTTGAGCAGG	600
55	CCTTAAACA AGCGGAAGTG TTTCGAGACA CAGTCCACAT GCTGTTGGAG TGGCTTTCTG	660
	AAGCAGAGCA AACGCTTCGC TTTCGGGGAG CACTTCCTGG ATGACACAGA GGCCCTGCAG	720
60	TCTCTCATTG ACACCCATAA GGAATTCATG AAGAAAGTAG AAGAAAAGCG AGTGGACGTT	780

	AACTCAGCAG TAGCCATGGG AGAAGTCATC CTGGCTGTCT GCCACCCCGA TTGCATCACA	840
5	ACCATCAAAC ACTGGATCAC CATCATCCGA GCTCGCTTCG AGGAGGTCCT GACATGGGCT	900
	AAGCAGCACC AGCAGCGTCT TGAAACGGCC TTGTCAGAAC TGGTGGCTAA TGCTGAGCTC	960
	CTGGAAGAAC TTCTGGCATG GATCCAGTGG GCTGAGACCA CCCTCATTCA GCGGGATCAG	1020
10	GAGCCAATCC CGCAGAACAT TGACCGAGTT AAAGCCCTTA TCGCTGAGCA TCAGACATTT	1080
	ATGGAGGAGA TGA CTCGCAA ACAGCCTGAC GTGGACCGGG TCACCAAGAC ATACAAAAGG	1140
15	AAAAACATAG AGCCTACTCA CGCGCCTTTC ATAGAGAAAT CCCGCAGCGG AGGCAGGAAA	1200
	TCCCTAAGTC AGCCAACCCC TCCTCCCATG CCAATCCTTT CACAGTCTGA AGCAAAAAAC	1260
	CCACGGATCA ACCAGCTTTC TGCCCGCTGG CAGCAGGTGT GGCTGTTAGC ACTGGAGCGG	1320
20	CAAAGGAAAC TGAATGATGC CTTGGATCGG CTGGAGGAGT TGAAAGAATT TGCCAACTTT	1380
	GACTTTGATG TCTGGAGGAA AAAGTATATG CGTTGGATGA ATCACA AAAA GTCTCGAGTG	1440
25	ATGGATTCTT TCCGGCGCAT TGATAAGGAC CAGGATGGGA AGATAACACG TCAGGAGTTT	1500
	ATCGATGGCA TTTTAGCATC CAAGTTCCCC ACCACCAAGT TAGAGATGAC TGCTGTGGCT	1560
	GACATTTTCG ACCGAGATGG GGATGGTTAC ATTGATTATT ATGAATTTGT GGCTGCTCTT	1620
30	CATCCCAACA AGGATGCGTA TCGACCAACA ACCGATGCAG ATAAAAATCGA AGATGAGGTT	1680
	ACAAGACAAG TGGCTCAGTG CAAATGTGCA AAAAGGTTTC AGGTGGAGCA GATCGGAGAG	1740
35	AATAAATACC GGTTCCTTCT CGGCAATCAG TTTGGGGATT CTCAGCAGTT GCGGCTGGTC	1800
	CGTATCTGTC GCAACCGTGA TGGTTCGCGT TGGTGGAGGA TGGATGGCCT TGGATGAATT	1860
	TTTAGTGAAA AATGATCCCT GCCGAGCAG AGGTAGAACT AACATTGAAC TTAGAGAGAA	1920
40	ATTTCATCCTA CCAGAGGGAG CATCCAGGG AATGACCCCC TTCCGCTCAC GGGGTCGAAG	1980
	GTCCAAACCA TCTTCCGGG CAGCTTCCCC TACTCGITCC AGCTCCAGTG CTAGTCAGAG	2040
45	TAACCACAGC TGTACATCCA TGCCATCTTC TCCAGCCACC CCAGCCAGTG GAACCAAGGT	2100
	TATCCCATCA TCAGGTAGCA AGTTGAAACG ACCAACACCA ACTTTTCATT CTAGTCGGAC	2160
	ATCCCTTGCT GGTGATACCA GCAATNAGTT CTTCCTCGGC CTCCACAGGT GCCAAAATA	2220
50	ATCGGGCAGA CCTAAAAAG TCTGCCAGTC GCCTGGGAG TCGGGCTGGG AGTCGAGCCG	2280
	GGAGTCGAGC CAGCAGCCGG CGAGGAAGTG ACGCTTCTGA CTTTGACCTC TTAGAGACGC	2340
55	ATTGCTTGTT CCGACACTTC AGAAAGCAGC GCTGCAGGGG GCCAAGGCAA CTCCAGGAGA	2400
	GGGCTAAACA AACCTTCCAA AATCCCAACC ATGTCTAAGA AGACCACCAC TGCTTCCCC	2460
	AGGACTCCAG GTCCCAAGCG ATAACACTGT CTAAGCACCC CCAAGCCACT ATCCACTTTG	2520
60	AATCCTGCTC CATACATTTG GTGTATATTT ATTCTGAACG GGAGAAGTTA TATTGTTAAA	2580

5 AGTGTAAG AATAATTGTG TTATGAAGCT GCCTTATTTT TTTCTTTTTT GTAAGTTACT 2640
 ATTTTCATGT GAATATTTAT GTAGATAAAA TTTGCCTCCT GGTAACCCCTG TAATGGATGG 2700
 GGGCCAGAAA TGAAATATTT GAGAAAAACA AGTGAAAAGG TCAAGATACA AATGTGTATT 2760
 AAAAAAAAAA AAGCCTATTA ATAGGGTTTC TCGCGGTGC AGGGTTGTAA ACCTGCTTTA 2820
 10 TCTTTTAGGA TTATTCCTAA ATGCATCTTC TTTATAAACT TGACTTGCTA TCTCAGCAAG 2880
 ATAAATTATA TTAATAAAT AAGAATCCTG CAGTGTAA GGAATCTTTT TTTGTAAAT 2940
 CACGGACACC TCAATTAGCA AGAAGTGGG GGAGGGCTTT TTCCATTGTT TAATGTTTGG 3000
 15 TGATTTTAG CTAAGAGAG GGAACCTCAT CTAAGTAACA TTTGCACATG ATACAGCAAA 3060
 AGGAGTTCAT TGCAATACTG TCTTTGGATA TTGTTTCAGT ACTGGGTGTT TAAAGGACAA 3120
 20 ATAGCTGCTA GAATTCAGGG GTAAATGTAA GTGTTTCAGAA AACGTCAGAA CATTTGGGGT 3180
 TTTAACTGA TTTGTGCTC CCTATCCAGC CTAGACACCA GTAATCTTTG TGTTCACCAG 3240
 GACCCAGACC CTTGGCAAGG GATAGGCTCG TTGGTGACAT TGTGAATTC AGATTTGTTT 3300
 25 TATCCACITT TTTTGCTATT TATTTAAATG GTGATCAAC TTCCACAAA CTGAGGAATG 3360
 AATTCACGA GCCTGTTCTG AAAATGTGGA CGTAAGACAA ACACGTGCTC GTCCTTTAAT 3420
 30 GGAGTTCACC AGCACACTTG TTAACCAGTC CTGTTTGCTT TCGTCTTTT TGTGCGTAA 3480
 TAAAGTCAAC TGACCAAGTG ACCATGAAAA GGGGCTGTCT GGGGCTCCTG TTTTTTAGCT 3540
 GCTGTTCTTC AGCTCCGACC ATGTTGCTGT GTGATTATCT CAATTGGTTT TAATTGAGGC 3600
 35 AGAACTGAA GCTCTACCA TGAAGTGTG AGAAACAAGA CACACTTTTG TATTAAAT 3660
 GCTTGCACTA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AACTCGAGG GGGGCCCGGT 3720
 40 ACCCAATTCG CCGTATATGA TCGTAAACAA TC 3752

45 (2) INFORMATION FOR SEQ ID NO: 128:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1144 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 128:

55 TGACCCCTCG CCTGCCGGGC TCAGTGCTGG ACGCTTCTCG TTTGTGCGA GTCGGTCCTC 60
 GGTAACACCA GCGGCTGTG GTCCACCACT CCATTCAGCA GCTCCATTTG GTCCAGCAAC 120
 60 CTTAGCAGCG CCTTCCTTC ACCACTCCAG CAAACACGCT GGCAAGCATC GGCCTCATGG 180

	GCACAGAAAA CTCCCCTGCT CCTCACGCTC CCTCCACCTC CAGTCCAGCT GACGACTTGG	240
	GACAGACCTA CAACCCGTGG CGGATATGGA GCCCCACGAT TGGAAGAAGA AGCTCGGACC	300
5	CTTGGTCTAA TTCGACTTTT CCTCACGAGA ATTAAATTAA GCAAAAAACA AACAAACATA	360
	GTGGGCCCTC GTCTAGATCA TGATGTGCCA GTTCTGAGA CATCTTTTTA AGGCTCTTAC	420
10	TGCAGCTCCC CTCCCCACCC TCCTCTTCTT TGCAAAACAG ACCCAAGCAG GGCAGGCTCA	480
	GACCACTCGC TTCTTTCAGA TCTTCTTGC AATTATGATA ACATGAGATT TGCTGTTGTG	540
	CTTTTAGAGA AAAGTCTGGA CTCAGCCACA AACTCTAATA AGACCTGTAC ATCTGAGAAC	600
15	CTTTCCCGTT ACTGCGTTTT CACCACCTGT CTCCCCATG CTTTATTTAT CTGTATGAAC	660
	ACAGATTTGA CATTACAGCT AAGGAAATAA TTTGAGTTGA TTCAGAAATC CTGGCATGTG	720
20	ACAATTTTGT TAAATTACCA AGTTTGSTTT TTAATAATTT CTCAATATTA TGCGCCAAGA	780
	TCTAATTTTA AACTGTATG AGGACTTTGT GCTGAAAATA GAGTATTTT TTAAGTAAG	840
	GCTGTCTTGG TTTAAAGCA GATTACAGAA ATGTAAGTCA ACTTAAGAAC RGTGAATGAA	900
25	TGTA AAAACA TTCAGTYGAG ACCATATGCA TTTTCTGTGC TGTTTGTACT TGAGGTATGT	960
	AACATTTGTA TACCTGAACT TATTTTAAAG ATGAACTGAA ATGCACATAG CCAAGTCTTG	1020
30	AGATACAAGA TTGAATGTGT ATTTCTTAAA AATACAACCT TGTGTTGTAC TTTGAAATAA	1080
	ATGATGCTTT TTTCAAAAAA AAAAAAAAAA AAAAAAAAC TCGAGGGGGG GCCCGGTACC	1140
	CAAT	1144
35		

(2) INFORMATION FOR SEQ ID NO: 129:

- 40 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1830 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- 45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 129:

	GCATGCAGAG GAGCACCTTG AGCGTGTGCC TGGAGCAGGC GGCCATSTTG GCACGGAGCC	60
50	ACGGGTTGCT GCCCAAGTGC ATCATGCAGG CCACGGACAT CATGCGGAAC AGGGCCCAAG	120
	GGTGGAGATT CTGGCCAAAA ACCTGCGAGT CAAGGACCAG ATGCCCCAGG GTGCTCCGCG	180
55	CCTCTACCGC CTCTGCCAGC CGCCGGTGGG TGGGACCTC TGAACACCCA AATGCCCCAC	240
	GCTGGGCCGC GGCTCTGGA GCTGGGATT GGGAGGACAC AGCAGGCAGC GCTGGCCTTC	300
	TCCAGGGATG GCCCAANGCT TCCGCARCCG CCCGTTCCGG GACCTGCCCA GCGTCTCCC	360
60	TGCCTCCTTC CGGACAAGC CTGGCCACCC TCCTGTGAT GACGAGCTGG CTGATTGGCC	420

	CTGGGCCGGC CCATTCTTCA CACGCCTGCC AGAAGCTGGA GGGGTGCTGG AGACCCATAG	480
5	AGCTGATGGG AGCAGCTGGT GCCTGGCCTT CGGCTCCTGC GTCCCCAGAA CCCAAGGGAA	540
	CGTCATGGAG GCCACATGGG GCCACCCGGC TCCCTCGGA TGGCTCCGCT GCACTTTTGA	600
	AACCCCGGTT TCCTTCAACG TCCACATTCC AGGTGACCAC ACGTGTCTCC TCCTCCTCAT	660
10	CTTAGCTTCC AGGTTCAACC TAACCCGTGA CTAACCTGCT TGGTGGACTT GGAAAAGACT	720
	TGGCTCTGTC GGGAAAGGAG AGACGGGGCC TCCATCACGC CTGTTACCAG AGGATCCCCG	780
15	AGAGCCACAC CAGCTCTGGA CATCACCGCC CCTGGAACTG GGGCCACCAG CCCTGGGCAC	840
	GAGATTTGCT CTGACTTTAT TTATATGGCA TGAAATCTCT GGTTTATTTT GGGATTTTTT	900
	GTTGTGGTG TTGTCAAAGT TTGTTTTTC TAAAGTGTG TGATTATATA TTTGACATTT	960
20	TACATTTCAA AGAAAGGTAT GTTGTCTAAC AGGGGACCAA CAGAAGGTAG TATTGACAAC	1020
	TGTTCTGCT TCTACTAAAA AAAAAAGAGC ACAAAGAAA AACTAAATTA TTGAAAAATT	1080
25	AAAAAATGTC ATTGTTTCCT GTTGTTAAT ATTAGGGTG TAAGGTGTCG TTTTGAGGTA	1140
	TCGACTGTA TTCTTCCCC CACCCTCCAT TCTCCAGCG TTGGCCGGTG TTAGAACTCG	1200
	CTCTCTTTGA GTGACTGGCT ACAAGGGCCT GAGAGGTGGC CAGCCAGGGT TGGAGCTGGA	1260
30	GGGGATGGAG CCCACCTGA GGTGCCGTGT CACACGGGT AGAGGGTCAC TGGGAAACAC	1320
	CGGGCGGTGG CTCTGTGAT TTATTTTCTT GATGGTAACT TCTCAGAGCA GGGCRATTGG	1380
35	GACATCACCA GCCAGAGCAC AGGAAGCCAC CCTGCCTGCT GGGGAGGAGG GACCCACACA	1440
	AGCCCCCTCG GCAGTTGTG CCCCAGCTT CGGTATGCCT TCAGGGAAAG GTCACAGCTG	1500
	GGGAGGAAGC GGGGGACGC CTGTCACCCC TGGCAGGTGG TGAGTTCAGG TGGGGGCTCC	1560
40	CTGCTKCCCC CAGGCCTGGG AGCTTGAAGC CCTCCCGCA TCTGGCATCC GAGCCTCCCG	1620
	CCCTCCAGGG TCGCTTCCC TCTCTTGCCG CAGCATACAC GAGGGCAGGC AGTGGCCTTG	1680
45	TCACTGTATC TTGCATCAGA GACAAAGGAG GACCCGCTTT AGCCCTGCTG CGGGAAATGG	1740
	GGGATGGCCC AGGGCCAGCG CATGTGTGCAC TGGTTTACTT TAAAATGTAC AGATTCTTCT	1800
50	CGTTAAATTC TTGATAGATT TTTTATTATT	1830

(2) INFORMATION FOR SEQ ID NO: 130:

- 55 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1864 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- 60

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 130:

	GGCCGCCCCG ATGGCGACCC CAGCCTCGGC CCCAGACACA CGGGCTCTGG TGGCAGACTT	60
5	TGTAGGTTAT AAGCTGAGGC AGAAGGGTTA TGTCTGTGGA GCTGGCCCCG GGGAGGGCCC	120
	AGCAGCTGAC CCGCTGCACC AAGCCATGCG GGCAGCKGGA GATGAGTTCT AGACCCGCTT	180
10	COGGCGCACC TTCTCTGATC TGGCGGCTCA GCTGCATGTG ACCCCAGGCT CAGCCCAACA	240
	ACGCTTCACC CAGGTCTCCG ATGAACTTT TCAAGGGGGC CCCAACTGGG GCCGCCTTGT	300
	AGCCTTCTTT GTCTTTGGGG CTGCACTGTG TGCTGAGAGT GTCAACAAGG AGATGGAACC	360
15	ACTGGTGGGA CAAGTGCAGG AGTGGATGGT GGCCTACCTG GAGACGCGGC TGGCTGACTG	420
	GATCCACAGC AGTGGGGGCT GGTATATCCCA GATCACTGAA GCTGAGATGG CTGATGAAGT	480
20	AATTTGCAGT GAAATTTTAA GCGACTGTGA CTCTGCTGCA AGTTCCCCAG ATCTTGAGGA	540
	GCTGGAAGCT ATCAAAGCTC GAGTCAGGGA GATGGAGGAA GAAGCTGAGA AGCTAAAGGA	600
	GCTACAGAAC GAGGTAGAGA AGCAGATGAA TATGAGTCCA CCTCCAGGCA ATGCTGGCCC	660
25	GGTGATCATG TCCATTGAGG AGAAGATGGA GGCTGATGCC CGTTCCATCT ATGTTGGCAA	720
	TGTGGACTAT GGTGCAACAG CAGAAGAGCT GGAAGCTCAC TTTCATGGCT GTGGTTCAGT	780
30	CAACCGTGTT ACCATACTGT GTGACAAATT TAGTGGCCAT CCCAAAGGGT TTGCGTATAT	840
	AGAGTTCTCA GACAAAGAGT CAGTGAGGAC TTCTTTGGCC TTAGATGAGT CCCTATTTAG	900
	AGGAAGGCAA ATCAAGGTGA TCCCAAAACG AACCAACAGA CCAGGCATCA GCACAACAGA	960
35	CCGGGGTTTT CCACGAGCCC GCTACCGCGC CCGGACCACC AACTACAACA GCTCCCGCTC	1020
	TCGATTCTAC AGTGGTTTTA ACAGCAGGCC CCGGGGTCGC GTCTACAGGG GCCGGGCTAG	1080
40	AGCGACATCA TGGTATTCCC CTACTAAAA AAAGTGTGTA TTAGGAGGAG AGAGAGGAAA	1140
	AAAAGAGGAA AGAAGGAAAA AAAAAAGAAT TAAAAAATAA AAAAAAATAA ACAGAAGWTG	1200
	MCCTTGATGG AAAAAAATA TTTTTTAAAA AAAAGATATA CTGTGGAAGG GGGGAGAATC	1260
45	CCATAACTAA CTGCTGAGGA GGGACCTGCT TTGGGGAGTA GGGGAAGGCC CAGGGARTGG	1320
	GGCAGGGGGC TGCTTATTTA CTCTGGGGAT TCGCCATGGA CACGTCTCAA CTGCGCAACT	1380
50	GCTTGCCCAT GTTCCCTGTC CCCACCCAC CCTCTTCTC CGGCTCCCTG CCCCTCCAGA	1440
	TTGCCTGGTG ATCTATTTTG TTTCTTTTGG TGTTTCTTTT TCTGTTTGA GTGTCTTTCT	1500
	TTGCAGTTT CTGTAGCCGG AAGATCTCCG TTCCGCTCCC AGCGGCTCCA GTGTAAATTC	1560
55	CCCTTCCCCC TGGGGAAATG CACTACCTTG TTTTGGGGG TTTAGGGGTG TTTTGTMTT	1620
	TCAGTTGTTT TGTTTTTTTG TTTTTTNTT TTTCTTTTGC CTTTTTTCCC TTTTATTTGG	1680
60	AGGGAATGGG AGGAAGTGGG AACAGGGAGG TGGGAGGTGG ATTTTGTTTA TTTTTTTAGC	1740

TCATTTCAG GGGTGGGAAT TTTTTTTAA TATGTGTCAT GAATAAAGTT GTTTTTGAAA 1800
AKAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA 1860
5 AAAA 1864

10 (2) INFORMATION FOR SEQ ID NO: 131:

(i) SEQUENCE CHARACTERISTICS:

15 (A) LENGTH: 2041 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 131:

20 GGCACGAGCG CGCGGCAGGG CCCTGGACCC GCGCGGCTCC CGGGGATGGT GAGCAAGGCG 60
CTGCTGCGCC TCGTGTCTGC CGTCAACCGC AGGAGGATGA AGCTGCTGCT GGGCATCGCC 120
25 TTGCTGGCCT ACGTCGCCTC TGTTTGGGGC AACTTCGTTA ATATGAGGTC TATCCAGGAA 180
AATGGTGAAC TAAAAATTGA AAGCAAGATT GAAGAGATGG TTGAACCACT AAGAGAGAAA 240
ATCAGAGATT TAGAAAAAAG CTTTACCCAG AAATACCCAC CAGTAAAGTT TTTATCAGAA 300
30 AAGGATCGGA AAAGAATTTT GATAACAGGA GCGCGAGGGT TCGTGGGCTC CCATCTAACT 360
GACAACTCA TGATGGACGG CCACGAGGTG ACCGTGGTGG ACAATTTCTT CACGGGCAGG 420
AAGAGAAACG TGGAGCACTG GATCGGACAT GAGAACTTCG AGTTGATTAA CCACGACGTG 480
35 TGGAGCCCCT CTACATCGAG GTTGACCAGA TATACCATCT GGCACTCTCA GCCTCCCCTC 540
CAAACCTACAT GTATAATCCT ATCAAGACAT TAAAGACCAA TACGATTGGG ACATTAAACA 600
40 TGTITGGGGCT GGCAAAACGA GTCGGTGGCC GTCTGCTCCT GGCCTCCACA TCGGAGGTGT 660
ATGGAGATCC TGAAGTCCAC CCTCAAAGTG AGGATTACTG GGGCCACGTG AATCCAATAG 720
GACCTCGGGC CTGCTACGAT GAAGGCAAAC GTGTTGCAGA GACCATGTGC TATGCCTACA 780
45 TGAAGCAGGA AGGCGTGGAA GTGCGAGTGG CCAGAATCTT CAACACCTTT GGGCCACGCA 840
TGCACATGAA CGATGGGCGA GTAGTCAGCA ACTTCATCCT GCAGGCGCTC CAGGGGGAGC 900
50 CACTCACGGT ATACGGATCC GGGTCTCAGA CAAGGCGGTT CCAGTACGTC AGCGATCTAG 960
TGAATGGCCT CGTGGCTCTC ATGAACAGCA ACGTCAGCAG CCCGGTCAAC CTGGGAACC 1020
CAGAAGAACA CACAATCCTA GAATTGCTC AGTTAATTAA AAACCTTGTT GGTAGCGGAA 1080
55 GTGAAATTCA GTTCTCTCTC GAAGCCCAGG ATGACCCACA GAAAAGAAA CCAGACATCA 1140
AAAAAGCAA GCTGATGCTG GGGTGGGAGC CCGTGGTCCC GCTGGAGGAA GGTTTAAACA 1200
60 AAGCAATTCA CTACTTCCGT AAAGAACTCG AGTACCAGGC AAATAATCAG TACATCCCCA 1260

	AACCAAAGCC TGCCAGAATA AAGAAAGGAC GGAATCGCCA CAGCTGAACT CCTCACTTTT	1320
5	AGGACACAAG ACTACCATTG TACACTTGAT GGGATGTATT TTGGCTTTT TTTGTTGTC	1380
	GTTTAAAGAA AGACTTTAAC AGGTGTCATG AAGAACAAAC TGGAATTTC TTTCTGAAGCT	1440
	TGCTTTAATG AAATGGATGT GCCTAAAAGC TCCCCTCAA AACTGCAGA TTTTGCCTTG	1500
10	CACTTTTTGA ATCTCTCTTT TTATGTAAAA TAGCGTAGAT GCATCTCTGC GTATTTTCAA	1560
	GTTTTTTTAT CTGCTGTGA GAGCATATGT TGTGACTGTC GTGACAGTT TTATTTACTG	1620
15	GTTCCTTTGT GAAGCTGAAA AGGAACATTA AGCGGGACAA AAAATGCCGA TTTTATTTAT	1680
	AAAAGTGGGT ACTTAATAAA TGAGTCGTTA TACTATGCAT AAAGAAAAAT CCTAGCAGTA	1740
	TTGTCAGGTG GTGGTGGGCC GGCATTGATT TTAGGCAGA TAAAGAATT CTGTGTGAGA	1800
20	GCTTTATGTT TCTCTTTTAA TTCAGAGTTT TTCCAAGTC TACTTTTGAG TTGCAAACTT	1860
	GACTTTGAAA TATTCCTGTT GGTCAATGATC AAGGATATTT GAAATCACTA CTGTGTTTTG	1920
25	CTGCGTATCT GGGGCGGGG CAGGTGGGG GGCACAAAGT TAACATATTC TTGGTTAACC	1980
	ATGTTAAAT ATGCTATTTT AATAAAATAT TGAAACTCAC CAAAAAATA AAAAAAATA	2040
	A	2041

30

(2) INFORMATION FOR SEQ ID NO: 132:

- 35 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 2012 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 132:

	TACCAAGCTG CAAGAATCTA CTATATCATG GCAGAAGAAG TAGAGTGGGA CTATTGCCCT	60
45	GACCGGAGCT GGAACGGGA ATGGCACAAC CAGTCTGAGA AGGACAGTTA TGGTTACATT	120
	TTCTGAGCA ACAAGGATGG GCTCCTGGGT TCCAGATACA AGAAAGCTGT ATTCAGGGAA	180
50	TACACTGATG GTACATTTCAG GNTCCCTCGG CCAAGGACTG GACCAGAAGA AACTTTGGGA	240
	ATCTTGGGTC CACTTATCAA AGGTGAAGTT GGTGATATCC TGACTGTGGT ATTCAAGAAT	300
	AATGCCAGCC GCCCCTACTC TGTGCATGCT CATGGAGTGC TAGAATCTAC TACTGTCTGG	360
55	CCACTGGCTG CTGAGCCTGG TGAGGTGGTC ACTTATCAGT GGAACATCCC AGAGAGGTCT	420
	GGCCTGGGC CAATGACTCT GCTGTGTTT CCTGGATCTA TTATTCTGCA GTGGATCCCA	480
60	TCAAGGACAT GTATAGTGGC CTGGTGGGC CCTTGGCTAT CTGCCAAAAG GGCATCCTGG	540

	NAGCCCCATG GAGGACGGAN TGACATGGAT CGGGAATTG CATTGTGTGTT CTTGATTTTT	600
	GATGAAAATA AGTCTTGGA TTTGGAGGAA AATGTGGCAA CCCATGGGTC CCAGGATCCA	660
5	GGCAGTATTA ACCTACAGGA TGAAACTTTC TTGGAGAGCA ATAAATGCA TGCAATCAAT	720
	GGGAAACTCT ATGCCAACCT TAGGGGTCTT ACCATGTACC AAGGAGAACG AGTGGCCTGG	780
10	TACATGCTGG CCATGGGCCA AGATGTGGAT CTACACACCA TCCACTTTCA TGCAGAGAGC	840
	TTCTCTATC GGAATGGCGA GAACTACCGG GCAGATGTGG TGGATCTGTT CCCAGGGACT	900
	TTTGAGGTTG TGGAGATGGT GGCCAGCAAC CCTGGGACAT GGCTGATGCA CTGCCATGTG	960
15	ACTGACCATG TCCATGCTGG CATGGAGACC CTCTTCACTG TTTTCTCTCG AACAGAACAC	1020
	TTAAGCCCTC TCACCGTCAT CACCAAAGAG ACTGAAAAAG CAGTGCCCCC CAGAGACATT	1080
20	GAAGAAGGCA ATGTGAAGAT GCTGGGCATG CAGATCCCCA TAAAGAATGT TGAGATGCTG	1140
	GCCTCTGTTT TGGTGGCCAT TAGTGTCAAC CTCTGCTCG TTGTTCTGGC TCTTGGTGGA	1200
	GTGGTTTGGT ACCAACATCG ACAGAGAAAG CTACGACGCA ATAGGAGGTC CATCCTGGAT	1260
25	GACAGCTTCA AGCTTCTGTC TTTCAAACAG TAACATCTGG AGCCTGGAGA TATCCTCAGG	1320
	AAGCACATCT GTAGTGCATC CCCAGCAGGC CATGGACTAG TCACTAACCC CAACTCAAA	1380
30	GGGGCATGGG TGGTGGAGAA GCAGAAGGAG CAATCAAGCT TATCTGGATA TTTCTTTCTT	1440
	TATTTATTTT ACATGGAAAT AATATGATTT CACTTTTCTT TTAGTTTCTT TGCTCTACGT	1500
	GGGCACCTGG CACTAAGGGA GTACCTTATT ATCCTACATC GCAAATTTCA ACAGCTACAT	1560
35	TATATTTCTT TCTGACACTT GGAAGGTATT GAAATTTCTA GAAATGTATC CTCTCACAA	1620
	AGTAGAGACC AAGAGAAAAA CTCAATTGATT GGGTTTCTAC TTCCTTCAAG GACTCAGGAA	1680
40	ATTTCACTTT GAACTGAGGC CAAGTGAGCT GTTAAGATAA CCCACACTTA AACTAAAGGC	1740
	TAAGAATATA GGCTTGATGG GAAATGAAG GTAGGCTGAG TATTGGGAAT CCAAATTGAA	1800
	TTTGTATTCT CCTTGGCAGT GAACTACTTT GAAGAAGTGG TCAATGGGTT GTTGCTGCCA	1860
45	TGAGCATGTA CAACCTCTGG AGCTAGAAGC TCCTCAGGAA AGCCAGTTCT CCAAGTTCTT	1920
	AACCTGTGGC ACTGAAAGGA ATGTTGAGTT ACCTCTTCAT GTTTTAGACA GCAAACCTTA	1980
50	TCCATTAAAG TACTTGTTAG AACACTGAAA AA	2012

55 (2) INFORMATION FOR SEQ ID NO: 133:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1669 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

60

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 133:

5	GAGCAGTATT TTAACCAACT TGTATTACAG ATGTTACAGT TCATGTTAGG AAGTCAGAAA	60
	AGACTTTGTT TGTCTTTGTT CTGCTGATGT GAGTCATGTT TTGTGGGGTC TTCCATGGCA	120
	CATTTACCTG TTGCTCCGTC CAGATGTTGA GGGCCAGTCT AGGCTGACAC ATCCTACCCG	180
10	AGGACAAGCC TGTTCCTCCAT TTCTTCACTC TCCCCTCCCC ATATAGCAAC TCTCCAGGT	240
	TTAGATTACC GTTTTCGACG ACAGATTAAAC CAAAAATGCC CCACACAGGT TTTATTACTG	300
15	TTATATACTA TACTTTTAAAC AGTACAGACC CTAAATTTTA TTATTTGTGTG CTCCCCCAAT	360
	CTGATACCAA ATGTTTAAAG TTGTTTGAAA TCCAAACATG GTAGTGTTC A TGGGTAAATA	420
	TTTCTAGGC TATGTAAGAG TTAGCAGCCC ATAGCATAGA AGTAATCAAG TAGCATCTGA	480
20	GACTGTTGGA GGCCTAGGG CCTCTCTGGG CCTAACAGCC TCACTTCCCC AGCCTCACCT	540
	TGCTGTCTC TGACACTGCC ATCAGGGCTG TTAGTGGCAC CTGTATGAGG CCAAGTGTGC	600
	GTCCAGGGGA ACAGCACAGG TTAATGCGTC TCCCTAGAAC TCATGAAGTC AGTTTAAATC	660
25	ATGCATGAAC ATGAGTTTAT TTTATGTTTT ATATAGCTTT CTTAGACATA CCAAACCATC	720
	ATTCATAAAT CAGATAAATT ATTCAGTTTT TGTGTTTGA AAGCTAAGTA TGTGTAGCTG	780
30	GAAACAAAAA TGAGCGTGTT TTCTCTCCTG TTAATCTAGA GTGTGCAGTT ACACATGTGT	840
	GGATAATTTT ATGTTCCAGG GGCGCTTGGC ATCTCCCATG GACTGATTCC CAGGAAGAAA	900
35	AGCCCCAAGG GAAACCCACG ATTCCTTTTCG AGTAGATGTG GGAAAGAGCC CATTTGAGGA	960
	TATGAGGTCC TGTGAAATTC AGTTGTGTGT GTGGCTCCTT GTTAGCAGTC ATGTTGACAT	1020
	GGTGTTAGGA GGCTCCCCAT CCACCCTTTA CATGATGTAG GGACCAGTGT CTTGTGAGAT	1080
40	TAACCTTGGG ACACAGTGGG TTAGCCTGGA GAAAATGAGA GGCCCTGCCT GGACCCAGGG	1140
	AGAGGAGCCA GTGACACAGG CAGAGCGGTG CAGCCCTCCT TCCCTTCCAT TTGGAGGAGG	1200
45	TGGTGCCAGG AGCCTGCCCG CTTACCTCTG CTGAAGCATA AGTGGACTTT GCTTTTGGGG	1260
	CTTATCTCTG ATACATGCTG GAGCCCTGCC TCTCCACTGC TAGATGGAAC CTGGAATCTC	1320
	TCATCTACCT CTTAGTCTGT CAGTTTCTAC GTGTGAGAAG CAAGCTTGTG GGCCAGTGTG	1380
50	CTTGATACAT CTGTAGCACT TAAAAAATAA TTCCAGGGTT CCCTGGAATA CCAGTCCCAG	1440
	GGTTCCCTATG ATCTGTAGTT TCTACCTGGA TTATAACTGG TTTTGGGTAC CTGAATTTTG	1500
55	ATTGGTTAGC CTTAATTATA GTCTGGCGTG ATCATGTAGA ATCTTTTCTG GTGAACAGAT	1560
	CATAAAGTTC TATCAAGGAG TTCTATCAAG GCATCCATGT CAGTGGTGCT ATGCTGGTTA	1620
60	CAACTTGAGA TTTTGTAAAT AAAAAATTTG TCATAAAAAA AAAAAAAA	1669

(2) INFORMATION FOR SEQ ID NO: 134:

5

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1565 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 134:

	CACTTTTGCT ATATAACCTA AGTGATAACC CTCTTTTAGT TACCTGCCAA ACTCTGGNCT	60
15	TGGTTTATAT TGCAGTTAAC ACAGTTACAA AGCTGTAATG GTGTCCTTTT TTCCCTTTGTA	120
	ACGGAATGTG TAAATCAAAG TATATACATT GTGTGGTGTT CCTGTTTCTG GAGTTTCATG	180
20	AGGATTTTACA CATGGCATTG AGTGTCTGT ATAGATCTGC CTACCTTTGT GAATTCATCT	240
	GTTAACCCCT CTTCCTTTGA GAGAGCACCG GCGATGGTGG TTAACCTCTT GTGTTTCTC	300
	TCTCTCCTAC TGGTTATTCT TGAATTAAGC ACAGACTCGT CAGCTCGGTT GCTTTATCAT	360
25	GAATAATGTG TGTGACCTTG CAGTTCTTCC ACAGTTCAGC AAACAAGTGC TAGCTTCACT	420
	GACCAAAAAT TAAGGAAGGA AAACACAGTT TTAAAAACGA TCCATCTTTT AACAGCCGAA	480
30	ACCGATGTGT CTATGGTGCT GCACCTTGCT GTTGTACTTC TGAAATCAGA CGTGTGTGAA	540
	CGATCATTTT TGACTTAACC GTGAGATGCT CACGAGTACC CTTCCTGTTG TTTTGTAGC	600
	ATTGAAATCG AGACTATTTA TTTGGAATAT ATACAACAGT GTTTTCCAC TGTATTTTCA	660
35	TTGCAAAAGT TGAGAAGTGC TTTCTCTACC TTTTGCAAAA TAATTGATAT TCCATATTGG	720
	ATTCTCAAAG ACTTCGATAT GGTGAACCTA TTAAACCTAG AAATTGTATT CATCCTTTCA	780
40	TGACTGTGGC CTGAGTTCCC CAGCCCCTCT CCTCCTTTTT TTTAGATGAG ATTTAGCACA	840
	CTCTCAGTTA TTAAACATG CAACATTTCT TGAGTATGTA TGTGAGGCC ATCTGAGCTC	900
	ATAGCTGATT CAGTAACCAG TTTTATGCTG TGTCAATCAC ACTCACTACT TAATACTGCC	960
45	ATGGTGAAAA TGTGGAGGAA AAATGTATCC ATGTGTGTCT GGAAGCATA TACACTTGTA	1020
	CATTTTTTAA TACTCTGATT CTGTAACATT TCTGAGTTT GTTTTGTTTT ACAGNAAAAA	1080
50	AAAAAAAAGT GATAAAGCAA TCAGAAGACC AAGAGGTTTA CTATTGATGC TTAGGGTCGT	1140
	CTGACCTTGG CTGGCCAATA GACCTACAG GCCAAATTAA TTTACGAGAG TAATAATTTT	1200
	TCAAAAGCCA ATTTTTTTT TGTATTTTCT GTATGAACT GCCAATATCA TGAATAGAAA	1260
55	GGGAGAACCA TAAAGGAGAA AGAACGTGAT GTTCTGTTAT GTTCATGTAA ACCTAAAGAA	1320
	ACAGTGTGGA GGCAGGCGCG ATCAGCCGAA CTCTAGGGAC TTGGTGTTC TTGGAAGGCA	1380
60	TCCATACCTG CATTTTGCAT TCTTCGTATG TAATCATATT GCCAAAGACA AACTATTTCA	1440

TCATTTATTG TAAATAACAC TTTTCCCCAG ACCTACCATA AAGTTTCTGT GATGTATTGT 1500
 CTTCCAGTTG CAATAAAAT TACTGAGTTG CATCAATTGA AGAAAAAAAA AAAAAAAAAA 1560
 5 CTCGA 1565

10 (2) INFORMATION FOR SEQ ID NO: 135:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2007 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 135:

20 TCTAAAGCC CCCTTATACC CCACTTTGTG CAGCAAAGAT CCCCGTGCAG GTCACAGCCT 60
 GATTTGTGGC CAGGCTGGAC AAATTCCTGA GGCACAACTT GGCTTCAGTT CAGATTTCAA 120
 GCTGTGTGG TGTGGGGACC AGCAGAAGGC AAACGTCCAG CCAACACACA GGA CTGTAAG 180
 25 AGGACTCTGA GCTACGTGCC CTGTGAAGAC CCCCAGGCTT TGTCATAGGA GGTCTGTCAG 240
 CTTCCTCCAAA GTCAGAGGTG ATTTGATTTG GGGAAGACTG AATATTCACT CCTAAGTCGT 300
 30 GAGCATATCC TGAGTTTATC TTCTTTATGG CTGCGCTCC AAGTTCTCTC TCTCATACAC 360
 ACACACACCC TTGCTCCAGA ATCACCAGAC ACCTCCATGG CTCCAGCTAT GGAACAGCT 420
 GCATTGGGGC TGCTTTCTG TTTGGCTTAG GAACTTCTGT GCTTCTTGTG GCTCCACTCG 480
 35 CGAGGCAGCT CGGAGGTGTG GACTCCGATT GGGCTGCAGG CAGCTCTGGG ACGGCACAGG 540
 GCGGGCGCTC TGATCAGCTC GTGTAAAACA CACCGTCTTC TTGGCCTCCT GGCAGTTCTT 600
 40 TCTGCGAATA GTCCTCTCCC TGGCCAGTTG AATGGGGGAA GCTGCTGGCA CAGGAAGGAG 660
 AGGCGATCCC GGCTGAGGCT TAGGAAATTG CTGGAGCCGG CTCCAAGCAG ATAATTCACT 720
 GGGGAGGTTT TCAGAGTCAA ACATCATTTCT GCCTGTGTTG GGGGCCAGGT GTGTACACAC 780
 45 AGCATCTCAA AGTCAAAAGC CATCTGGGGC TGCTGCTTCT CTTTCTCAGG CTCTGGGGAA 840
 AGGAATCTCC CTCTCCTCTC ACTTGATTCC AAGTGTGGTT GAATGTCTG GAGCACTGGG 900
 50 ACTTTTTCCT TCTTTTCCTT GATGGACCAA CAGTGCAAAT GCAATCTCGC CATTTAACTT 960
 TCAGGTCGAT TTCTTTCTCT GATCAGACAT CTTGTGCCC CCTTTAGGAA GGAAAAGAAT 1020
 ACACCTACGA TGTGCCAGGC ACTGTGTTAG GCGCTTTTAT ATAGATCCTC GTTAGGATGA 1080
 55 GACTAAGGGA TGAGGACATC TCTTTATAAA AGGCCCTTAA GTAATGGATA AACAGAAACA 1140
 CTTAGAGGTG AGAAGGTCTG TCTTCAAGAT CCAAGGTAAG ATTGCCTTCA GTCTGATGTT 1200
 60 TGTTCCTCAAG GACTTATCCC CTACAATATT CTCCACTCC ATACTTCTCC TTCTACCCCA 1260

5 CCATGTGCTC CCGTGCACCTC CTCAGATGGT CAGAGGGGTA ACCCAAGTCC TTAGAGAATT 1320
 TGGGGACCAA TAGAATATGT GATGTGTGAA TTTTCTTTAA AAAACTTAAG GAGTCTTTGC 1380
 TACCTTCTGC TTGTTGAGTT GTTTTGGCAT TCATATTAAA AGCCAGCATC TCACTATTTA 1440
 TTGACAGGTT GGGCTGTGTG TGTGCGCATG TGTGTATACA TTTCCAGGCG TGCTGTGTC 1500
 10 CTGTAGCTTT TTAAGGAA ACCCAGTCAT CCCACTATGA ATCTGGCATC TTCTTATGCT 1560
 TCTAGTGTTC TGGCCATACA TCAACCAAGG GGTTAATTT ATCCAATGCT TGACGACATG 1620
 TTCAGGAGGG GCTGGATCAA ATTTTGAGAG GGTATGGGA AAGGAGGGG GAGAAGAAAT 1680
 15 TGACATTTAT TTTATTATTT ATTTTAAATG TTTACATCTT CTTTATGTTG TATCAAGCCT 1740
 GAATAGAAAC TGATAGCATT AAAATACTCC GTTCCTCTCT CTCCTCTCGC TTCCTTTTTT 1800
 20 TTTTTTTTTT AATTAGGAT AACACATTTT TGTTCTAAA GTGATTTGTG ATTTGTGCTG 1860
 TATAACTGT ATAAAAGGT CTGTTTTTAA AGGTGGATTT TCATTCCTCT GGGACAGTG 1920
 25 GTGCCAAGA CATCTACATT GTAAGAGAAC ACAGTGAAG ATCCTGTCCT GATTCTCAA 1980
 AATTATTTTC TCTGTATGAT TAAAAGT 2007

30

(2) INFORMATION FOR SEQ ID NO: 136:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1291 base pairs
 35 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 136:

40 CTTTTAACCC TCCCCCTCA CACACATACA TATCAGGTTG TTTTCTAGTT AAAAACCCAA 60
 GTAGCTCAGA TTCTACTTTA ATGTCAGTGC AGATTGTCAT TGAATCATGC CATTATGTTT 120
 45 TTTCTCATTT TTATGCTGTT GGGTCTTAGT TTTTAAATG ATATAAGAA CTCAGCAATG 180
 GTTTTATTTT CTACTCATAC TTAGGGTTTA GGAAACACTA CCACTAGTTA TCATTTAATC 240
 AACTTCAATG GTCTACTGAA ACAAAAATGG TAACTTTCA TTAGTGGATT ATTTAGAGTT 300
 50 ATAGTAGTTG TTTCCAGAAA ACACTTCCTC ACAATTGTAC TTCCCAATCA AATCATGTGA 360
 TCATACAGTT ATTCCCATGA AAGGCAGAAT GTTTGTTTCA AAATTAATCT AGTTTTCTGT 420
 55 ACATTTAAAT TTGAGAAGGT GACAACTGGC TCTTTCCAG TCTTCCTTCA TGTCAGTTTT 480
 CTGATAGACC ACTATTGGCA AACAGTATCT GTCAACTACC AAATGTGTAA AATTTTCTGT 540
 60 ATTTCACTTT GTCTTATTTG TAAATAGTGA ACTAAACTT TTGGCAGATC AGCAACATTT 600

GCTGAGCCTG TTTTSTAAGC TAATGTGTAT TCTTACTAAT GTTCCTATCA AGAATGGATT 660
 TGTAATATAT GCTGTCTATT TCTAATGTTC ACATTCATAT TTTGAGGTTC TATCTTATTT 720
 5 TAATAGAGAA CAGACTTCTC AAAAAATCTT CAGAAGCAGC TTATTATTGA AATATCGAAA 780
 TATTGAAATA AACCCGGTGG GTTAGATTAC TCATCTGTCC ACCAAGTGGG ACATTTGCAT 840
 10 GGACTGGGGG CTTAAAGGAC TTAGAAGAGA CCTGTAAGTA AATCCTGAAA ATGAGCCAAT 900
 CCCCCTTGA ATGGTTACTG GAGTAAACCC ACCTTTACCA CCCCAATTAC AGCACCCGAG 960
 GCCGATAAAC CAACTTGGCT CTGGTTCATT TTTCTTTTCT TCATTTGTGA TGCTCAGATT 1020
 15 CAAAATGTGT GTTCTACACT GTTACAGGCT TCTCTTTTGT TTGATTAAAG ATTTTAGTCC 1080
 TACTTTTGTA TGGACACATT AGAATATTCA GAGACCAAAA TAGAAGAATT TGCTGTTAGA 1140
 TATTTTTCAG AAGTCAGCAG ATTTGTGGCA AATCATTTAT TTGCCTTTT AAAAATTCAT 1200
 20 TTAAGCAGTT CAGAGAGTAG ACTACTCAGA AAATTATTTT ACGTAATTGT CTAAGAGGTC 1260
 AATATTTTTT AATGCATATT GAATCAAATA A 1291

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(2) INFORMATION FOR SEQ ID NO: 137:

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- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1906 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 137:

GGCACGAGGA CCTACTTTTG TAACAGACCA TGGTTGTGTC CAAGGTAAAA CCACAGTGAT 60
 40 ATTTTGGGAT GCTTTGTCTG CAATCTTGAC TTGTTTGTGC AGTATCATTA TTCAGACTTC 120
 AAATTGTGAA TCTTTTAAAC ATCTTGATAA TTGTTGTGTC AGAGCTGTTC ATTCTAAAAT 180
 45 GTAATGAAAT TCAGTCTAGT TCTGCTGATA AAGATCATCA GTTTTGAAAG GTTACTGATT 240
 TTCTCTTCC CTCTTAGTTT TTTACCCAAT ATATGGAGAA GAGTAATGGT CAATCTTAAC 300
 ATTTTGTTTT AATTGTTTAA TAAAGCTGCT GGCAGTGGT GCAGCATTC TACCTAGTGT 360
 50 CATAAAAGCA AAATACTTAC ATAGCTTTCT TAAAATATAG GAATGACATT ACATTTTATAG 420
 GAGAAAGTAA GTTGCTTTGC ACCGCCTACT TAATTCCTTT CCATATATTG TGATACAAAC 480
 55 TTTTGAATAT GGAATCTTAC TATTTGAATA GAAATGTGTA TGTATAATAT ACATACATAC 540
 ATAAGCATAT ATGTGTGTGT GTGTGTGTAT ATATATATAT ATGCATGCTG TGAAACTTGA 600
 CTACACAACA TAAATCACTT TTTAAATTCC AGGAACGGGT AGTCTGACAC GGTGATTATC 660
 60 CTTTGTAGGC TGAATCCGTT ATTAACCTGT TATTTAGGTT TTAATCCCAG TAGCAAGGGA 720

	TTCTAAGTTA GTTGCACTTA CATGATTATT GTGATTTAAA ACTAAGAATA AAGGCTGCAT	780
5	TTTCAAAGAT AAATTGGAAT TGCTGTTGGT GAAATAACAA CAAAATACT GAATCTGATG	840
	TACATACAGG TTTCTACAGG AAGAGATGGT ATAATTTACA ATTTGGAGAT TTAATAACCA	900
	GGGCTACCCA GAAAAAGTGA CTTGATAACA TGGTACCAAT AAGTAAGGA TGCTCTCTCG	960
10	GTTTGCTTTT GCCACTTTCA AGATTTTAAC TTCTCAGGTT ATTAATCAAA ATTATTGTAT	1020
	AAGTTAGCCA ATAGAATTTT TAGGTTAAAA CAACAGATGG GGGGTTTGTG GAGTGTTTAA	1080
15	TGTCATGGGC ATTTTtagTA GCATAGACCC TTGTGTTCTGC ATTTGAATGT TTCGTATATT	1140
	TTTGTTCAC AGTTAATCTT CCTCCCAA GTTTGCTATT CAAATCAACT GCCTGAATGA	1200
	CATTCTAGT AGTCTGATGT ATTTTCTGA GGAATAGTTT GTGATTCCAA TGCAGGTGTC	1260
20	TTCATTACCA TTACCTCTAC ACTGCAGAAG AAGCAAACT CCTTTATTAG AATTACTGCA	1320
	CATGTGTATG GGGAAAATAG TTCTGAAAGG CTAGAATGAT ACAAGTGAGC AAAAGTTGGT	1380
25	CAGCTTGCT ATGGAGTGGT GGCAATAATC TCTAAACATT CCAAAGACC ATGAGCTGAA	1440
	CCTAAACTCC CTTGGGAATC TGAACAAAG GAATATGAAA ATTGCCATTT GAAAACTGAC	1500
	CAGCTAATCT GGACCTCAGA GATAGATCAG CCAGTGGCCC AAAGCCATTT CAAGTACAGA	1560
30	AATTATAGAG ACTACAGCTA AATAAATTTG AACATTAAAT ATAATTTTAC CACTTTTGT	1620
	CTTTATAAGC ATATTTGTAA ACTCAGAACT GAGCAGAAGT GACTTTACTT TCTCAAGTTT	1680
35	GATACTGAGT TGACTGTTCC CTATCOCTC ACCCTTCCCC TTCCCTTTCC TAAGGCAATA	1740
	GTGCACAACT TAGGTATTTT TTGCTTCCGA ATTTGAATGA AAAACTTAAT GCCATGGATT	1800
	TTTTCTTTT GCAAGACACC TGTTTATCAT CTTGTTTAAA TGTAAATGTC CCCTTATGCT	1860
40	TTTGAAATAA ATTTCTTTT GTAAAAAAA AAAAAAAA AAAAAA	1906

45 (2) INFORMATION FOR SEQ ID NO: 138:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1935 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 138:

55	TCTGAACTAA TGCTAACAGA TCCCCCTGAG GGATTCTTGA TGGGCTGAGC AGCTGGCTGG	60
	AGCTAGTACT GACTGACATT CATGTGATG AGGGCAGCTT TCTGGTACAG GATTCTAAGC	120
60	TCTATGTTTT ATATACATTT TCATCTGTAC TTGCACCTCA CTTACACAA GAGGAACTA	180

	TGCAAAGTTA GCTGGATCGC TCAAGGTCAC TTAGGTAAGT TGGCAAGTCC ATGCTTCCCA	240
	CTCAGCTCCT CAGGTCAGCA AGTCTACTTC TCTGCCTATT TTGTATACTC TCTTTAATAT	300
5	GTGCCTAGCT TTGGAAGTC TAGAATGGGT CCTGGTGCY TTTTACTTT GAAGAAATCA	360
	GTTTCTGCCT CTTTTTGAA AAGAAAACAA AGTGCAATTG TTTTTTACTG GAAAGTTACC	420
10	CAATAGCATG AGGTGAACAG GACGTAGTIN AGGCCTTCCT GTAAACAGAA AATCATATCA	480
	AAACACTATC TTCCCATCTG TTTCTCAATG CCTGCTACTT CTGTAGATA TTTCATTCA	540
	GGAGAGCAGC AGTTAAACCC GTGGATTTTG TAGTTAGGAA CCTGGGKTCA AACCCCTCTC	600
15	CACTAATTGG CTATGTCTCT GGACAAGTTT TTTTTTTTTT TTTTTTTTAA ACCCTTCTG	660
	AACPTTCACT TTCTATGTCT ACCTCAAAGA ATTGTGTGA GGCTTGAGAT AATGCATTTG	720
20	TAAAGGTCT GCCAGATAGG AAGATGCTAG TTATGGATT ACAAGGTTGT TAAGGCTGTA	780
	AGAGTCTAAA ACCTACAGTG AATCACAATG CATTTACCCC CACTGACTTG GACATAAGTG	840
	AAAAGTAGCC AGAAGTCTCT TTTCAAATT ACTTACAGT TATTCAATAT AAAATTTTGT	900
25	TAATGGATAA TCTTATTTAT CTAACTAAA GCTTCCTGTT TATACACACT CCTGTTATTC	960
	TGGGATAAGA TAAATGACCA CAGTACCTTA ATTTCTAGGT GGGTGCCTGT GATGGTTCAT	1020
30	TGTAGGTAAG GACATTTTCT YTTTTTCAGC AGCTGTGTAG GTCCAGAGCC TCTGGGAGAG	1080
	GAGGGGGTA GCATGCACCC AGCAGGGGAC TGAAGTGGGA AACTCAAGGT TCTTTTACT	1140
	GTGGGTTAGT GAGCTGCCTT TCTGTGATCG GTTTCCTAG GGATGTGCT GTTCCCTCC	1200
35	TTGCTATTCTG CAGCTACATA CAACGTGGCC AACCCAGTA GGCTGATCCT ATATATGATC	1260
	AGTGCTGGTG CTGACTCTCA ATAGCCCCAC CCAAGCTGGC TATAGGTTTA CAGATACATT	1320
40	AATTAGGCAA CCTAAAATAT TGATGCTGGT GTTGGTGTGA CATAATGCTA TGGCCAGAAC	1380
	TGAAACTTAG AGTTATAATT CATGTATTAG GGTTCCTCCAG AGGGACAGAA TTAGTAGGAT	1440
	ATATGTATAT ATGAAAGGGA GGTATATTAG GAGAACTGGC TCCCACAGTT AGAAGGCGAA	1500
45	GTGCGACAAT AGGCCGTCTG CAAGCTGGGT TAGAGAGAAG CCAGTAGTGG CTCAGCCTGA	1560
	GTTCAAAAAC CTCAAAACCTG GGAAGCTGA CAGTGCAGCC AGCCTTCAGT CTGTGGCCAA	1620
50	AGGCCAAGAG CCCCTGGCAA CCAACCCACT GTTGCAAGTC CTAGATTCCA AAGGCTGAAG	1680
	AACCTGGAGT CTGATGTCCA AGAGCAGGAA GAGTGAAGA AAGCCAGAAG ACTCAGCAAA	1740
	CAAGGTAGAC AGTGTCTACC ACCAYAGTGG CCATACCAA GAGGCTACCG ATTCTTCTCT	1800
55	GCTACCTGGA TCCCTGAAGT TGCCCTGGTC TCTGCACCTT CTAAACCTAG TTCTTAAGAG	1860
	CTTTCCATTA CATGAGCTGT CTCAAAGCCC TCCAATWAAT TCTCAGTGTA AGYTTCAAAA	1920
60	AAAAAAAAA AAAAA	1935

(2) INFORMATION FOR SEQ ID NO: 139:

5

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1446 base pairs

(B) TYPE: nucleic acid

10

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 139:

15	NGCCCCCTTG GCACAAGTCA GATGAAGCAC GTTCTGCCGG GGAGGCCCTC AMCTTCCAGA	60
	GAGGACAGAC ACAGATTTC TGTCTGGGGA GGGAGGAGTC CACGCATCCT GATGCTGCCT	120
	GGAAGCTTAT TTTCCCGTGG CCAGGATGCA TTCTCTGAG TGGAAACAGG TTCTTGCATG	180
20	TGGATGTGTG TTTCCCCAGG CAGACGGCC CTCTYTTCCC AGCACTTCCC TGCCTCCCCC	240
	AGGCCTCAGG CCAGCACCCA GTTCTCTCTC ACATGGCAGG TGAGCACAGA CTTCTAGTTG	300
	GCAGGAGCTG AGGAGGGTGA ACAACCCCG AGGGAGGCC GGCCCTTGCT CCCGAGTTGG	360
25	GGGAGGGGG TGTGGCAACG TGCCCCCGC AGAGGCCACG CATGTTTGAC CAAAGCCCTC	420
	ATTGTGGTCC GAGGACAGCC TTTTCCCCAG GCCTCARAGC ATTGCTCATC CGTGCCAAAC	480
30	TGGTAGGTG GATTTGAGCG GAAAGACTCC CAAAATGTGC CAAGAATTTC CCRGTCCCAG	540
	GCAGGCGAGG GGAAACTAAG GGCAAGCAGG ATACAGGGCG AGGGATGTGG CAGGTGAGGG	600
	GGCTCCCGCC TGTGCCCCCT CTCCTCACCA TGCTCCCCC ACCCTGCCTC AGTTCTCCGT	660
35	TCCCCITCAT CTCGTCCCC CTCTTTGAAG CTGTCCCCAT CTCAGTGTCA GACCAGCCTT	720
	CTCTCAKCT GACCACCCTC CTCTGACCSA CGCCCCCTCC TTGTCTGAAA AAAGGAGCCT	780
40	TGAATGGTGG AGGGAGGCAG TGGGAGAAA GGTCTACCG GACAGGTGG GAGAATGAGG	840
	TCAGCGGTGC TGGGAACAG ATGGAGGGG CAGTGGGAC AGGGCTTGGG CAGACACCAG	900
	CAGGAATAAT TTGAAATGTG TGAGGTGACT CCCCAGAGGC CTTGGGCTTG GGCATTTGGG	960
45	AAAAGAATGA TGTCTGGAAG GGCTTAAGGG ACACAGTGA CGAGGGGAGA GTCTCATCT	1020
	GCTGGCATTT TGTGGGTGT TAGTGCCAAA CTTGAATAGG GGCTGGGGTG CTGTCTTCCA	1080
50	CTGACACCCA AATCCAGAAT CCCTGGTCTT GAGTCCCAG AACTTTGCCT CTTGACTGTC	1140
	CCTTCTCTTC CTACCTCCAT CCATGGAAAA TTAGTTATTT TCTGATCCTT TCCCCTGCCT	1200
	GGTCTAGCTC CTCTCCAAAC AGCCATGCCC TCCAAATGCT AGAGACCTGG GCCCTGAACC	1260
55	CTGTAGACAG ATGCCCTCAG AATTGGGGCA TGGGAGGGG GSTGGGGGAC CCCATGATTG	1320
	AGCCACGGAC TCCAATGCCC AGCTCCTCTC CCCAAAACAA TCCCGACAAT CCCTTATCCC	1380
60	TACCCCAACC CTTTGC GGCT CTGTACACAT TTTTAAACCT GGCAAAAGAT GAAGAGAATA	1440

TTGTAA

1446

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(2) INFORMATION FOR SEQ ID NO: 140:

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(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1109 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 140:

TTTTTTTTTT TTTGATATGA AATTGTCTTT CTCCATTGCA GAAATAAGCT AGGGAAACAC 60
TAACCCAAAA ACTTTCTGTA GAGCTGTTCC TTTGGAGGCA GCATCACTTA TTGGCAGTAA 120
AGACTCAGTA TAAAAGCACC AGCATCCCTA CTTGGGTGAT GGGGATTAAT TTTATAGCAT 180
TCCATTTTCC TAGTGCCACA TGTGAAATTG GATTTTGATG ATCTTAATCT ATATTCTACC 240
CTTATAATAA AAGATCAAAA GATATATCTC CTATGAACAG ATTGGAGATA GGAGATGAAA 300
AGTTGGGAGG ATGTCTTTAT TCTAATGTGA GGTAGGGAA AATGTGGATA ACATTACTGG 360
GGTGARGGAG GCATTGTTCT TTAGTTGGAG TTCTCATTTT TATTCTCCAG TACTGACTTG 420
TGGGGAAGC ATACTTTTTC ACTGCCAGGT ACTGAATGCA GAGGCTCAGT GAAGTATATA 480
TGTGGGAAGT GCATGCATTT CGTTTATTAG CAAACATAGC TGGATTAAGA CAAAGTTGTT 540
GGTTTGAAAA GGGGTAAAG CCTTAAGTGA ACAAATCTAG CTAACAGTGA ATGAACTAGG 600
TAATATAACT TGCATATTTT TAATTTCCCTT TGGTTAAAGG TCCCCATAC TTCTCTGTTT 660
GGAGACATGA GAAGTATGAT TACTTCAGTG TTAGTTTCTT TAATTTTTTT TTCCCTAT 720
TTGTCCCTTG TCACTTTGTT GCAAGCTAGA AATCTGTGGG TTATACATAG GGCAGCTCTT 780
TGTGAAAGTG GTTTATTCCA CTGGAGAAAG GGGATTGAAA ATCAGTTAGA ACCAATGTAT 840
TTCTTGCCCC ACGGAACACT ATTCTATAA GATAGCTGAA AGAAGCTGCT GTGAGGAGCT 900
CAGCTCCAAA CACAGGATCA GCACCTTGTA TAGGAATTCC CATGAATTAT GACTTCTCAT 960
TCTGTTTAT CAGAGTGCAT ATATGTCCTA CTTCAGGAAA AGTAAAACAG TCATTTACGA 1020
AAGAAAGTCA ATCTGTATCC TAAGCATTTT AATAAAAAGT TAAACAAAA AATTAAAAGG 1080
GACACTCGAG GGGGGGCCCG AAACCCAAT 1109

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(2) INFORMATION FOR SEQ ID NO: 141:

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(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 497 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 141:

TAGGACTAAC TTAAATCTT TTATTCATCT TTTATTTATT AAAAAATTTT ATTTCTTTGA 60
10 ATTTTCCTGT AATTTCTTA RGCTCTTCTA TAAAATGTTA TATTCATGTG AACCATACCT 120
CATTATCCTT AACATTTACT CTCAAAAAGC TTTTATTTT TATTTTTTTG AAGGTAGTTT 180
15 TTCTGTGTGT ACTCTGTAAC ATGATTTTGC TTTCAAATCA TTGTTGTGCC CCCATACAAA 240
ATGCCCTTTA TTTTGTAGGA TCGTGGACTT TTTAGTATGG CATGAGTGTG CTAAAAGCCA 300
GATATCTTTC CACATTCACT GGTGGCTTTG ACACCTAGTT TTTAATCTCC CATCCTTACT 360
20 TTAAACCCGT ACAGTGCAGT CCTCAGTCAG GGCCAGGACC GGGCTGAGGC CCTTTGTGGA 420
GATGCTGCAC CACCAGCAGA AGGCTGAGAC CTGGTTACCT GTACCTGTTT ACTTGTAAATA 480
AAAAGAATTA TCTAAAA 497
25

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(2) INFORMATION FOR SEQ ID NO: 142:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 269 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
35 (D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 142:

ATGAGGCAGA GGCAAGCTGC CTGCCAACC CCTCCCTCAA GGAATGGCCT TGCCCAGGAA 60
40 TGCCCACCAC ACATACCTC TTCTTTTTT CTAGTCAAAC TCTGTATTAT TCCTTGGCTT 120
GCCTCCCTCC TTCTCTCCC TCTCAACCT TACTTCTGG TTTCTATTTC ATGGGATTTG 180
45 GGGTTGAAGT TAACTTACA ACAGTGCCGC CAACACCAAG TCTTGCAGGA AAAAAATACA 240
AAGAAATTTA ACAAAAAAAA AAAAAAAA 269

50

(2) INFORMATION FOR SEQ ID NO: 143:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1269 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
55 (D) TOPOLOGY: linear

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60

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 143:

	TTGATTGACT ATGGTCTCTC CGGCTACCAG GAAGAGTCTG CCGAAGTGAA GGCCATGGAC	60
5	TTATCACCT CCACAGCCAT CCTGCCCCTG CTGTTGGCT GCCTGGGCGT CTTGGGCTC	120
	TTCCGGCTGC TGCAGTGGGT GCGCGGAAG GCCTACCTGC GGAATGCTGT GGTGGTGATC	180
	ACAGGCGCCA CCTCAGGGCT GGGCAAAGAA TGTGCAAAG TCTTCTATGC TGCGGTGCT	240
10	AAACTGGTGC TCTGTGGCCG GAATGGTGGG GCCCTAGAAG AGCTCATCAG AGAACTCACC	300
	GCTTCTCATG CCACCAAGGT GCAGACACAC AAGCCTTACT TGGTGACCTT CGACCTCACA	360
15	GACTCTGGG CCATAGTTC AGCAGCAGCT GAGATCCTGC AGTGCTTTGG CTATGTCGAC	420
	ATACTGTCA ACAATGCTGG GATCAGCTAC CGTGGTACCA TCATGGACAC CACAGTGGAT	480
	GTGGACAAGA GGGTCATGGA GACAACTAC TTTGGCCAG TTGCTCTAAC GAAAGCACTC	540
20	CTGCCCTCCA TGATCAAGAG GAGCAAGGC CACATGTTC CCATCAGCAG CATCCAGGGC	600
	AAGATGAGCA TTCCTTTTCG ATCAGCATAT GCAGCCTCCA AGCACGCAAC CCAGGCTTTC	660
25	TTTGACTGTC TGCCTGCCGA GATGGAACAG TATGAAATTG AGGTGACCGT CATCAGCCCC	720
	GGCTACATCC ACACCAACCT CTCTGTAAAT GCCATCACCG CGGATGGATC TAGGTATGGA	780
	GTTATGGACA CCACCACAGC CCAGGGCCGA AGCCCTGTGG AGGTGGCCCA GGATGTTCTT	840
30	GCTGCTGTGG GGAAGAAGAA GAAAGATGTG ATCCTGGCTG ACTTACTGCC TTCCTTGGCT	900
	GTTTATCTTC GAACTCTGGC TCCTGGGCTC TTCTTCAGCC TCATGCCTCC AGGGCCAGAA	960
35	AAGAGCGGAA ATCCAAGAAC TCCTAGTACT CTGACCAGCC AGGGCCAGG CAGAGAAGCA	1020
	GCACTCTTAG GCTGTCTTAC TCTACAAGG ACAGTTGCAT TTGTTGAGAC TTTAATGGAG	1080
	ATTTGTCTCA CAAGTGGGAA AGACTGAAGA AACACATCTC GTGCAGATCT GCTGGCAGAG	1140
40	GACAATCAAA AACGACAACA AGCTTCTTCC CAGGGTGAGG GGAAACACTT AAGGAATAAA	1200
	TATGGAGCTG GGGTTTAAAC CTAAAACTA GAAATAAACA TCTCAAACAG TAAAAAATAA	1260
45	AAAAAAAC	1269

(2) INFORMATION FOR SEQ ID NO: 144:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1944 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 144:

60	AAAAGGCAAA CTATAGGATA ACACAGAGCC CTTTTTGAAA ATAAATTGGC ATTGGAGTGT	60
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	TTTACCCTCT	AGCTGTTTTA	CTTAGAATGT	AACATATGCT	GCCTACCCAC	CTCAAAATGT	120
	CTGTACTGCA	AGAGGGCCCT	GGGCCTCTGC	TTTCCATATT	CACGTTTGGC	CAGAGTTGTA	180
5	GTCCCAAAGA	AGAGCATGGG	TGGCAGATGG	TAGGGAATTG	AACTGGCCTG	TGCAATGGGC	240
	ATGGAGCACA	AGGGGTCACA	GCATGCCTCC	TGCCTTACCG	TGGCAGTACG	GAGACAGTCC	300
10	AGAACATGGT	CTTCTTGCCA	CGGGGTGTTG	TGTCTCTCTG	TGGTGCTGCA	TGTCTGTGGC	360
	TCACCTTTAT	TCTTGAAACT	GAGGTTTACC	TGGATCTGGC	TACTGAGGCT	AGAGCCCACA	420
	GCAGAATGGG	GTTGGGCCTG	TGGCCCCCAA	ACTAGGGGGT	GTGGGTTTCAT	CACAGTGTG	480
15	CCTTTTGTCT	CCTAAAGATA	GGGATCTACT	TTTGAAGGGA	ATTGTTCTCT	CCAAATAAAT	540
	TTGCTTTACC	TTGGTCCTTT	CTTTTGTGCC	AGTATTCAAG	TGGTATAGCT	CTGAGCAGGG	600
20	TCACATTTGG	CCAAACCTGA	CACTGTCTTG	CTGCATTCTC	CTTTGGCAAA	CATCAGGGTC	660
	AGAATTCAGG	ATAGCCCTTC	CTAGGGCACT	GGACTTTCTG	GCATGGGGGC	TGTGTTTGCA	720
	CAAGTTATTT	TCATGTTACC	TGGAGAGTGT	CCAGAGGCTG	CTCTGAGGCT	GAGGTGTGTT	780
25	CCCCCTTGCC	TGGTTCCAGC	TGTCAGAGGG	ATACCATCCT	AGGGTCTGGG	AATCCAAGGC	840
	CACGAGACTC	CTTGGTTTGT	GGTCCGAGAT	CCTGTACTAA	GGAGGGTCTG	GCCAGAGGAA	900
30	CAGACCAGCT	TTTGACAAAT	GAAGCGCAAG	GGAACAAGTG	GTTTGCTCTG	TGTCTTACCT	960
	GTCCTGAACC	TGGTCTGTG	GGCCATTGAA	AAGTTAGATC	TGTGATCTCT	GGGTTTMTG	1020
	TGGCTTTGTT	CAATGCTTCC	ACTCTAGGGC	AGGCAGAGCA	GTCTATACTC	TCCCAAGCCT	1080
35	GCTTGACCTC	CAAGTAGAGC	TGATACAGAG	ATCTGTGAAT	ATTGTGATAG	AAATTCTTTG	1140
	GTATTTCATC	ATTTTCAGCTG	CAAGTCAGCA	ATTTCCAGG	TACCATGTAA	GCTATAAAAC	1200
40	AGTCATTCTT	AAAGACAGAG	GATAGCTGTG	ACTCATGGGA	TCATGAGGTC	CATGGCTGGT	1260
	TGCAGGTTC	CTTTTTCCTT	CCTCAGGTTT	TGTCTCTTCC	TGTGTTGTCC	CCAGCAAGGG	1320
	AGAGACTGTG	GGGTGGATTG	GGAGAACAGA	TTAGGAGTAT	AGCAAATGAA	CCCAGAATGG	1380
45	AACAGTGGGG	AGCTAACTGT	GAATGAGGAG	AGTACCTGCT	GCAGGACCTG	GAGGTCAGGT	1440
	GTGAATGCTG	TATTGGCACA	GGGAATAAAT	ATCCTGGCGT	CTGGAGCCTT	CACCTCTCCG	1500
50	TCAAGTCCTT	CCTGTGATAC	TGCCATGGCA	CAGGATCTGA	GTTGCAGCTC	TGCACCCTAA	1560
	ATCACACCCT	GGGCATTGTC	TGGGCTGCAG	GGCTGCCAGG	TTCTGTACTT	GTGTCCAGCT	1620
	GTGGCCCTGG	ATGCTGGAGC	TGGAGGGTTT	TCTGTGCTCA	GACTGTAGCC	TGTAGCTCTT	1680
55	GGCCTGTGTA	GAGCCCCCTC	CTGTGCCCTC	AGTGGCTGTC	GTTTGTTAAC	ATCATCAGGA	1740
	AGATGGGAAA	GGTCAGGCAG	AATTTTCTG	CCCTACAAAG	GGTGAAGAG	AAAGGACACA	1800
60	GTATTTTCAT	GAATTTACCA	TATATCTTTG	TTTTTCTTCA	ACGAAAAAGT	TAATTGAGGC	1860

AATGTCATCT GCTCAAAGTT GAGTGGTTTA TTCACAATAA ACTGTAAGTT TCTGATTATA 1920
AAAAAAAAAA AAAAAAAAAA AAAG 1944

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(2) INFORMATION FOR SEQ ID NO: 145:

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(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1021 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 145:

TCGACCCACG CGTCCGGGGT GCGCAACGGG GAGTTCGGC TGGAGACCCG TGCTCTGGGC 60
20 CGGCGCCTTC ACCATGGCCT CGGCAGAGCT GGACTACACC ATCGAGATCC CGGATCAGCC 120
CTGCTGGAGC CAGAAGAACA GCCCCAGCCC AGGTGGGAAG GAGGCAGAAA CTCGGCAGCC 180
25 TGTGGTGATT CTYTTGGGCT GGGGTGGCTG CAAGGACAAG AACCTTGCCA AGTACAGTGC 240
CATCTACCAC AAAAGGGGCT GCATCGTAAT CCGATACACA GCCCCGTGGC ACATGGTCTT 300
CTTCTCCGAG TCACTGGGTA TCCCTTCACT TCGTGTMTTG GCCCAGAAGC TGCTCGAGCT 360
30 GCTCTTTGAT TATGAGATTG AGAAGGAGCC CCTGCTCTTC CATGTCTTCA GCAACGGTGG 420
CGTCATGCTG TACCGCTACG TGCTGGAGCT CCTGCAGACC CGTCGCTTCT GCCGCTGCG 480
35 TGTGGTGGGC ACCATCTTTG ACAGCGCTCC TGGTGACAGC AACCTGGTAG GGGCTCTGCG 540
GGCCCTGGCA GCCATCCTGG AGCGCCGGGC CGCCATGCTG CGCCTGTTCG TGCTGGTGGC 600
CTTTGCCCTG GTGGTCGTCC TGTTCACGT CCTGCTTGCT CCCATCACAG CCNTCTTCCA 660
40 CACCCACTTC TATGACAGGC TACAGGACGC GGGCTCTCGC TGGCCCGAGC TCTACCTCTA 720
CTCGAGGGCT GACGAAGTAG TCCTGGCCAG AGACATAGAA CGCATGGTGG AGGCACGCCT 780
GGCACGCCGG GTCCTGGCGC GTTCTGTGGA TTTCGTGTCA TCTGCACACG TCAGCCACCT 840
45 CCGTGACTAC CCTACTTACT ACACAAGCCT CTGTGTCGAC TTCATGCGCA ACTGCGTCCG 900
CTGCTGAGGC CATGTCTCCA TCTACCTCT GCTCCAGAAA TAAATGCCTG ACACCTCCCC 960
50 ACAAAAAAAAA AAAAAAAAAA ACTCGAGGGG GGGCCCGGTA CCCAATTTCG CCTATAAAGG 1020
T 1021

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(2) INFORMATION FOR SEQ ID NO: 146:

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(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1285 base pairs

(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 146:

GGCAGGAGGA GGGCCACGGC AGCCATCGCG CTTTGCACTT CGGTCTCCTG GTGTACGGCC 60
AACGCCAAGT AGGGGATTGC GTTCCCTCCA GTCGCAGACC CTATCAGATT TGGATATGTC 120
10 CTTTCATATTT GATTGGATTT ACAGTGGTTT CAGCAGTGTG CTACAGTTTT TAGGATTATA 180
TAAGAAAAC TGGTAACTGG TATTTCTTGG ATTGGATAAT GCAGGAAAAA CAACATTGCT 240
15 ACACATGCTA AAAGATGACA GACTTGGACA ACATGTCCCA ACATTACATC CCACCTCCGA 300
AGAACTGACC ATTGCTGGCA TGACGTTTAC AACTTTTGAT CTGGGTGGAC ATGTTCAAGC 360
TCGAAGAGTG TGGAAAAACT ACCTTCCTGC TATCAATGGC ATTGTATTTT TGGTGGATTG 420
20 TGCAGACCAC GAAAGGCTGT TAGAGTCAAA AGAAGAACTT GATTCACTAA TGACAGATGA 480
AACCATTGCT AATGTGCCTA TACTGATTCT TGGGAATAAG ATCGACAGAC CTGAAGCCAT 540
25 CAGTGAAGAG AGGTTGCGAG AGATGTTTGG TTTATATGGT CAGACAACAG GAAAGGGGAG 600
TATATCTCTG AAAGAACTGA ATGCCCGACC CTTAGAAGTT TTCATGTGTA GTGTGCTCAA 660
AAGACAAGGT TACGGAGAAG GCTTCCGCTG GATGGCACAG TACATTGATT AACACAACT 720
30 CACATTGGTT CCAGGTCTCA ACGTTCAGGC TTAATCAGAG ATTTGATTGC TCAACATGCA 780
TAACTTGAAT TCAATAGACT TTTGCTGGTT ATAAACAGA TGTTTTTTAG ATTATTAATA 840
35 TTAAATCAAC TTAATTGAA TGAGAATTGA AAAGTATTC AAGTAAGTTT GAGTATCACA 900
ATGTTAGCTT TCTAATTTCA TAAAGTACT TGGTTTTTAC AGTTTATAAT CTGACATCAC 960
CCCAGCGCCA TTTGTAAAGA GCAACTTTCC AGCAGTACAT TTGAAGCACT TTTTAAACAAC 1020
40 ATGAAACTAT AAACCATATT TAAAGCTCA TCATGTTAAA TTTTTTATGT ACTTTTCTGG 1080
AACTAGTTTT TAAATTTTAG ATTATATGTC CACCTATCKT AAGTGACAG TTAATAATTA 1140
45 GCTTATTCAA TGATTGCATG ATGCCTTACA GTTTTCAATA ACTTTTTTTC TTATGCAAAC 1200
GTCATGCAAT AAAACAACT CTAATGTTTG GCAAAAAAAA AAAAAAAAAA NTCGAGGGGG 1260
50 GGCCCGTACC CAATTCGCCC TAAAG 1285

55 (2) INFORMATION FOR SEQ ID NO: 147:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1386 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
60 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 147:

5	GGCACGAGGT GCGCAGGGG TCAGTGGTTC TCTCGGGTCT CGGGACAGGT GAGCACCTTG	60
	ATGAAGGCCA CGGTCTGAT GCGGCACCTG GCGGGGTGCA GGAGATCGTG GCGGCCCTCC	120
	GCAAGGGCGS CGGAGACCGG TTACAGGTGA TTTCTGATTT TRACATGACC TTGAGCAGGT	180
10	TTGCATATAA TGGAAAGCGA TGCCCTTCTT CTTACAATAT TCTGGATAAT AGCAAGATCA	240
	TCAGTGAGGA GTGTGGAAA GAGCTCACAG CGCTCCTTCA CCACTATTAC CCAATTGAGA	300
	TCGACCCACA CCGACCGTC AAGGAGAAGC TACCTCATAT GGTGGAATGG TGGACCAAAG	360
15	CGCACAACTCT CCTATGTCAG CAGAAGATTC AGAAGTTTCA GATAGCCAG GTGGTTAGAG	420
	AGTCCAATGC AATGCTCAGG GAGGGATATA AGACCTTCTT CAACACACTC TACCATAACA	480
20	ACATTCCTTCT TTTCACTTTT TCTGCGGGCA TTGGTGATAT CCTGGAAGAA ATTATCCGAC	540
	AGATGAAAGT GTTCCACCCC AACATCCACA TCGTGTCTAA CTACATGGAT TTTAATGAAG	600
	ATGGTTTCTT CCAGGGATTT AAGGGCCAGC TGATACACAC ATACAACAAG AACAGCTCTG	660
25	TGTGTGAGAA CTSTGGTTAC TTCCAGCAAC TTGAGGGCAA AACCAATGTC ATCCTGCTGG	720
	GAGACTCTAT CGGGACCTC ACCATGGCCG ATGGGGTTCC TGGTGTGCAG AACATTCTCA	780
30	AAATTGGCTT CCTGAATGAC AAGGTGGAGG AGCGGCGGA NCGCTACATG GACTCCTATG	840
	ACATCGTGCT GGAGAAGGAC GAGACTCTGG ATGTGGTCAA CGGGCTACTG CAGCACATCC	900
	TGTGCCAGGG GGTCCAGCTG GAGATGCAAG GCGGCTGAAG GCGCAGGCTN CCAGNCCGCC	960
35	TGCAGGCCGT GGTGAGGAGG GCGGCCTCCC CAGAGTCTGC TCCCCCGTGA ACACAGAGCA	1020
	GANGCCAGGG TGGCCAGCAG TGGCTGGGTC CTTCCGCGCC CCTCCGTCTT CCTTTCCCTG	1080
40	AGCACCTTCA TCACCAGAGG CTTGAAGGAA CCCCGCCATG TGGCAGGGCA CAGGCACTGT	1140
	TCCTGGTGAA CCTTGGACCA CAGCATGTCA GTGCTCTAGG GATTGTCTAC TCCAGGGATT	1200
	TTCTTCAAAA TTTTAAACA TGGGAAGTTC AAACAAATAT AATGTGTGAA ACAGATCAAA	1260
45	ATTTTAAAAA TGAAAAAAA GCTGCTCTGA TTCAGGGGAT GTGGGTCGGG GTAGAACCTG	1320
	GACCTCTTGG CCTGGGGGCA CATGGGATGC TTCTAGGAAC ACAGTTTGAG AACCACCAA	1380
50	AAAAAA	1386

55 (2) INFORMATION FOR SEQ ID NO: 148:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2098 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

60

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 148:

5	AGCCCTTCTC CCCGCGCTTG GGA CTCTGAC ATCTTAAGGC TGCACGGTCG TGTCTTGTGTC	60
	TGGGTGAGGC CATGTCTGTG ATCCAAGGTT CCTGGAAGTC ACACAGGAAG GGGCTGTGAA	120
	CCCTAAGTGG GTGTMATCTC CTCCRACCGA GGCTTCTMAC CCTGGAGATG GCAGTTACTC	180
10	CTGGCCATGG TTGCTGAGCA TGGGCAGACC AGTGGAGGCC ACCCTACTGT GPTATCTGCG	240
	CCTTCRATGA AGTGAGACCC TTGGGGAGAA CGGGCTGTGG ATGAAGGAGT GGA CTGCAGC	300
15	CTTGGCCTAG CCACTGGGCT GGGATCTTCT GGGTCATGTG ACTGTGTATC CAGGAGCAGA	360
	AACTTGTAAT CTCAGGATTC AGGATCTACC CAGCACCAAA GATGTATTTT CAGGAGAACA	420
	GACCTAGAAA TGGCCCTGTC TGGCATTTCA GAGTCAGGCA AAGCAGGCAG GGCCAGGGAG	480
20	CTTCTGTGGG TCTACACAAG AAGGTTCCTG TGAGGGCTAT CAGTTGTTGC CTTCTAGCTT	540
	GCTGTAAGT TTGGCGCCTC CGCCAAGCCC TGCCAGACTC CCCTGGCTGT GATGGCATTC	600
25	TGTGCCATCC TGCCCTGTCC CCAGCCTCTG CAGGATGCCC TCCCTACCCA MCTYTYCCTG	660
	GGCCTTCCCT GTCCACTGGG CTGGATTCAT GTTCAAACCA CTGGACTGGC AGGGCAACGA	720
	CTTCTTCCCA CCTCAAGATG AGGTCTCTGC CCCCTTGTCT TGGCATAAAA ACACCTTTAA	780
30	AGCATGAGCC ATGTGCTTCT TTGCCCTTCT CTGTCTGTGT CCAATCTTCT GCCTCCAGT	840
	CACTCCCTGG GGA CTATGGG ATCACTGTCC CCCCACCTGT GTGGCCACAC CATGTGTCTT	900
35	GTCAATCCAG AACTGCCTCT GAGCTCCAGG CTGACCACAG ATCAGCCACA GCCTGATGCC	960
	TGCAGCCCCA CTTTGCTCAC CCTTCCCTC CCCTCCTCCT TCCTTCCACA CAGCAAGCCT	1020
	ACCTTTYTCC ATCCATGCTC ACCATAGCCC CCTTCCTTGT GACCTGGACC CTCCAATTGA	1080
40	CCTGGCTGAG ACTGTGAGCC TCCTGGAGGA GTGGGGTCCA CCTTCTTCTT GCCCTATGCA	1140
	GTGCAAGCTT CACTTCTCAC CCAGCAAGGT TGA CTATCT GCCTCCATGT CTCTGGGGCT	1200
45	TTGCTGTGTC CCTGAAACCT AGCTGGGCTG GTCTTGCTCC CAGCTTGCTT CCCCCTCCTC	1260
	GGATGTCCCT TTGCAGGCCC CTGTCTGTCC TCCGGCACCA GTGTCTTGG CTGCCATGGC	1320
	AAGCTCATCA GGGGCTTGTA CCCTGGTCAC CAAGCATGGT AGCAGCTGCC TGCATTGTAT	1380
50	CTCCATCTGG TCACTGCAGG TGCCAACCTT TCATCCCCCA TGTTTTCTCT GGCCATGGAG	1440
	GGCTGACCTC CGTTTCTGGG GAATGTGGCT GAGCTGTGGT AACCAGCTAC ACCCCAGGTG	1500
55	CTCTTTCCAT GGTGGTGCTT GCTCATCTTG CTGATGCAAA CTAGGAAGTT AGGCTGCATC	1560
	TCGGAGTGGC TTTCTGCTGA GAGGTGCTTT GCTGTCTCTC AGACTCAGTC ACTGTGTTCC	1620
60	CTCCCCGCTT CTCATTATCT CATGGCTGTT TGCAGCTCTC CCAGGTACTT TGGGGTCTGA	1680

GCTGGAATTC CTTTGTGGTT TGCTCTTCTG CTTCTCACTC TTGTATTAAAG AAGGATTCCA 1740
 CAAAGGGAGA GTGGCATCCC TGCTGCTGCT GTGCCAGACC AGAGTTTCCT GAGGGGCCCT 1800
 5 GACCCTAACC CTCCAGCTCA GCCCTGTACA CCTGACCCCTG TAAATGAGTG GGGTTTGCTG 1860
 ACTGTAATCC CTGACACCAG TAAAACCAAA AGGACTCTTG GGGGCTCAGT GTGAGAGCCA 1920
 GGGTTACCTA CTCTGCCAAG TGAGGACAAA CTGCTAGGCT GTATCCATA ATTTCAAGAT 1980
 10 GAGAAACATT AACAAATAAA ATTTGTAGTA AACATAACCT CATGANGACT AAAAAAAAAA 2040
 AAAAACYGG GGGGGGGCCC GTAACCCATT GGGCCCTTNG GGGGGGNGTT TTAAAATT 2098

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(2) INFORMATION FOR SEQ ID NO: 149:

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- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1847 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 149:

TCGACCCACG CGTCCGAACT GAGCGGCGG CGGGAGCCGG TTGGKGTCTG GTCTTCGCGT 60
 30 CGGCCCCGCG GACCAGACGC TGCCCCCGGC GCGGGGAGAA GATGGTGCKK AGCGGCCTCG 120
 GGGCCGCCAC GCGCCGCCAC GAGTGAGCCC AGCGCGACCG CGGGCGTCCG CCGAGCAGCT 180
 GGGCCGGCTG GGGCCGGGCG GCGCANTGCC CGCCGGGGCG GGGTGGAGCT GATCAGAATA 240
 35 ATGTTTCAGCA TCAACCCCTT GGAGAACCTG AAGGTGTACA TCAGCAGTCG GCCTCCCTTG 300
 GTGGTCTTCA TGATCAGCGT AANGCCCATG GCCATAGCTT TCCTGACCCT GGGCTACTTC 360
 40 TTCAAAATCA AGGAGATTAA ATCCCAGAA ATGGCAGAGG ATTGGAATAC TTTTCTGCTA 420
 CGGTTCAATG ATTTGGACTT GTGTGTATCA GAGAATGAAA CCCTCAAGCA TCTCACAAC 480
 GACACCACAA CTCCGGAAAG TACAATGACC AGCGGGCAGG CCGAGCTTC CACCCAGTCC 540
 45 CCCCAGGCC TGGAGGACTC GGGCCCGTG AATATCTCAG TCTCAATCAC CCTAACCTG 600
 GACCCACTGA AACCTTTCGG AGGTATTCC CGCAACGTCA CCCATCTGTA CTCAACCATC 660
 50 TTAGGGCATC AGATTGGACT TTCAGGCAGG GAAGCCACG AGGAGATAAA CATCACCTTC 720
 ACCCTGCCTA CAGCGTGGAG CTCAGATGAC TGCGCCCTCC ACGGTCCTG TGAGCAGGTG 780
 GTATTACAG CCTGCATGAC CCTCACGGCC AGCCCTGGGG TGTTCCCCGT CACTGTACAG 840
 55 CCACCGCACT GTGTTCTGA CACGTACAGC AACGCCACGC TCTGGTACAA GATCTTCACA 900
 ACTGCCAGAG ATGCCAACAC AAAATACGCC CAAGATTACA ATCCTTTCTG GTGTTATAAG 960
 60 GGGCCATTG GAAAAGTCTA TCATGCTTTA AATCCCAAGC TTACAGTGAT TGTTCAGAT 1020

	GATGACCGTT CATTAAATAA TTGTCATCTC ATGCACACCA GTTACTTCCT CTTTGTGATG	1080
5	GTGATAACAA TGTTTTGCTA TGCTGTTATC AAGGCAGAC CTAGCAAATT GCGTCAGAGC	1140
	AATCCTGAAT TTTGTCCCGA GAAGGTGGCT TTGGCTGAAG CCTAATTCCA CAGCTCCTTG	1200
	TTTTTTGAGA GAGACTGAGA GAACCATAAT CCTTGCCTGC TGAACCCAGC CTGGGCCTGG	1260
10	ATGCTCTGTG AATACATTAT CTTCGATGT TGGGTTATTC CAGCCAAAGA CATTTCAAGT	1320
	GCCTGTAACT GATTGTGACA TATTTATAAA AATCTATTCA GAAATTGGTC CAATAATGCA	1380
15	CGTGCTTTGC CCTGGGTACA GCCAGAGCCC TTCAACCCCA CCTTGGACTT GAGGACCTAC	1440
	CTGATGGGAC GTTTCACGT GTCTCTAGAG AAGGATTCCT GGATCTAGCT GGTACGACG	1500
	ATGTTTTCAC CAAGTCACA GGAGCATTCG GTCGCTGATG GGGTTGAAGT TTGGTTTGGT	1560
20	TCTGTATTCA GCCCAATATG TAGAGAACAT TTGAAACAGT CTGCACCTTT GATACGGTAT	1620
	TGCATTTCOA AAGCCACCAA TCCATTTTGT GGATTTTATG TGTCTGTGGC TTAATAATCA	1680
25	TAGTAACAAC AATAATACCT TTTTCTCCAT TTTGCTTGCA GGAAACATAC CTTAAGTTTT	1740
	TTTTGTITIG TTTTGTITTT TTGTITTTTT GTTTTCCTTT ATGAAGAAAA AATAAAATAG	1800
30	TCACATTTTA ATACTACCAA AAAATGGACA AAAAAAGTCG AGGGGGG	1847

(2) INFORMATION FOR SEQ ID NO: 150:

- 35 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1569 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

- 40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 150:

	GACGCTGACG AGAGAAGGCC TCTTCCTTGA GGGTTGGTGC TGTGTTGCAG TGACCGTGGC	60
45	GGATTACGCC AACTCGGATC CGGCGTCTGT GAGGTCTGGA CGAGTCAAGA AAGCCGTAGC	120
	CAACGCTGTT CAGCAGGAAG TAAATCTCTT TTGTGGCTTG GAAGCCTCTC AGGTTCCTGC	180
50	AGAGGAAGCT CTTTCTGGGG CTGGTGAGCC CTGTGACATC ATCGACAGCA GTGATGAGAT	240
	GGATGCCCCAG GAGGAAAGCA TCCATGAGAG AACTGTCTCC AGAAAAAGA AAAGCAAGAG	300
	ACACAAAGAA GAACTGGACG GGGCTGGAGG AGAAGAGTAT CCCATGGATA TTTGGCTATT	360
55	GCTGGCCTCC TATATCCGTC CTGAGGACAT TGTGAATTTT TCCCTGATTT GTAAGAATGC	420
	CTGGACTGTC ACTTGCACTG CTGCCTTTTG GACCAGGTTC TACCGAAGCA CTACACGCTG	480
60	GATGCTTCCC TGCCTTTGCG TCTGCGACCA GAGTCAATGG AGAAGCTGCG CTGTCTCCGG	540

	GCTTGTGTGA TCCGATCTCT GTACCATATG TATGAGCCAT TTGCTGCTCG AATCTCCAAG	600
	AATCCAGCCA TTCCAGAAAG CACCCCCAGC ACATTAAAGA ATTCCAAATG CTTACTTTTC	660
5	TGGTGAGAA AGATTGTTGG GAACAGACAG GAACCAATGT GGAATTCAA CTTCAAGTTC	720
	AAAAAACAGT CCCCTAGGTT AAAGAGCAAG TGTACAGGAG GATTGCAGCC TCCCGTTCAG	780
10	TACGAAGATG TTCATACCAA TCCAGACCAG GACTGCTGCC TACTGCAGGT CACCACCCCTC	840
	AATTTTCATCT TTATTCGAT TGTTCATGGA ATGATATTTA CTCTGTTTAC TATCAATGTG	900
	AGCACGGACA TCGGGCATCA TCGAGTGAGA CTGGTGTTC AAGATTCCCC TGTCCATGGT	960
15	GGTCGGAAAC TCGCAGTGA ACAGGGTGTG CAAGTCATCC TGGACCCAGT GCACAGCGTT	1020
	CGGCTCTTTG ACTGGTGGCA TCCTCAGTAC CCATTCTCCC TGAGAGCGTA GTTACTGCTT	1080
20	CCCATCCCTT GGGGGCAGCC TCGAGTGTAG TCCATTAGTA ATCAGATTCC AGTTTGGACA	1140
	GGGTGGCTGG ATTGTATATC TCGTTAGTAA TGTACATGCT CTTCAGGTTC TAGGGCTCCT	1200
	GTTAGGGGAG GGAGAAATGT TGAATCAAGA GGGAAAACAA CTACTATGAT TTATAAACAT	1260
25	ATTTTAATGT AAAAATTGTC ATTTAAAAGG AGTGGCCCTG TTTTCTGTGT TAAAACCCCA	1320
	TTTGGTGCTA TTGAGTTTGT TCTTTATTCT TTTATCCCAG TGAAAATGT TGATCTTGCT	1380
30	GTAGGGAAAA ATTAACTCT TTGAATCTCC AAACAAGGAA GTTTCAGCAT TCCCTTATGG	1440
	ATCAGAGGAA CCTTAGAGGC CTGAAATTGT TGCTTCCAGT TTAGCTGCCC CTCAAATTCA	1500
	AGTGAATATT TTCCCTTCTC CCTTTACCCT TCTCCAGAAA TAAAGCAGGT GACAGGGTTT	1560
35	CAGAATCTT	1569

40 (2) INFORMATION FOR SEQ ID NO: 151:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1540 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 151:

50	CCCACGCGTC CGGAAGGATT GACCAGTTAA CCAACATCTT AGCCCCCATG GCTGTTGGCC	60
	AGATTATGAC ATTGGGCTCC CCAGTCATCG GCTGTGGCTT TATTTGCGGA TGGAACCTGG	120
55	TATCCATGTG CGTGGAGTAC GTCCTGCTCT GGAAGGTTTA CCAGAAAACC CCAGCTCTAG	180
	CTGTGAAAGC TGGTCTTAAA GAAGAGGAAA CTGAATTGAA ACAGCTGAAT TTACACAAAG	240
	ATACTGAGCC AAAACCCCTG GAGGGAAGTC ATCTAATGGG TGTGAAAGAC TCTAACATCC	300
60	ATGAGCTTGA ACATGAGCAA GAGCCTACTT GTGCCTCCCA GATGGCTGAG CCCTTCCGTA	360

	CCTTCCGAGA TGGATGGGTC TCCTACTACA ACCAGCCTGT GTTCTGGCT GGCATGGGTC	420
5	TTGCTTTTCTT TTATATGACT GTCCTGGGCT TTGACTGCAT CACCACAGGG TACGCCTACA	480
	CTCAGGGACT GAGTGGGTTT CATCCTCAGT ATTTTGATGG GAGCATCAGC TATAACTGGA	540
	ATAATGGGAA CTGTAGCTTT TACTTGGCTA CGTCGAAAAT GTGGTTTGGT TCGGCAGGTC	600
10	TGATCTCAGG ATTGGCACAG CTTTCCTGTT TGATCTGTG TGATGCTCT GTATTTCATGC	660
	CTGGAAGCCC CCTGGACTTG TCCGTTTCTC CTTTGAAGA TATCCGATCA AGGTTTCATT	720
15	AAGGAGAGTC AATTACACCT ACCAAGATAC CTGAAATTAC AACTGAAATA TACATGTCTA	780
	ATGGGTCTAA TTCTGCTAAT ATTGTCCCGG AGACAAGTCC TGAATCTGTG CCCATAATCT	840
	CTGTCACTCT GCTGTTTGCA GCGTCATTG CTGCTAGAAT CCGTCTTTGG TCCTTTGATT	900
20	TAAGTGTGAC ACAGTTGCTG CAAGAAAATG TAATTGAATC TGAAAGAGGC ATTATAAATG	960
	GTGTACAGAA CTCCATGAAC TATCTTCTTG ATCTTCTGCA TTTCATCATG GTCATCCTGG	1020
25	CTCCAAATCC TGAAGCTTTT GGCTTGCTCG TATTGATTTT AGTCTCCTTT GTGGCAATGG	1080
	GCCACATTAT GTATTTCCGA TTTGCCCAA ATACTCTGGG AAACAAGCTC TTTGCTTGCG	1140
	GTCTTGATGC AAAAGAAGTT AGGAAGGAAA ATCAAGCAA TACATCTGTT GTTTGAGACA	1200
30	GTTTAACTGT TGCTATCCTG TTAGTAGATT ATATAGAGCA CATGTGCTTA TTTTGTACTG	1260
	CAGAATTCCA ATAAATGGCT GGGTGTTTTG CTCTGTTTTT ACCACAGCTG TGCCTTGAGA	1320
35	ACTAAAAGCT GTTTAGGAAA CCTAAGTCAG CAGAAATTAA CTGGATTAAT TTCCCTTATG	1380
	TTGAGGGCCA TGGRAAAAAA ATTGGGAAAA GGAAAACTC AGTTTAAAT ACGGGAGACT	1440
	ATAATGGATA AACTGGRATT CCCCTATTTC TCATGAGTAG ATACAATCTT ACGTAAAAGA	1500
40	GTGGTTAGTC ACGTGAATTC AGTTATCAAT TGACAGATTC	1540

45 (2) INFORMATION FOR SEQ ID NO: 152:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1719 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 152:

55	TACTTATGAG GTCAATTGGA AATAAGAACA CCATTTTACT GGGTCTAGGA TTTCAAATAT	60
	TACAGTTGGC ATGGTATGGC TTTGGTTCAG AACCTTGGAT GATGTGGGCT GCTGGGGCAG	120
60	TAGCAGCCAT GTCTAGCATC ACCTTTCCTG CTGTCACTGC ACTTGTTCGA CGAACTGCTG	180

	ATGCTGATCA ACAGGGTGTC GTTCAAGGAA TGATAACAGG AATTCGAGGA TTATGCAATG	240
	GTCTGGGACC GGCCTCTAT GGATTCATTT TCTACATATT CCATGTGGAA CTAAAGAAC	300
5	TGCCAATAAC AGGAACAGAC TTGGGAACAA ACACAAGCCC TCAGCACCAC TTTGAACAGA	360
	ATTCCATCAT CCCTGGCCCT CCCTTCCTAT TTGGAGCCTG TTCAGTACTG CTGGCTCTGC	420
10	TTGTTGCCTT GTTTATTCCG GAACATACCA ATTTAAGCTT AAGGTCCAGC AGTTGGAGAA	480
	AGCACTGTGG CAGTCACAGC CATCTCATA ATACACAAGC GCCAGGAGAG GCCAAAGAAC	540
	CTTTACTCCA GGACACAAAT GTGTGACGAC TGAATCAGG AAGATTTTTC TATCAGCACC	600
15	CAGGTCTTAG TTTTCACCTC TAGTCTGGA TGTACATTCC ATTTCCATCC ACAGTGTACT	660
	TTAAGATTGT CTTAAGAAAT GTATCTGCAT GAACTCCGTG GGAATAAAG GAAGTGGGAA	720
20	CTTAGAACCA GACAGTTTTC CAAAGATGTT ACAATTCTT TTGAAAAACC TTTTGTATTAT	780
	TAGCACCAAT TTCTYGCAC TAAGCTATTT GTTTTATTAT ACATCCTTTA ATTAAAACT	840
	ATATATGTAA CTTCCTAGAT ATTAGCAAAT GTCTCTGCTA CCAITTCCTT AAGGTGTTGA	900
25	GCTTTAACTC TATGCTGACT CAGTGAGACA CAGTAGGTAG TATGGTTGTG GACCTATTTG	960
	TTTTAACATT GTAAAAATTT GAGTCAGATT TTAATATTGT AAAATCTGG GTCAAATAAT	1020
30	TCAAAGCCTT AATGCAGATG CACTAAAACA AAGAAATGGT AAATGAATTG TTTGCATTTA	1080
	AAAAAAAAAA CTCTTAAGAA AACTGTACTA AATCTGAATC ATGTTTTGAG CTGTGTTGCA	1140
	GTACTTTTAA ACATTATICA CTAAGTGT TTGAAGTAGA AAGTATCAGC CATTTAGCAT	1200
35	TTAAGTGGG GTATTTAGAG CCTGTAATCT AAATGCTGGC TCAAATTTAT TCCCCAGCTA	1260
	CTTCTTATAC CACTATTCTT TTAATGTTTG CATAATCATA AGCACCTCAA CACTTGAATA	1320
40	CATAATCTAA AAATTATATA GTAAAGCTGG TAGCCTTGAA AATGTCAGTG TGATATCTAT	1380
	TATGTAGATA AATATATATA GTGGCCTTTC AGGACTGTCA CAGTAACACT TTATTTACAG	1440
	AGCTAATGTT TGTCCTAAAT TTTCAGGACC CTAGAGGAGA GCTTTATACA ATTACCGATG	1500
45	TGAATTTCTC TAAAGTGTAT ATTTTGTGT CCAGTTATAT TATTTAAAAA AGTGTACTT	1560
	TGTAAAAATT GTATATAAAG AACTGTATAG TTTACTGT TTTTCATCTG TGTGTGGTTA	1620
50	TTGCTTAATG CTTTTTAAAC TTGGAACACT CACTATGGTT AAATAAGGTC TTAAGAGAAA	1680
	TGTAAATATT YGTTAATAA AGTTAAATAT TTAAATGAT	1719

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(2) INFORMATION FOR SEQ ID NO: 153:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 863 base pairs

(B) TYPE: nucleic acid

60

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 153:

5
GGCACGAGGG AAGCCGGGAC GATGTCCGCA TGACAACCGA CGTTGGAGTT TGGAGGTGCT 60
TGCCTTAGAG CAAGGGAAAC AGCTCTCATT CAAAGGAACT AGAAGCCTCT CCCTCAGTGG 120
10 TAGGGAGACA GCCAGGAGCG GTTTCCTGGG AACTGTGGGA TGTGCCCTTG GGGCCCCGAG 180
AAACAGAAG GAAGATGCTC CAGACCAGTA ACTACAGCCT GGTGCTCTCT CTGCAGTTCC 240
TGCTGCTGTC CTATGACCTC TTTGTCAATT CCTTCTCAGA ACTGCTCCAA AAGACTCCTG 300
15 TCATCCAGCT TGTGCTCTTC ATCATCCAGG ATATTGCAGT CCTCTTCAAC ATCATCATCA 360
TTTTCCTCAT GTTCTTCAAC ACCTTCGTCT TCCAGGCTGG CCTGGTCAAC CTCCTATTCC 420
20 ATAAGTTCAA AGGGACCATC ATCTGACAG CTGTGTACTT TGCCCTCAGC ATCTCCCTTC 480
ATGTCTGGGT CATGAACTTA CGCTGAAAA ACTCCAACAG CTTCATATGG ACAGATGGAC 540
TTCAAATGCT GTTTGTATT CAGAGACTAG CAGCAGTGTG TACTGTCTAC TTCTATAAAC 600
25 GGACAGCCGT AAGACTAGGC GATCCTCACT TCTACCAGGA CTCTTTGTGG CTGCGCAAGG 660
AGTTCATGCA AGTTCGAAGG TGACCTCTTG TCACACTGAT GGATACTTTT CCTTCCTGGA 720
30 TAGRAGGCCA CATTTGCTGC TTTGCAGGGG AGAGTTGGGC CCTATGCATG GGGCAAAACA 780
GGTGGGATTT TCCAAGGGAA GGGTTCAGAA TTAGGCNTGT TGTTTCAGCC ATTTCCAAGG 840
AAGGGAAGG GTTCCCTNC CCT 863
35

(2) INFORMATION FOR SEQ ID NO: 154:

40

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1101 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

45

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 154:

50 AACAGCAAAA AAGAATGATT TCTTCTGAAA TTGTGGAACA TGAGGATTCA AGTTTTTATT 60
TTGTACTAG GTGCTGGAGG AACATCCAG TTCACAAAGC CCCCATCTCT TCCTCTGGAG 120
CCAGAGCCTG CGGTGGAATC AAGTCCAAC GAAACATCAG AACAAATAAG AGAGAAATAA 180
55 GAATAGAATG AATGACCCCA AAATARGGTT TTCTTGGGCG AGGATGTGCT GGATTAGGAA 240
AGGTGACATG ACACAGGCAG AGCAGAGTGG CACCCACCAC AGAATACAGT GTGTGTTATT 300
ACGAGGAGCC AGCAGTTGAG CCTAAGGTCC TTCTACCTAC CTGGTATTGG CATTTGAGGT 360
60

CGGAAACCCCT CTA CTGCCCC ATAAGCCAGG AAAAGTGAAA AGAGAACACA GTTCCTTTTAA 420
 GAACTGGCAG CAAGGCTTGA GGCCTTATGT ATGTAGCTGA GTCAGCAAGG TACATGATGC 480
 5 TGTCTGCTTT CAAAAGGACT TTTCTCTCCT AGCTGACTGA CTCCTTCCTT AGTTCAAGGA 540
 ACAGCTGAGA CAGACCTCTG CTGAGTAGCT CTGTGATGAC AAAGCCTTGG TTAACTGAG 600
 GTGATCCTCA GGTGTGAGG TTTATTAGTC CCCAAGGCAA ACACAAATAT TAGATTAATA 660
 10 ATCCAACTTT AATAGTATAC ATTTAAAAGA AAAAAACAA AAGCCCTGGA AGNTTGAGGC 720
 CAAGCCTGCT GAGTATTGCA GCTGCATTTG CCCAAAGGGA ATCCAGAACA AGTCCCTCCC 780
 15 TGTATTTTGT TCTTGAGAGG GGTCACTCTA GAAGCTAGAT CCTATCAGGA TGAGGAGCAG 840
 CAGCCAGGG CTGTCTGGA TCAGCACCAA CGATTTTAAA GAAAAAGGA AGAGTTTCTT 900
 AGATGAGTAA TTGTTATTGA AGATAGTCAG TGATAACCAC TGACCAGATG CTATCAATAC 960
 20 ACTATGTGTC CTTTTAGAA TAAAGATTAC ATATCATCAT TCCTTTGGGG AAAATTGTTA 1020
 TTCAGGTATA AAAACAAGAG ATTATAATAA AAAANTAAAA GAACCTAAA AAAAAAAAC 1080
 25 CTCGTGCCGA ATCCCTGCA G 1101

30 (2) INFORMATION FOR SEQ ID NO: 155:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2031 base pairs

(B) TYPE: nucleic acid

35 (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 155:

40 CAATTAACCC GTTTGAGGCC TAGGTTGTTT GGCAAGCCCC NGGCCTAAAG TTTTAATTCG 60
 GCAGAGCCAA GGCCTGAAA GGAAGGGAAA GGGGAGGGTA GCGGGAGGGT AGCAGGTGAG 120
 TTCCTAGGGC TGAAGGTTT AGCAGCAGCC TGGTGCACTG CCCTGTCATC AAGACAAACC 180
 45 CACGGTCCTC CTGGGTGCCT ACCAAGCTTG GTTTGTACAA AAGCAAGGTG GGAGTCTATT 240
 TTTGTACATG AGATACATCA CACTTACCTG TGGGCCAGTA TTGTGAAGTG AGTCTGAGTT 300
 50 GTTTTACTG ATGCCCTCCC TGCCACCCAC AAATTGTGTA CATAGTCTTC AGAATGATAC 360
 CACCCCTTTC CCCAGCTCCC AACCAAGAGC TGGTTCTAGG CCTGTGTTAT ATGTCATATT 420
 TAGCGTTTTT ATATATGACC TTTGATTCTT GTTGTGTTGTA TTTTAGCACA GTGTATGCAC 480
 55 CTTCAATTA AATACATCTGT GTGCATACAG ATACGCATAT ATGTGTGTGC GTATGCATAT 540
 ATCTCTCATC TGTAGTTTCC AAGAGTTCAG CTGAAGCAGA TGGAGTCCTG CAGCCAGGA 600
 60 GACACCCCTG ATCCCTGCTA ATAGTGTGTT CCACAAGTAT TAGTGAGTCT TCCTTATTAA 660

TATTTTCATT TCAGAAGACT GAAGCAAAGC TGATAGTGTT TGCTGTTTCT TTGGCAGCTA 720
 AGTGAGGGTC TTGGGATGAC TTGCTGTGTT CCTCAAGCTG CACTTTGGGG CCATCTCTGC 780
 5 AGTATTAAAGC CCCCTTTTTCG CTGGGTGGTA CTCTGTCTGT GCCTGTGTGT GTGTGTGATA 840
 GTCACCTCTG CATGGCTTCC ATGTCTGGTT TGTGGCATTG GGGGATAAGT GCTGAACCAG 900
 10 AGCATTTGCA GTTTGTTTGA GGCTCGTTG CCAATGATAG ATCACTCCTG TTGACCTGGT 960
 ATGTCTGCTT GCTTGCTGCT TTTCCTTGCT TTCTCTTGGA AGAGGAAAGG ACTCTGGTCA 1020
 15 GGCCAGGCT GAGTGAGATG AGCTGCAGCT GGCTCATGGC CTTCTTAGAG CAGAGAGAGG 1080
 AGTATGTCAT TTTACTAAGT TCCTAAACAA ACATTTATGC AGGCAACACT CCTTGCAGAT 1140
 CCAGAACTG AGGCACAATA GGGTTATGAC TTGCTCAAGA ATATGTAGCT GCTAGGGGGT 1200
 20 AAATCAAGGC ATCACAATT CTGTCAGCG GGCAGGAATA GGCTGTGAAT TGCTAGCACT 1260
 TTTTTTTTAA GCAATTACTT TTTGACTTGT TCCTCTGAAA GTGCAAGAGG CGTACACCTT 1320
 TCCCAAATGT AGACTAGAAT CTGCAGGATG CCACCCACTG TATAGTTCTG CTTTCCAGA 1380
 25 GAGGAAGAAC TTTTAGAAAC CAAATGATCT TAATTGTTAT TGCCACCCC TGGCTTTTCC 1440
 GGGTAGAAAA TTCACAGTAG GAATGATTGT TAAGAGAGAG TGCTTGGAAC CATGGGTAA 1500
 30 CAGGAAAGGC TACCTAATT CACATATCTG CAACCAGAGC AGCCACCAAG CATTACTTAG 1560
 CAGCAGGAAA ATGATTGTAT TTGAGTTCTT GTGTGTCCAA AACTGAGGCA CCATGTTCTT 1620
 TGAAAACATG CCACCTCAAG GCTGGGCGCG GTGGCTCACA CCTGTTAATC CCAGCACTTT 1680
 35 GGGAGGCCGA GCGGGCGGA TCACCGAGT CGGGAGTTT GAGACCAGCC TGGACCAACA 1740
 TGGGAGAAAC CCCATCTCTA CCTAAAAATA CAAAATTAGC CGGGCGTGGT GGCATGCGCC 1800
 40 TATAATCTCA GCTACTTGGG AGGGYTGAGG CAGGRGAATT GCTTGAACCC RGGANGGCGG 1860
 AGGTTTGCGG TTGAGTTGAG GATCGTGCCA TTGCACTTCC GGGCCTTGGG GCAACAACAG 1920
 45 CAAAAAYTCC GTCTTCAAMW MRTGCCGAAT TCGATATCAA GCTTATCGAT ACCGTCGACC 1980
 TCGAGGGGGG GCCCGGTACC CAATCGCCC TATAGNGATC GTATTACAAT C 2031

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(2) INFORMATION FOR SEQ ID NO: 156:

(i) SEQUENCE CHARACTERISTICS:

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- (A) LENGTH: 1981 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

60

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 156:

	CCTGCACCCCT GAGCCCTTCA CCCCTCCGAG TTCCCCCAG GTTGGCTTCC TTCGATTCT	60
	TTCTCTGGTA TCAACGTTTG ATTGGAAGAA CAACCCCTC TTTGTCAACC TCAATAATGA	120
5	GCTCACTGTG GAGGAGCAGC TCGGGCACAG CTCMCCGYA TGGTCATTGT TACCCCCAA	180
	GACCGCAAAA ACTCTGTGTG GACACAGGAT GGACCTCAG CCCAGATCCT GCAGCAGCTT	240
10	GTGGTCCTGG CAGCTGAAGC CCTGCCCATG TTAGAGAAGC AGCTCATGGA TCCCCGGGA	300
	CCTGGGGACA TCAGGACAGT GTTCCGGCCG CCCTTGGACA TTTACGACGT GCTGATTGCG	360
	CTGTYTCTC GCCATATCCC GCGGCACCGC AGGCTTGTGG ACTCGCCAGY TGCTCTCTC	420
15	TGCCGGGGCC TGCTCAGCCA GCCGGGGCCC TCATCCCTGA TGCCCGTGCT GGGTINATGAT	480
	CCTNCTCAGC TCTATCTGAC GCAGCTCAGG GAGGCCTTTG GGGATCTGGC CCTTTTCTC	540
20	TATGACCAGC ATGGTGGAGA GGTGATTGGT GTCTCTGGA AGCCACCAG CTTCAGCCG	600
	CAGCCCTTCA AGGCCTCCAG CACAAAGGGC CGCATGGTGA TGTCTCGAGG TGGGGAGCTA	660
	GTAATGGTGC CCAATGTGA AGCAATCCTG GAGGACTTTG CTGTGCTGGG TGAAGGCCTG	720
25	GTGCAGACTG TGGAGGCCCG AAGTGAGAGG TGGACTGTGT GATCCAGCT CTGGAGCAAG	780
	CTGTAGACGG ACAGCAGGAC ATTGGACCTC TAGAGCAAGA TGTCAGTAGG ATGACCTCCA	840
30	CCCTCCTTGG ACATGAATCC TCCATGGAGG GCCTGCTGGC TGAACATGCT GAATCATCTC	900
	CAACAAAACC CAGCCCCAAC TTTCTCTCTG ATGCTCCAGC ATTGGGGCAG GGGCATGGTG	960
	GCCCATGTAG TCTCCTGGGC CTCACCATCC CAGAAGAGGA GTGGGAGCCA GCTCAGAGAA	1020
35	GGAAGTGAAC CCAGGAGATC CATCCACCTA TTAGCCCTGG GCCTGGACCT CCCTGCGATT	1080
	TCCCCTCCT TTTCTAGTCT TCTTCCAGAA ACAGAGAAGG GGATGTGTGC CTGGGAGAGG	1140
40	CTCTGTCTCC TTCTGTCTGC CAGGACCTGT GCCTAGACTT AGCATGCCCT TCACTGCAGT	1200
	GTGAGGCTT TAGATGGGAC CCAGCGAAAA TGTGGCCCTT CTGAGTCACA TCACCGACAC	1260
	TGAGCAGTGG AAAGGGGCTA TATGTGTATG AATAGACCAC ATTGAAGGAG CACAATGCC	1320
45	TCCTGTGTG ATGCCACTTC CCAGGGTGA GACAGTGGA AAGAACCGAG GACAGGAAAG	1380
	GATTGGGTAG GTGAAGGGGT CAGGGGACTG GTAGTCACCC AATCTTGGAG AGGTGCAAAA	1440
50	AGCACTGGGG GCTACCCGTT AGCTGCATCT GCCTGGCTG TTTGCCCGTT CATGTCACAA	1500
	ACTGCCACTA CTATGTACCT GCAGTGGGT TGCAGAGATG GGGGAGACTC AAGTCTTACT	1560
	CCCCAGGAGC TCCCAGGGCC CAAGGAGGAG AATGCTGCCT CCTTTCAGTC TGGTCTACAC	1620
55	CCACTTCTG GTAGCCTCTC TGCTTCTGT AATTCTGGCT GTTTTCCAG ACTCAGCTCA	1680
	AATAGTCCCC CTCTTAAGC CCATCCCTCG CCCCAGCCT GAGGTGATCT TTCCCTCCTC	1740
60	TGAAGTATTA GAGCAGTTAC TGTCTGTTCA GTTCGTTTGG CAGGCACACA CAGTGGCATA	1800

AATTCTATTG TTTTGAATC TGATTTAAAA TTAAATTGCA GCTGGGCGTG GTGGCTCATG 1860
CTTGTAATCC CAACACTTAG GGAGTMAGGR GAATCACTTG ASCYCAGGAG TYCTAGACCA 1920
5 ATCTGGGCAA MAGAGAGACC CCATCTCTTT TAAATAAAAA GTTAAATTGC TTAAAAAAA 1980
A 1981

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(2) INFORMATION FOR SEQ ID NO: 157:

(i) SEQUENCE CHARACTERISTICS:
15 (A) LENGTH: 915 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 157:

GAATTCGGCA CGAGCGCGGC CATGGCGCTC CTGCTTTCGG TGCTGCGTGT ACTGCTGGGC 60
GGCTTCTTCG CGCTCGTGGG GTTGCCCAAG CTCTCGGAGG AGATCTCGGC TCCAGTTTCG 120
25 GAGCGGATGA ATGCCCTGTT CGTGCAGTTT GCTGAGGTGT TCCCGCTGAA GGTATTTGGC 180
TACCAGCCAG ATCCCCTGAA CTACCAAATA GCTGTGGGCT TTCTGGAAGT GCTGGCTGGG 240
30 TTGCTGCTGG TCATGGGCCC ACCGATGCTG CAAGAGATCA GTAACCTGTT CTTGATTCTG 300
CTCATGATGG GGGCTATCTT CACCTTGGCA GCTCTGAAAG AGTCACTAAG CACCTGTATC 360
CCAGCCATTG TCTGCCTGGG GTTCTCTGCTG CTGCTGAATG TCGGCCAGCT CTTAGCCCAG 420
35 ACTAAGAAGG TGGTCAGACC CACTAGGAAG AAGACTCTAA GTACATTCAA GGAATCCTGG 480
AAGTAGAGCA TCTCTGTCTC TTTATGCCAT GCAGCTGTCA CAGCAGGAAC ATGGTAGAAC 540
40 ACAGAGTCTA TCATCTTGTT ACCAGTATAA TATCCAGGGT CAGCCAGTGT TGAAAGAGAC 600
ATTTTGTCTA CCTGGCACTG CTTTCTCTTT TTAGCTTTAC TACTCTTTTG TGAGGAGTAC 660
ATGTTATGCA TATTAACATT CCTCATGTCA TATGAAAATA CAAAATAAGC AGAAAAGAAA 720
45 TTATAATCAA CCAAAATTCT GATGCCCCAA ATAACCACTT TTAATGCCIT GGTGTAAGTA 780
TACCTCTGAA CTTTTTCTG TGCCTTTAAA CAGATATATA TTTTTTTTWA ATGAAAATAA 840
50 AACCATATAT CCTATTTTAT TTCCTCCTTT TAAAACCTTA TAACTATAA MAAAAAAAAA 900
AAAAAAAAA CTCGA 915

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(2) INFORMATION FOR SEQ ID NO: 158:

(i) SEQUENCE CHARACTERISTICS:
60 (A) LENGTH: 2117 base pairs

(B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

5	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 158:	
	AGAGCGAAGC GAGGGTGGCG CGGGTCCGGG CATGAAGCTG GGCCGGGCGG TGCTGGGCCT	60
	GCTGCTGCTG GCGCCGTCCG TGGTGCAGGC GGTGGAGCCC ATCAGCCTGG GACTGGCCCT	120
10	GGCCGGCGTC CTCACCGGCT ACATCTACCC GCGTCTCTAC TGCTCTTCG CCGAGTGCTG	180
	CGGCAGAAG CGGAGCCTTA GCCGGGAGGC ACTGCAGAAG GATCTGGACG ACAACCTCTT	240
15	TGGACAGCAT CTTGCAAAGA AAATCATCTT AAATGCCGTG TTTGGTTTCA TAAACAACCC	300
	AAAGCCCAAG AAACCTCTCA CGCTCTCCCT GCACGGGTGG ACAGGCACCG GCAAAAATTT	360
	CGTCAGCAAG ATCATCGCAG AGAATATTTA CGAGGGTGGT CTGAACAGTG ACTATGTCCA	420
20	CCTGTTTGTG GCCACATTGC ACTTTCCACA TGCTTCAAAC ATCACCTTGT ACAAGGATCA	480
	GTTACAGTTG TGGATTCGAG GCAACGTGAG TGCTGTGCG AGGTCCATCT TCATATTTGA	540
25	TGAAATGGAT AAGATGCATG CAGGCCTCAT AGATGCCATC AAGCCTTTCC TCGACTATTA	600
	TGACCTGGTG GATGGGGTCT CCTACCAGAA AGCCATGTTT ATATTTCTCA GCAATGCTGG	660
	AGCAGAAAGG ATCACAGATG TGCTTTTGA TTTCTGGAGG AGTGGAAAGC AGAGGGAAGA	720
30	CATCAAGCTC AAAGACATTG AACACGGGTT GTCTGTGTCG GTTTTCAATA ACAAGAACAG	780
	TGGCTTCTGG CACAGCAGCT TAATTGACCG GAACCTCATT GATTATTTTG TTCCCTTCCT	840
35	CCCCCTGGAA TACAAACACC TAAAAATGTG TATCCGAGTG GAAATGCAGT CCGAGGCTA	900
	TGAAATTGAT GAAGACATTG TAAGCAGAGT GGCTGAGGAG ATGACATTTT TCCCCAAAGA	960
	GGAGAGAGTT TTCTCAGATA AAGGCTGCAA AACGGTGTTT ACCAAGTTAG ATTATTACTA	1020
40	CGATGATTGA CAGTCATGAT TGGCAGCCGG AGTCACTGCC TGGAGTTGGA AAAGAAACAA	1080
	CACTCAGTCC TTCCACACTT CCACCCOCAG CTCCTTTCCC TGAAGAGGA ATCCAGTGAA	1140
45	TGTTCCCTGT TGATGTGACA GGAATTCTCC CTGGCATTGT TTCCACCCCC TGGTGCCTGC	1200
	AGGCCACCCA GGGACCACGG GCGAGGACGT GAAGCCTCCC GAACACGCAC AGAAGGAAGG	1260
	AGCCAGCTCC CAGCCCACTC ATCGCAGGGC TCATGATTTT TTACAAATTA TGTTTTAATT	1320
50	CCAAGTGTTT CTGTTTCAAG GAAGGATGAA TAAGTTTTAT TGAAAATGTG GTAACTTTAT	1380
	TTAAAATGAT TTTTAACATT ATGAGAGACT GCTCAGATTC TAAGTTGTTG GCCTTGTTGTG	1440
55	TGTGTTTTTT TTTAAGTTCT CATCATTATT ACATAGACTG TGATGTATCT TTAAGTGGAAA	1500
	TGAGCCCAAG CACACATGCA TGGCATTGTG TCCACAGGAG GGCATCCCTG GGGATGTGGC	1560
60	TGGAGCATGA GCCAGCTCTG TCCCAGGATG GTCCCAGCGG ATGCTGCCAG GGGCAKTGAA	1620

GTGTTTAGGT GAAGGACAAG TAGGTAAGAG GACGCCTTCA GGCACCACAG ATAAGCCTGA 1680
 AACAGCCTCT CCAAGGGTTT TCACCTTAGC AACAAATGGGA GCTGTGGGAG TGATTTTGGC 1740
 5 CACACTGTCA ACATTTGTTA GAACCACTCT TTTGAAAGAA AAGTATTTCC AACTTGTAC 1800
 TTGCCAGTCA CTCOGTTTGG CAAAAGGTGG CCCTTCACTG TCCATTCCAA ATAGCCCACA 1860
 10 CGTGCTCTCT GCTGGATTCT AAATTATGTG AATTTTGCCA TATTAAATCT TCCTCATTTA 1920
 TACTATTATT TGTTACGTTT AATCAGAATC CCCGAAACCT CCTATAAAGC TTAGCTGCCC 1980
 CTTCTGAGGA TGCTGAGAAC GGTGTCTTTC TTATATAATG CAAATGGCTA CCGTTTACA 2040
 15 ATAAATTTT GCATGTGCAA AAAAAAAAAA ANAAAAAAAA AAAATCCCGG GGGGGGGCCG 2100
 GTAACCAATT TGNCCCC 2117

20

(2) INFORMATION FOR SEQ ID NO: 159:

25 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 2395 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 159:

TGTTCCTTAA TCCCTTTTCT AAAAAGGGGG GAAAATCCCG ATGGATTTTA GGGATTGGTC 60
 TGGTGTGAGC TGTTTMTAT TGCACACCTA AATCCTGATT ATAGGCTTTT CATTTCTCCG 120
 35 CAAAGCCTTT ATTTTGGCAG TTAAGCCAAA TGTGTTTTCC AGAAAGTTAG TTATTTTCTC 180
 CTCTTTCTTT CCTTCTTTT CTCCCTTTT CCCGTCTGAC CCCAAACGTT ATTGTCCAAA 240
 40 CATGACTGGA CAGCAGCTTT TGTTCTTGA CCCTGTAATA TGACAGTCTG CTAATATTGA 300
 CAGAAGGTGC AGTTTTTGGG TTATAGTCGT GATTTTCGCT AATCAATCAT ATTAGCAGGA 360
 AAAAAAAGA CTGTCTCTG TTGTACTTGA GTCTTAAGAA AAAGTGGCCC ATAGTTTAGT 420
 45 GGACAATTTT CAAAGGCTTT AGTACCACCT GTATTTCAAA ATGGGGGACC CAAACTCCCG 480
 GAAGAAACAA GCTCTGAACA GACTACGTGC TCAGCTTAGA AAGAAAAAG AATCTCTAGC 540
 50 TGACCAGTTT GACTTCAAGA TGTATATTGC CTTTGTATT CAGGAGAAGA AGAAAAAGTC 600
 AGCACTTTT GAAGTGTCTG AGGTATATACC AGTCATGACA AATAATTATG AAGAAAATAT 660
 CCTGAAAGGT GTGCGAGATT CCAGCTATT CTTGGAAAGT TCCCTAGAGC TTTTACAGAA 720
 55 GGATGTGGTA CAGCTCCATG CTCCTCGATA TCAGTCTATG AGAAGGGATG TAATTGGCTG 780
 TACTCAGGAG ATGGATTTC TTTTGGCC TCGGAATGAT ATTGAAAAA TCGTCTGTCT 840
 60 CCTGTTTTCT AGGTGAAAG AATCTGATGA GCCTTTTAGG CCTGTTCAGG CAAATTTGAG 900

	TTTCATCATG GTGACTATGA AAAACAGTTT CTGCATGTAC TGAGCCGCAA GGACAAGACT	960
5	GGAATCGTTG TCAACAATCC TAACCAGTCA GTGTTTCTCT TCATTGACAG ACAGCACTTG	1020
	CAGACTCCAA AAAACAAAGC TACAATCTTC AAGTTATGCA GCATCTGCCT CTACCTGCCA	1080
	CAGGAACAGC TCACCCACTG GGGCAGTTGG CACCATAGAG GRTCACCTCC GTCCTTATAT	1140
10	GCCAGAGTAG AGTACTGACC AGCAAAATGG AGAAGATCAG AGAATGCAGC AGCAGTTTTT	1200
	TTTCTTGTTT TCTTACCACT TTATCTTTC AGAGTTTAAA GAAAATGGAC TCATGCACAG	1260
15	AACACTATGC ATTTTGAAAC TTGTTCAATCC TGGATTTTTT TAAATCATTT TTATCTCAGA	1320
	ACTTAAACAA AAATTAGATG TCGTGCACGG ACTGTGTGAA AGAAGATGCT TTGCATATTT	1380
	GCTGCACTGC ATCAGTATCT TACTAAAAAT GTGAAATGAA AGGACTATIG TACACTGAAA	1440
20	TGCTTAAATG TATCTGAAAG CACAAGGTGA TACTCATTTT TATGGTCTTC CCATTTGTGC	1500
	TGGTTTTGTC CTCTTTGACA TCTGTCATCA GTATTTAGAG GGTGAGAAGT GAATGTAACA	1560
25	GGTATAATA ACATTTTTAA AAACAATAAC TTGCTATAA TCACAGTTGT TCCAGAGCAC	1620
	TGTCAGATAC ATTCTAATGA CCAGAACTGG TTTAAAAAA GAAAATACAA CCATGGGAAA	1680
	GAAATCTTAA ATGAAAAACG CATCTCATTG TAGGCATTTT TGCCTCATAT TTTACTGGGC	1740
30	CATGTTTGTT TCCTGGTACT CATGTATTTT TTTTTCCAG ATCTCTTTCC CCAAGTTGCT	1800
	ATTGTAAGAG TATCTGCTG CGTGTGGATG CAGTTATACA CATTAAAGCA GATCTGGAGT	1860
35	CTGAAGTAGC TATAAAGCAG CTATAAAACA GAAATACATG CATAGCTGCA GAAACCATGA	1920
	TAGGTAGAGG ACTTTTCTTT TGGTTTTGTT TTGTTTTGTT TTGTTTTGTT TTTGGTTTTA	1980
	CAGAGAAGAG ATTTTATTTA CAAAGAAAAA AATTCCAGTG AATGTGTCAG AAATGCTGGT	2040
40	TTTTACACCA TCCTAAAGAA AAACTTTACA AGGGTGTITT GGAGTAGAAA AAAGTTATA	2100
	AAGTTGGAAT CTTAAATTGT AAAATTAACC ATTGAGTGTG AAAGTTCTAA AAGCAGAACT	2160
45	CATTTTGTGC AATGAACATA AGGAAAGACT ACTGTATAGG TTTTTTTTTT TTCTCCTTTT	2220
	AAATGAAGAA AAGCTTTGCT TAAGGGTTGC ATACTTTTAT TGGAGTAAAT CTGAATGATC	2280
	CTACTCCTTT GGAGTAAAAC TAGTGCTTAC CAGTTTCCAA TTGTATTTAG CTTCTGGTTG	2340
50	GAATTTGAAA AAAAAAGAAA AAAAGAAAAA GAAAACCTAA ATAAAATAGG TGAAA	2395

55 (2) INFORMATION FOR SEQ ID NO: 160:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2120 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

60

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 160:

5	CCCCGATAC CGCCTGACGT AGTGCCAATC ACACCTCTCG CGTCTCGGCG CCTCGGAGGC	60
	TAATGAGGAC GCCTGGCGAA ACGCAGTAAC GGATTTCGG GTGGACCTTC GCTTTACGGC	120
10	TCGTGAGTTC TTCCGCCCAA CCCAGAGGAA GCGGGAGAGC AGTTTACGAC AGCGCCGGTC	180
	GTGTTTACGG CGGCGCCCGC TGC GCGCGCA TGTTCCTCT TTTCTGGTT TCTCAAGAGT	240
	GCTGCTGTA ACGCGGTCCC CGGCACGCAC CATCTGTTC CATCCCGGCC GGCCGAGGCA	300
15	TTGCAGATT TGAAGATGG CAAAGTTCAT GACACCCGTG ATCCAGGACA ACCCCTCAGG	360
	CTGGGGTCCC TGTGCGGTTC CCGAGCAGTT TCGGGATATG CCCTACCAGC CGTTCAGCAA	420
	AGGAGATCGG CTAGGAAAGG TTGCAGACTG GACAGGAGCC ACATACCAAG ATAAGAGGTA	480
20	CACAAATAAG TACTCTCTC AGTTTGGTGG TGAAGTCAA TATGCTTATT TCCATGAGGA	540
	GGATGAAAGT AGCTTCCAGC TGGTGGATAC AGCGCGCACA CAGAAGACGG CCTACCAGCG	600
25	GAATCGAATG AGATTTGCCC AGAGGAACCT CCGCAGAGAC AAAGATCGTC GGAACATGTT	660
	GCAGTTCAAC CTGCAGATCC TGCCTAAGAG TGCCAAACAG AAAGAGAGAG AACGCATTCTG	720
	ACTGCAGAAA AAGTTCCAGA AACAATTGG GGTTAGGCAG AAATGGGATC AGAAATCACA	780
30	GAAACCCCGA GACTCTTCAG TTGAAGTTCG TAGTGATTGG GAAGTGAAAG AGGAAATGGA	840
	TTTTCTCTCAG TTGATGAAGA TCGCTACTT GGAAGTATCA GAGCCACAGG ACATTGAGTG	900
35	TTGTGGGGCC CTAGAATACT ACGACAAAGC CTTTGACCGC ATCACCACGA GGAGTGAGAA	960
	GCCACTGCGG ASATNCAAGC GCATCTTCCA CACTGTACC ACCACAGACG ACCCTGTCTAT	1020
	CCGCAAGCTG GCAAAAATC AGGGGAATGT GTTTGCCACT GATGCCATCC TGGCCACGCT	1080
40	GATGAGCTGT ACCCGCTCAG TGTATTCCTG GGATATTGTC GTCCAGAGAG TTGGGTCCAA	1140
	ACTCTTCTTT GACAAGAGAG ACAACTCTGA CTTTGACCTC CTGACAGTGA GTGAGACTGC	1200
45	CAATGAGCCC CCTCAAGATG AAGGTAATTC CTTCAATTCA CCCCACAACC TGGCCATGGA	1260
	GGCAACCTAC ATCAACCACA ATTTCTCCCA GCAGTGCTTG AGAATGGGGA AGGAAAGATA	1320
	CAACTTCCCC AACCCAAACC CGTTTGTGGA GGACGACATG GATAAGAATG AAATCGCCTC	1380
50	TGTTGCGTAC CGTTACCGCA GTGGNAAGCT TGGAGATGAT ATTGACCTTA TTGTCCGTTG	1440
	TGAGCACGAT GCGTCATGA CTGGAGCCAA CGGGGAAGTG TCCTTCATCA ACATCAAGAC	1500
55	ACTCAATGAG TGGGATTTCA GGCACGTGTA TGGCGTTGAC TGGCGTCAGA AGCTGGACTC	1560
	TCAGCGAGGG GCTGTCTATT CCACGGAGCT GAAGAACAAC AGCTACAAGT TGGCCCGGTG	1620
60	GACCTGCTGT GCTTTGCTGG CTGGATCTGA GTACCTCAAG CTTGGTTATG TGTCTCGGTA	1680

CCACGTGAAA GACTCCTCAC GCCACGTCAT CCTAGGCACC CAGCAGTTCA AGCCTAATGA 1740
 GTTTGCCAGC CAGATCAACC TGAGCGTGGA GAATGCCTGG GGCATTTTAC GCTGCGTCAT 1800
 5 TGACATCTGC ATGAAGCTGG AGGAGGGCAA ATACCTCATC CTCAAGGACC CCAACAAGCA 1860
 GGTCATCCGT GTCTACAGCC TCCCTGATGG CACCTTCAGC TCTGATGAAG ATGAGGAGGA 1920
 AGAGGAGGAG GAAGAAGAGG AAGAAGAAGA GGAAGAACT TAAACCAGTG ATGTGGAGCT 1980
 10 GGAGTTTGTC CTCCACCGA GACTACGAGG GCCTTTGATG CTTAGTGGAA TGTGTGTCTA 2040
 ACTTGCTCTC TGACATTTAG CAGATGAAAT AAAATATATA TCTGTTTAGT CTTAAAAAAA 2100
 15 AAAAAAAAAA AAAAAAAAAAN 2120

20 (2) INFORMATION FOR SEQ ID NO: 161:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 900 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 161:

30 GGAAGCTGAA GTCCTTCCAG ACCAGGGACA ACCAGGGCAT TCTCTATGAA GCTGCACCCA 60
 CCTCCACCCCT CACCTGTRAC TCAGGACCAC AGAAGCAAAA GTTCTCACTC AACTTGATG 120
 CCAAGGATGG GCGCTTGITC AATGAGCAGA ACTTCTTCCA GCGGGCCGCC AAGCCTCTGC 180
 35 AAGTCAACAA GTGAAGAAG CTGTACTCGA CCCCACTGCT GGCCATCCCT ACCTGCATGG 240
 GTTTCGGTGT TCACCAGGAC AAATACAGGT TCTTGGTGTT ACCCAGCCTG GGGAGGAGCC 300
 40 TTCAGTCGGC CTGGATGTC AGCCCAAAGC ATGTGCTGTG CAGAGAGGTC TGTGCTGCAG 360
 GTGGCCTGCC GGCTGCTGGA TGCCCTGGAG TTCTCCATG AGAATGAGTA TGTTCATGGA 420
 AATGTGACAG CTGAAAATAT CTTTGTGGAT CCAGAGGACC AGAGTCAGGT GACTTTGGCA 480
 45 GGCTATGGCT TCGCNTTCCG CTATTGCCCA AGTGGCAAAC ACGTGGCCTA CGTGGGAAGGC 540
 AGCAGGAGCC CTCACGAGGG GGACCTTGAG TTCATTAGCA TGGACCTGCA CAAGGGATGC 600
 50 GGGCCCTCCC GCGCRGCGA CCTCCAGAGC CTGGGCTACT GCATGCTGAA GTGGCTCTAC 660
 GGGTTTCTGC CATGGACAAA TTGCCTTCCC AAMAMTGAGG ACATCATGAA GCAAAAACAG 720
 AAGTTTGTG ATAAGCCGGG GCCCTTCGTG GGACCCTGCG GTCCTGGAT CAGGCCCTCA 780
 55 GAGACCTGC AGAAGTACCT GAAGTGGTG ATGGCCCTCA CGTATGAGGA GAAGCCGCC 840
 TACGCCATGC TGAGGAACAA CCTAGAAGCT TTGCTGCAGG ATCTGCGTGT GTCTCCATAT 900

60

(2) INFORMATION FOR SEQ ID NO: 162:

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(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1003 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 162:

GGCACCAGAT GAGGGGCACC CAGTGCTTCT AGGGCAGGCT GGGTGGTGGT CCCCTAGGTA 60
15 TCAGCCTCTC TTACTGTACT CTCCGGGAAT GTTAACCTTT CTATTTTCAG CCTGTGCCAC 120
CTGTCTAGGC AAGCTGGCTT CCCCATTTGC CCCTGTGGGT CCACAGCAGC GTGGCTGCCC 180
20 CCCAGGGCCA CCGCTTCTTT CTGTATCCTC TTTCCTTAAC AGTGACTTGG GCTTGAGTCT 240
GGCAAGGAAC CTTGCTTTTA GCTTCACCAC CAAGGAGAGA GGTGACATG ACCTCCCCGC 300
CCCCTACCA AGGCTGGGAA CAGAGGGGAT GTGGTGAGAG CCAGGTTCTT CTGGCCCTCT 360
25 CCAGGTGTGT TTCCACTAGT CACTACTGTC TTCTCCTTGT AGCTAATCAA TCAATATTCT 420
TCCCTTGCCT GTGGGCAGTG GAGAGGCTGC TGGGTGTACG CTGCACCTGC CCACTGAGTT 480
GGGGAAGAG GATAATCAGT GAGCACTGTT CTGCTCAGAG CTCTGATCT ACCCCACCCC 540
30 CTAGGATCCA GGACTGGGTC AAAGCTGCAT GAAACCAGGC CCTGGCAGCA AACCTGGGAA 600
TGGCTGGAGG TGGGAGAGAA CCTGAACTTC TCTTCCCTC TCCCTCCTCC AACATTAATG 660
35 GAACTCTATC CTGTTAGGAT CTTCTGAGCT TGTTCCTTG CTGGGTGGGA CAGAGGACAA 720
AGGAGAAGGG AGGTCTAGA AGAGGCAGCC CTTCTTTGTC CTCTGGGGTA AATGAGCTTG 780
ACCTAGAGTA AATGAGAGA CAAAAGCCT CTGATTTTAA ATTTCCATAA AATGTTAGAA 840
40 GTATATATAT ACATATATAT ATTTCTTTAA ATTTTGGAGT CTTTGATATG TCTAAAAATC 900
CATTCCCTCT GCCCTGAAGC CTGAGTGAGA CACATGAAGA AACTGTGTT TCATTTAAAG 960
45 ATGTTAATTA AATGATTGAA ACTTGAAAAA AAAAAAAAAA AAA 1003

50

(2) INFORMATION FOR SEQ ID NO: 163:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2196 base pairs

(B) TYPE: nucleic acid

55

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 163:

60 AAGAAGCGGC ACACGGATGT GCAGTTCTAC ACAGAAGTGG GAGAGATAAC CACGGACTTG 60

	GGGAAACATC AGCATATGCA TGACCGAGAT GACCTCTATG CTGAGCAGAT GGAACGAGAA	120
5	ATGAGGCACA AACTGAAAAC AGCCTTTAAA AATTTCAATTG AGAAAGTAGA GGCTCTAACT	180
	AAGGAGGAAC TGGAATTTGA AGTGCCTTTT AGGGACTTGG GATTTAACGG AGCTCCCTAT	240
	AGGAGTACCT GCCTCCTTCA GCCCACTAGT AGTGCCTGG TAAATGCTAC GGAATGGCCA	300
10	CCTTTTGTGG TGACATTGGA TGAGGTAGAG CTGATCCACT TTRAGCGGT CCAGTTTCAC	360
	CTGAAGAACT TTGATATGGT AATCGTCTAC AAGGACTACA GCAAGAAAGT GACCATGATC	420
15	AACGCCATTC CTGTAGCCTC TCTTGACCCC ATCAAGGAAT GGTGTGAATTC CTGCGACCTG	480
	AAATACACAG AAGGAGTACA GTCCCTCAAC TGGACTAAAA TCATGAAGAC CATGTGTGAT	540
	GACCTGAGG GCTTCTTCGA ACAAGGTGGC TGGTCTTTCC TGGAGCCTGA GGGTGAGGG	600
20	AGTGATGCTG AAGAAGGGGA TTCAGAGTCT GAAATGAAG ATGAGACTTT TAATCCTTCA	660
	GAAGATGACT ATGAAGAGGA AGAGGAGGAC AGTGATGAAG ATTATTCATC AGAAGCAGAA	720
25	GAGTCAGACT ATTCTAAGGA GTCATTGGGT AGTGAAGAAG AGAGTGGAAA GGATTGGGAT	780
	GAAGTGGAGG AAGAAGCCCG AAAAGCGGAC CGAGAAAGTC GTTACGAGGA AGAAGAAGAA	840
	CAAAGTCGAA GTATGAGCCG GAAGAGGAAG GCATCTGTGC ACAGTTCGGG CCGTGGCTCT	900
30	AACCGTGGTT CCAGACACAG CTCTGCACCC CCCAAGAAA AGAGGAAGTA ACTTCTGAAC	960
	TTTGGCCCTG AGCTCCATTC TTCTCCAGC CAACCCCTGA AAATTTTACA TGACATAGAA	1020
35	ACTGTATTTT TCCTTTCTGT TTCATTTGAA GTTTTGCCAT TTGTGTTTAT GGGTTTAGGG	1080
	GGCCATTTGT GTGGACCAAT CTACTCGGG AATTCCAGGC CCACCAGGAC ACGTGCCAAT	1140
	GGCCCCATTC AGATGGCAAG GGAGGAGGTG TTCTTGAAGA CAGGAGGAGG CTCCCGCTGT	1200
40	TAATAAATAT TGTTTCAATC TTCTCTCTC CTGTCACCTT CTGCCAAGAC ATTGATGGCT	1260
	CTGACATCT TATTTGGTGT CTCAAAGCTG TATTTCCAAG ACAGTGGTAC AAGGTGACCC	1320
45	TTAATTACCC GTATCATGGT TCTTGACCAG CACATTCAAT CCTCCAACCT ACCCTACTGC	1380
	CATGACCTTC CGCACATCTC TAAGTTTAT CTTTGCAATA CTCAAGGTTT TCGGAAATTT	1440
	GCTAATGGTT GTGATAAACC ATACAGCTTG AGCCAGTGAG GCAGATTGGG CTGGTGCCCT	1500
50	CGTCTGAGTT TTCTGCTTT CCTGCCTCGT GCAGATTCTG AGGTATATCT GCTGCCTTGG	1560
	AAGACATAAG AAGCAGTGAT ACTCCCTGGC TCGGTATTTT TCTCCATACA ATGCACACAT	1620
55	GGTACAATGA TAGAAGGCAA AATTGCCACT GTCTTCTTTT TTTTCTCATA TATCTAAGGA	1680
	AGATATATCA GGTGTGTCCT CATGTACCGC TTCTAGTGAA ATGTAGAGGA AGGCTCAAAG	1740
	GAGTCAACAT TTAGATCTGG AAGGGACAAG TCATGCCTTG GCCTAGAAAT ACCCTGATGA	1800
60	GAAAAGAGAA GAGGAAGGGA GGCCATATCT ACAACANCAN CCTCTCGGCA CTGTGCTCC	1860

TTATTTTAAC TTGTCTTGC ATTGTCTGT ATTTATCACA GTTCTGTGTG AACAGCTTTT 1920
 5 CAAGTATTTG GGGAGTTTAT CTTGCCATCC TCCCCTTCTG GTTCTCTGCA CCCACCTGTC 1980
 CCACTGCAGT TCCTTCCGTG CTCTGTGACT TTAAGAGAAG AAGGGGGGAG GGGTCCCGGA 2040
 TTTTATGTTT GTTGTTTTTT TCTCCTTAGC AGTAGGACTT GATATTTTCA ATTTTGGAAG 2100
 10 AACTAAAAGA TGAATAAACT GGGTTTTTTT TGTGTTTTGT TTTTGTA AAAA 2160
 AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAA 2196

15

(2) INFORMATION FOR SEQ ID NO: 164:

20 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1945 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 164:

GCACAGAGTC GGGCGGACGG ACAGGGAGAG GAGGAGAGGG GGTCTGCCGG CGGCCCGCTAC 60
 CCAGAAAGCCA GCGGACGGCA GCACGGAGTG GGCTGTCCCC GAGCCAGGCC CCGAGCGAGC 120
 30 CCCCCCCCCG CCCCCGMAGG ACGCGCCTYC CAGCCAGCCC GACTYCTAGG AGGAGGGGAG 180
 GCGGGAAAGC AGCTCAAGCC TCACCCACCG CCTGCCCC AGCCCCGCCA CTCCCAGGCT 240
 35 CCTCGGGA CTGCGGGTCC TCCTGGGAGT CTCGGAGGGG ACCGGCTGTG CAGACGCCAT 300
 GGAGTTGGTG CTGGTCTTCC TCTGCAGCCT GCTGGCCCC ATGGTCTCTG CCACTGCAGC 360
 TGAAAAGGAG AAGGAAATGG ACCCTTTTCA TTATGATTAC CAGACCCTGA GGATTGGGGG 420
 40 ACTGGTGTTC GCTGTGGTCC TCTTCTCGGT TGGGATCCTC CTTATCCTAA GTCGCAGGTG 480
 CAAGTGCAGT TTCAATCAGA AGCCCCGGGC CCCAGGAGAT GAGGAAGCCC AGGTGGAGAA 540
 45 CCTCATCACC GCCAATGCAA CAGAGCCCCA GAAAGCAGAG AACTGAAGTG CAGCCATCAG 600
 GTGGAAGCCT CTGGAACCTG AGGCGGCTGC TTGAACCTTT GGATGCAAAT GTCGATGCTT 660
 AAGAAAACCG GCCACTTCAG CAACAGCCCT TTCCCCAGGA GAAGCCAAGA ACTTGTGTGT 720
 50 CCCCCACCCT ATCCCCCTTA ACACCATTC TCCACCTGAT GATGCAACTA ACATTGCCT 780
 CCCCCTGCA GCCTGCGGTC CTGCCACCT CCGGTGATGT GTGTGTGTGT GTGTGTGTGT 840
 55 GTGACTGTGT GTGTGTGCTA ACTGTGGTCT TTGTGGCTAC TTGTGTGTGG ATGGTATTGT 900
 GTTGTGTAGT GAACTGTGGA CTCGCTTTC CAGGCAGGGG CTGAGCCACA TGGCCATCTG 960
 60 CTCCTCCCTG CCCCCGTGGC CCTCCATCAC CTCTGCTCC TAGGAGGCTG CTTGTGTGCC 1020

	GAGACCAGCC CCCTCCCCTG ATTTAGGGAT GCGTAGGGTA AGAGCACGGG CAGTGGTCTT	1080
	CAGTCGTCTT GGGACCTGGG AAGGTTTGCA GCACTTTGTC ATCATTTCTC ATGGACTCCT	1140
5	TTCACCTCTT TAACAAAAAC CTGCTTCCT TATCCACCT GATCCAGTC TGAAGGTCTC	1200
	TTAGCAACTG GAGATACAAA GCAAGGAGCT GGTGAGCCCA GCGTTGACGT CAGGCAGGCT	1260
10	ATGCCCTTCC GTGGTTAATT TCTTCCAGG GGCTTCCAG AGGAGTCCCC ATCTGCCCCG	1320
	CCCCTTCACA GAGCGCCCGG GGATTCCAGG CCCAGGCTT CTACTCTGCC CCTGGGGAAT	1380
	GTGTCCCTG CATATCTTCT CAGCAATAAC TCCATGGGCT CTGGGACCCT ACCCTTCCA	1440
15	ACCTTCCCTG CTTCTGAGAC TTCAATCTAC AGCCAGCTC ATCCAGATGC AGACTACAGT	1500
	CCCTGCAATT GGGTCTCTGG CAGGCAATAG TTGAAGGACT CCTGTTCCGT TGGGGCCAGC	1560
20	ACACCGGGAT GGATGGAGGG AGAGCAGAGG CCTTTGCTTC TCTGCCTACG TCCCCTTAGA	1620
	TGGGCAGCAG AGGCAACTCC CGCATCCTTT GCTCTGCTG TCRGTGGTCA GAGCGGTGAG	1680
	CGAGGTGGGT TGGAGACTCA GCAGGCTCCG TGCAGCCTT GGGAACAGTG AGAGGTGAA	1740
25	GGTCATAACG AGAGTGGGAA CTCAACCCAG ATCCCGCCCC TCCTGTCTC TGTGTTCCCG	1800
	CGGAAACCAA CCAAACCGTG CGCTGTGACC CATTGCTGTT CTCTGTATCG TGATCTATCC	1860
30	TCAACAACAA CAGAAAAAAG GAATAAAATA TCCTTTGTTT CCTAGTGAAA AAAAAAAAAA	1920
	AAAAAAAAA AAAAAAAAAA CTCGA	1945

35

(2) INFORMATION FOR SEQ ID NO: 165:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 2933 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

40

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 165:

45

	GGGTCGACCC ACGCGTCCG CAGCCGTCGT TTGAGTCGTT GCTGCCGCTG CCCCCTCCCG	60
	GATCAGGAGC CAGTGTATAC CGCCCGCCA CGCCTTGGT GCCGCTAGAG GAAACGAGAA	120
50	GGAGGCCGCC TCGGTTTGT CGCCGAGCT CGCCCMYGY CYGGRAGAGC CGAGCCCCG	180
	CCAGTCGGT CGCTGCCAC CSCTCGTAGC CGTTACCCGC GGGCCGCCAC AGCCGCCGGC	240
55	CGGAGAGGC GCGGCCATG GCTCTGGAG CCGATTCAA AGGTGATGAC CTATCAACAG	300
	CCATTCTCAA ACAGAAGAAC CGTCCAATC GGTAAATTGT TGATGAAGCC ATCAATGAGG	360
	ACAACAGTGT GGTGCTCTG TCCAGCCCA AGATGGATGA ATTGCAATTG TTCCGAGGTG	420
60	ACACAGTGT GCTGAAAGGA AAGAAGAGAC GAGAAGCTGT TTGCATCGTC CTTCTGATG	480

	ATACTTGTTC TGATGAGAAG ATTCCGGATGA ATAGAGTTGT TCGGAATAAC CTTCGTGTAC	540
5	GCCTAGGGGA TGTCAATCAGC ATCCAGCCAT GCCCTGATGT GAAGTACGGC AAACGTATCC	600
	ATGTGCTGCC CATTGATGAC ACAGTGGAAAG GCATTACTGG TAATCTCTTC GAGGTATACC	660
	TAAAGCCGTA CTTCTCGGAA GCGTATCGAC CCATCCGGAA AGGAGACATT TTTCTTGTCC	720
10	GTGGTGGGAT GCGTGCTGTG GAGTTCAAAG TGGTGGAAAC AGATCCTAGC CCTTATTGCA	780
	TTGTGTCTCC AGACACAGTG ATCCACTGCG AAGGGGAGCC TATCAAACGA GAGGATGAGG	840
15	AAGAGTCCTT GAATGAAGTA GGGTATGATG ACATTGGTGG CTGCAGGAAG CAGCTAGCTC	900
	AGATAAAGGA GATGGTGGAA CTGCCCCCTGA GACATCCTGC CCTCTTTAAG GCAATTGGTG	960
	TGAAGCCTCC TAGAGGAATC CTGCTTTACG GACCTCCTGG AACAGGAAAG ACCCTGATTG	1020
20	CTCGAGCTGT AGCAAATGAG ACTGGAGCCT TCTTCTTCTT GATCAATGGT CCTGAGATCA	1080
	TGAGCAAATT GGCTGGTGAG TCTGAGAGCA ACCTTCGTAA AGCCTTTGAG GAGGCTGAGA	1140
25	AGAATGCTCC TGCCATCATC TTCATTGATG AGCTAGATGC CATCGCTCCC AAAAGAGAGA	1200
	AAACTCATGG CGAGGTGGAG CGGCGCATTG TATCACAGTT GTTGACCCTC ATGGATGGCC	1260
	TAAAGCAGAG GGCACATGTG ATTGTTATGG CAGCAACCAA CAGACCCAAC AGCAATTGACC	1320
30	CAGCTCTACG GCGATTGGT CGCTTTGACA GGGAGGTAGA TATTGGAATT CCTGATGCTA	1380
	CAGGACGCTT AGAGATTCTT CAGATCCATA CCAAGAACAT GAAGCTGGCA GATGATGTGG	1440
35	ACCTGGAACA GTAGCCAATG AGACTCACGG GCATGTGGGT GCTGACTTAG CAGCCCTGTG	1500
	CTCAGAGGCT GCTCTGCAAG CCATCCGCAA GAAGATGGAT CTCATTGACC TAGAGGATGA	1560
	GACCATTGAT GCCGAGGTCA TGAAGTCTCT AGCAGTTACT ATGGATGACT TCCGGTGGGC	1620
40	CTTGAGCCAG AGTAACCCAT CAGCACTGCG GGAAACCGTG GTAGAGGTGC CACAGGTAAC	1680
	CTGGGAAGAC ATCGGGGGCC TAGAGGATGT CAAACGTGAG CTACAGGAGC TGGTCCAGTA	1740
45	TCCTGTGGAG CACCCAGACA AATTCCCTGAA GTTTGGCATG ACACCTTCCA AGGGAGTTCT	1800
	GTTCTATGGA CCTCCTGGCT GTGGGAAAAC TTTGTGGCC AAAGCCATTG CTAATGAATG	1860
	CCAGGCCAAC TTCAATCTCCA TCAAGGGTCC TGAGCTGCTC ACCATGTGGT TTGGGGAGTC	1920
50	TGAGGCCAAT GTCAGAGAAA TCTTTGACAA GGCCCGCCAA GCTGCCCCCT GTGTGCTATT	1980
	CTTTGATGAG CTGGATTCTGA TTGCCAAGGC TCGTGGAGGT AACATTGGAG ATGGTGGTGG	2040
55	GGCTGCTGAC CGAGTCATCA ACCAGATCCT GACAGAAATG GATGGCATGT CCACAAAAA	2100
	AAATGTGTTT ATCATTTGGC CTACCAACCG GCCTGACATC ATTGATCCTG CCATCCTCAG	2160
	ACCTGGCCGT CTTGATCAGC TCATCTACAT CCCACTCCT GATGAGAAAT CCCGTGTTC	2220
60	CATCTCAAG GCTAACCTGC GCAAGTCCCC AGTTGCCAAG GATGTGGACT TGGAGTTCCT	2280

5 GGCTAAATG ACTAATGGCT TCTCTGGAGC TGACCTGACA GAGATTGGCC AGCGTGCTTG 2340
 CAAGCTGGCC ATCCGTGAAT CCATCGAGAG TGAGATTAGG CGAGAACGAG AGAGGCAGAC 2400
 AAACCCATCA GCCATGGAGG TAGAAGAGGA TGATCCAGTG CCTGAGATCC GTCGAGATCA 2460
 CTTTGAAGAA GCCATGCGCT TTGCGCGCCG TTCTGTCACT GACAATGACA TTCGGAAGTA 2520
 10 TGAGATGTTT GCCCAGACCC TTCAGCAGAG TCGGGGCTTT GGCAGCTTCA GATTCCCTTC 2580
 AGGGAACCAG GGTGGAGCTG GCCCCAGTCA GGGCAGTGGA GCGGCACAG GTGGCAGTGT 2640
 ATACACAGAA GACAATGATG ATGACCTGTA TGGCTAAGTG GTGGTGGCCA GCGTGCAGTG 2700
 15 AGCTGGCCTG CCTGGACCTT GTTCCCTGGG GGTGGGGGCG CTGCCCAGG AGAGGGACCA 2760
 GGGTGCGCC CACAGCCTGC TCCATTCTCC AGTCTGAACA GTTCAGCTAC AGTCTGACTC 2820
 20 TGGACAGGGG GTTCTGTGTG CAAAAATACA AAACAAAAGC GATAAAATAA AAGCGATTTT 2880
 CATTTGGTAA AAAAAAAAAA AAAAAAAAAAT CCGGGGGGGG GCCCGAACCA TTT 2933

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(2) INFORMATION FOR SEQ ID NO: 166:

30 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 2243 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 166:

TCGGAGAGCC GCGGGGCGNG CGCCTCTCGG CCAGGAAGCG CCTCTTGGAC GCGTGTNACC 60
 40 GATGCCCAGA AGTGGCCTTG GGCTGGGGAT CACCATAGCT TTTCTAGCTA CGCTGATCAC 120
 GCAGTTTCTC GTGTATAATG GTGTCTATCA GTATACATCC CCAGATTTC TCTATATTCG 180
 TTCTTGGCTC CCTTGTATAT TTTTCTCAGG AGGCGTCACG GTGGGGAACA TAGGACGACA 240
 45 GTTAGCTATG GGTGTTCTTG AAAAGCCCCA TAGTGATTGA GTCTTCAAAA CCACCGATTC 300
 TGAGAGCAAG GAAGATTTTG GAAGAAAATC TGAAGTGTGA TTATGACAAA GATTATCTTT 360
 50 TTTCTTAAGT AATCTATTTA GATCGGGCTG ACTGTACAAA TGACTCCTGG AAAAACTCT 420
 TCACCTAGTC TAGAATAGGG AGGTGGAGAA TGATGACTTA CCCTGAAGTC TTCCCTTGAC 480
 TGCCCGCACT GCGCCTGTC TGTGCCCTGG AGCATCTGTC CCAGGCTACG TGGGTTTCAGG 540
 55 CAGGTGGCAG CTTCCCAAGT ATTGATTTT ATTATGTGA TTAACAACAG TTGCCATATT 600
 TCAAAGCCTT GAACCTAAGAC TCAATTACCA ACCCGCAGTT TTGTGTCACT GCCCAAAGGA 660
 60 GGTAGGTGTA TGGTGCTTAA CAAACATGAA GTATGGTGTG ATAGGAATAA TATTTATCCA 720

	AAAGATTTTT AAAAATAGGG CTGTGTTTAA AAAAAAAAC AAAACARGAA AAGCAGCAGT	780
	GATTATAGAG AGGTCACACT CTAAGTGGGG TCGCGGCGTG GCCACGCTTC ACGGTCACGC	840
5	TCGTCCGTCC TGCAGTGGCG TGTTTACATG GTCACACGTG TGTGTATCAC CAGTGGGTCA	900
	ACTGCTTGTC ATTCTCCCG TGGCAGTTTG TGTAGACAAT CTTACTGAGC AAAAGGCAAT	960
10	GAAAAGTCTT GGTTCACACA CTGCGATATA TTGGAATTTT CACCTCAGTT TATGAAGTTT	1020
	ATTTGCAAAT CCATAGTCAT CTAAGAATGA ATACCTGTCT GCCATGTATT TCAATCTTAG	1080
	TGAGCCAAAA TTGTTTGTIT GTTACTACAG AATAGAGATG ACTGTTTTTT GCCACAGCCC	1140
15	TATGGRATTT GCAATCTGTG ATTGCCTTGT AAAAAGGAGA GTGCATATGG CACTGCATTA	1200
	AACGTGTGGT GTTCTAGTC AATGATATG GTGAGCACAA TGTATTCATT TAATGGCATA	1260
20	GACCATACCA GACCTAATTT GCAAGTATG GGTCTTAAAC TTCAAGTGCA ATGTATATGA	1320
	AAACCAATCT GAGCCTTGTA TCTCTTAAAT ATTTATTTTT TTAAACGTGT GAGATGTTTG	1380
	AGAGAAGGTT CTCCATTCAT TTCAGTGCTG CCTGGAGGAA ACTCGGCAAT GATTTCTTTC	1440
25	AGTTGTGAAG TTCCTTTCGT GTTACACCCT CCACTGAACC CTCAACCTTC GAAATACTCC	1500
	AGTTTGTGG GTTTGGTCAT TTTTACTTAT AAATTACCT TTTTGTATTT TGCAATTTAC	1560
30	ATGTGTTTGG TTTGTTTAA ATTCTGTGAA AGTGGCTTGA TTTAAAGACT CCTTTTAAAT	1620
	GGAAGCCACC AGTCAGCAGA ATGGAAGCTT AGAGGAACCT GCCTGTGAGC GCTGGTCTTT	1680
	GTGTTTGGTT TTGTGATGTA ACGATCTTTG CTGGGGTTTT TTGCTTTGTT TTGAGGGAAA	1740
35	TGCTTTGGAG TAAATTTTAA GTTCTGGAG TTAATTTGTT TTACAGGAAT TTTGTTTTTT	1800
	AAAAAATAG GATCATCTCG AACTTTGGAA TGACCCCTT ATATATTTTC TGAAAATGAA	1860
40	AACAGTTACA TGAAAAAAT TTCCAATGAA GATGTCAGCA TTTTATGAAA AACCAGAAGT	1920
	TATTAGATGA AAGCAGCGAG TGAATCTTTA AAACAGACTT GATCAGCAC ACACAATAAG	1980
	TCTTTCTCTC CGAAACCGGA AGTAAATCTA TATCTGTTAG AAATAATGTA GCCAAAAGAA	2040
45	TGTAAATTTG AGGATTTTTT TGCCAATAGT TTATAGAAAA TATATGAACC AAAGTGATTT	2100
	GAGTTTGTA AAATGTAAAA TAGTATGAAC AAAATTGCA CTCTACCAGA TTTGAACATC	2160
50	TAGTGAGGTT CACATTCATA CTAAGTTTTT AACATTGTGT TCTTTTTGCA TTCATTTTTT	2220
	ACTTTTATTA AAGGTTCAAA ACC	2243

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(2) INFORMATION FOR SEQ ID NO: 167:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1816 base pairs

(B) TYPE: nucleic acid

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(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 167:

5	GGTGGGNAGC TTTNAATTTT CCCTTACWGG GGCCTMTAA GGGGAAACCT TCCCGGAATT	60
	TTCGGGTCGA CCCACGGTC CGGCCAGCCT AGGAGAAGAA GTTCGTAGTC CCAGAGGTGA	120
10	GGCAGGAGGC GGCAGTTTCT GCGGGGTGAG GCGGAGCTG AAGTGACAGC GGAGGCGGAA	180
	GCAACGGTCG GTGGGGCGGA GAAGGGGGCT GGCCCCAGGA GGAGGAGGAA ACCCTTCCGA	240
	GAAAACAGCA ACAAGCTGAG CTGCTGTGAC AGAGGGGAAC AAGATGGCGG CGCCGAAGGG	300
15	GAGCCTCTGG GTGAGGACCC AACTGGGGCT CCCGCCGCTG CTGCTGCTGA CCATGGCCTT	360
	GGCCGGAGGT TCGGGGACCG CTTGGGTGA AGCATTTGAC TCGGTCTTGG GTGATACGGC	420
20	GTCTTGCCAC CGGGCCTGTC AGTTGACCTA CCCCTTGCAC ACCTACCTA AGGAAGAAGA	480
	GTTGTACGCA TGTACAGAGG GTTGCAGGCT GTTTTCAATT TGTCAAGTTG TGGATGATGG	540
	AATTGACTTA AATCGAATA AATTGGAATG TGAATCTGCA GTACAGAAG CATATTCCCA	600
25	ATCTGATGAG CAATATGCTT GCCATCTTGG KTGCCAGAAT CAGCTGCCAT TCGCTGAACT	660
	GAGACAAGAA CAACTTATGT CCCTGATGCC AAAAATGCAC CTACTCTTTC CTCTAACTCT	720
30	GGTGAGGTCA TTCTGGAGTG ACATGATGGA CTCCGCACAG AGCTTCATAA CCTCTTCATG	780
	GACTTTTAT CTTCAAGCCG ATGACGGAAA AATAGTTATA TTCCRGTTA AGCCAGRAA	840
35	TCCCAGGTAC GCACCACATT TGGAGCCAGG AGCCCTACCA AATTTGRGRG RAWCTCTCT	900
	AAGCAAAATG TCCNTCAKMT CGSMAATGAG AAATTCACAA GCGCACAGGA ATTTTCTTGA	960
	AGATGGAGAA AGTGATGGCT TTTTAAGATG CCTCTCTCTT AACTCTGGGT GGATTTTAAC	1020
40	TACAACTCTT GTCCTCTCGG TGATGGTATT GCTTTGGATT TGTGTGCAA CTTGTGTCTA	1080
	CACGCTGTG GACGCAGTAT AGTTTCCCTC TGAGAAGCTG AGTATCTATG GTGACTTGA	1140
45	GTTTATGAAT GAACAAAAGC TAAACAGATA TCCAGCTTCT TCTCTTGTGG TTGTTAGATC	1200
	TAAAACTGAA GATCATGAAG AAGCAGGGCC TCTACCTACA AAAGTGAATC TTGCTCATTC	1260
	TGAAATTTAA GCATTTTCT TTTAAAAGAC AAGTGAATA GACATCTAAA ATTCCACTCC	1320
50	TCATAGAGCT TTTAAATGG TTTCAATTGGA TATAGGCCTT AAGAAATCAC TATAAAATGC	1380
	AAATAAAGTT ACTCAATCT GTGAAAAAA AAAAAAAAC AAAAAAAAC TCGAGGGGGG	1440
55	GCCCGTTACC AAKTCGCCCT ATWGTGADTB GTATTMITAT TTTACTAATA TCTGTAGCTA	1500
	TTTTGTTTTT KGCTTKGGTT ATKGTTTTTY TCCCTTYTCT WAGCTATRAG CTGATCATKG	1560
	CYSCPTCTCA CCTCTGCCA TGATACTGTC AGTTACCTTA GTTAACAAGC TGAATATTTA	1620
60	GTAGAAATGA TGCTTCTGCT CAGGAATGGC CCACAAATCT GTAATTTGAA ATTTAGCAGG	1680

5 AAATGACCTT TAATGACACT ACATTTTCAG GAACTGAAAT CATTAAAAAT TTATTTGAAT 1740
AATTATGTGC TGAACAAAAA AAAAAAAAAA AMWMRARASK RRWWACTCGA GGGGGGGCCC 1800
GGTACCCNAT TCGCCG 1816

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(2) INFORMATION FOR SEQ ID NO: 168:

15 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 945 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 168:

AGAAACCGTT GATGGGACTG AGAAACCAGA GTTAAACCT CTTGGAGCT TCTGAGGACT 60
CAGCTGGAAC CAACGGGCAC AGTTGGCAAC ACCATCAACT TCTCCCAAGC AGAGAAACCC 120
25 GAACCCACCA ACCAGGGGCA GGATAGCCTG AAGAAACATC TACACGCAGA AATCAAAGTT 180
ATTGGGACTA TCCAGATCTT GTGTGGCATG ATGGTATGA GCTGGGGAT CATTTTGGCA 240
TCTGCTTCCT TCTCTCCAAA TTTTACCCAA GTGACTTCTA CACTGTTGAA CTCTGCTTAC 300
30 CCATTCATAG GACCCCTTTT TTTTATCATC TCTGGCTCTC TATCAATCGC CACAGAGAAA 360
AGGTTRACCA AGCTTTTGGT GCATAGCAGC CTGGTTGGAA GCATTCTGAG TGCTCTGTCT 420
35 GCCCTGGTGG GTTTCATTAT CCTGTCTGTC AAACAGGCCA CCTTAAATCC TGCCTCACTG 480
CAGTGTGAGT TGGACAAAAA TAATATACCA ACAAGAAGTT ATGTTTCTTA CTTTATCAT 540
GATTCACTTT ATACCAAGGA CTGCTATACA GCCAAAGCCA GTCTGGCTGG AWCTCTCTCT 600
40 CTGATGCTGA TTGCACTCT GCTGGAATC TGCTAGCTG TGCTCACTGC TGTGCTGCGG 660
TGGAACAGG CTTACTCTGA CTTCCCTGGG AGTGTACTTT TCCTGCCTCA CAGTTACATT 720
45 GGTAATTCTG GCATGTCCTC AAAATGACT CATGACTGTG GATATGAAGA ACTATTGACT 780
TCTTAAGAAA AAAGGGAGAA ATATTAATCA GAAAGTTGAT TCTTATGATA ATATGGAAAA 840
GTTAACCATT ATAGAAAAGC AAAGCTTGAG TTTCTTAAAT GTAAGCTTTT AAAGTAATGA 900
50 ACATTAAAAA AAACCATTAT TTCCTGTCA TTAAAGATA ATGTG 945

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(2) INFORMATION FOR SEQ ID NO: 169:

60 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 902 base pairs
(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 169:

5
GGCAGAGCCA CAGGAAGGAT GAGGAAGACC AGGCTCTGGG GGCTGCTGTG GATGCTCTTT 60
GTCTCAGAAC TCCGAGCTGC AACTAAATTA ACTGAGGAAA AGTATGAACT GAAAGAGGGG 120
10 CAGACCCTGG ATGTGAAATG TGA CTACTACAG CTAGAGAAGT TTGCCAGCAG CCAGAAAGCT 180
TGGCAGATAA TAAGGACGG AGAGATGCCC AAGACCCTGG CATGCACAGA GAGGCCCTCA 240
AAGAATTCCT ATCCAGTCCA AGTGGGGAGG ATCATACTAG AAGACTACCA TGATCATGGT 300
15 TTACTGCGCG TCCGAATGGT CAACCTTCAA GTGGAAGATT CTGGACTGTA TCAGTGTGTG 360
ATCTACCAGC CTCCAAGGA GCCTCACATG CTGTTGATC GCATCCGCTT GGTGGTGACC 420
20 AAGGGTTTTT CAGGGACCCC TGGCTCCAAT GAGAATTCTA CCCAGAATGT GTATAAGATT 480
CCTCTACCA CCACTAAGGC CTGTGCCCCA CTCTATACCA GCCCCAGAAC TGTGACCCAA 540
GCTCCACCCA AGTCAACTGC CGATGTCTCC ACTCCTGACT CTGAAATCAA CCTTACAAAT 600
25 GTGACAGATA TCATCAGGT TCCGGTGTTC AACATTGTCA TTCTCCTGGC TGGTGGATTG 660
CTGAGTAAGA GCCTGGTCTT CTCTGTCTG TTTGCTGTCA CGCTGAGGTC ATTTGTACCC 720
30 TAGGCCACG AACCCACGAG AATGTCTCT GACTTCCAGC CACATCCATC TGGCAGTTGT 780
GCCAAGGGAG GAGGGAGGAG GTAAAGGCA GGGAGTTAAT AACATGAATT AAATCTGTAA 840
35 TCACCRGCTA AAAAAAAAAA AAAAAAACN CGANCCTNGG TTTTCAGCTC CATCAGCTCC 900
TT 902

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(2) INFORMATION FOR SEQ ID NO: 170:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1883 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 170:

50
AGAAAACAAC TGAAAACCA CATTTTCTA CATACTAGT GGGAGGTAGC TGAGAACTTG 60
GCACTGCGCA CACATACTAG GTTGAAAGAG AGTTGAGGAA ACCAGAAGGC CAAGTGGATC 120
55 TGCTGGCAAA CCCTGAACCT GTCTCTGCG CTGTCTCTAC AGTTCTGAAG TTGAAAATCC 180
TTTTCATGCC TAGCATCTGC TTGAGTTATA AACCCCAAGG CAGCCATGTC ATAGACTAGT 240
GTTTACTCTT GTTTTGAATT TGTMTTAATG CTTCTAAGA CCCAAGTGCC TCCTGCTGTT 300
60

	TCCTCCTTTG TGGTAGCCTC TGGCCATCTG GGACCTCAAT CCCCAGCTTT CCCACTTTCA	360
	GCAGTCCTTT GCTCTCTTTG CTTCTACCTC AAATAGCCCC AGGAGTGGGC TTTAGTCTCC	420
5	AATATGGAGC ATYTCAAGCT TCTCCTGGGG GATGGGGATT GGGATGGGCA GAATCTGTTT	480
	TGGWTCCTCG GGTATTTCCT AGTGGGTGTA AAAGCAGAGC TGGGCCCTTC CCTCTCTTAT	540
10	CCCTGAGGGT GGGTAAGAAG GACTGTATCT ACACCTGTTT TTCCTACCT TCTCTTTTGT	600
	TAGGGAGGCC TCATTCTAAG TTCTCAAGA GAGTCTTTGG CTTAAAGCTG TAGCAAGGGT	660
	GTGCTAGGTG GGGGATTGG AGCAAAACCG TCGAGTAGGC ATGATACTGG TATGGAGTGG	720
15	GCCTGCAAAA TCAGACAGAA ATGGCTTGAG AAGCCGCAGG GGAGCATGCC TGTCTCTCAG	780
	TGATAGAGTA TGGGAGGGAC CTCCCTAGCT TGGAAAATGA GAATTGAAGG GGTATGAAC	840
	AAATAGGATG CCTAGTTGAG GATGTTCCCA AAGTTTGTCT CAATCTTATC ATTAGTAGAT	900
20	TTTATAAGCC ACAGAGACAA ACCAGAAACG GAATAATGTT ACTTTGGATG CTTTATTTTT	960
	TTGTTCTAGG TGTGGCTTTG TACATGCAGA AGAATGCTAT ATGCTGCACA TTTTGCCTTT	1020
25	AAAGTCTTAC GACTTTCCCC ATTTTAGTCT AATGGGAAGA TACAGATGTG CAAGTCTGCT	1080
	TTTTTGTTTT TTGTTATTAT TTTTTTTTTT TTGCTCTGTG TTATGGACAT TTTCAGACAT	1140
30	GCACAGAAGT GGAGAGGATG GTCCTTGAC CCCATGTGTC CATCACCTAG CTGCATCACT	1200
	TATCAGCTAT GGTCAACCTG GTTTCATCTG TATCTCTCTC TTTTCACCTG TATTGTTTAT	1260
	TGAAAATCCA AGACACTATG CCAATGCAAC CGTGACTACT TTGGGAGATT GGTAGTCTCT	1320
35	TTTGATGGTG ATAGTGATGG GGTGCACTAT CATAATCACA TCAGGTCTGC TTTTGTCTTT	1380
	TAATGTTAAC TAATGAAGTT CCAGAGATGG GCCTTAGAAA TGTGTTTTAA GAATTAACAA	1440
40	GGAGTCTCAA AAAGAAATGA GAGGGATGCT TCCTTTCCCC TTGCATCTAC AAAACAAGAG	1500
	AGAGACTGTT CTGTGTGAAA ACTCTTTCAA AAATTCTGAT ATGGTAAGGT ACTTGAGACC	1560
	CTTCACCAGA ATGTCAATCT TTTTTTCTGT GTAACATGGA AACTTGTGTG ACCATTAGCA	1620
45	TTGTTATCAG CTTGTACTGG TCTCATAACT CTGGTTTTGG AAGAATAATT TGGAAATTGT	1680
	TGCTGTGTTT TGTGAAAATA ACCTCCCCAA AATAATTAGT AACTGGTTGT TCTACTTGGT	1740
50	AATTTGACAC CCTGTTAATA ACGCAATTAT TTCTGTGTTT TTAACAGTA TAAATAGTTG	1800
	TAAGTTTGCA TGCATGATGG AAAAATAAAA ACCTGTATCT CTGTTAAAAA AAAAAAAAAA	1860
	AAAAAAAAAA AAAAAAAAAA AAA	1883
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(2) INFORMATION FOR SEQ ID NO: 171:

60 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2100 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 171:

	TACTTTTAGA TTTACTGCCT TCAAAAAGTG CCTATTCTGA GCAACATAAA CGTTATTCCT	60
10	TACATATGTA TGTACACACG GTACCCAGAG TCGTACTGTG GCAGCCTTCA AAAACATACC	120
	ATCAGAAAGA GTAGGTGCTG AGATAAGGNA ACTTTGCCAA ATGNAAGAAA GTCACCTCACT	180
15	TCCAATATCC CCTCTTCAAG CGGCTACCGT GRAASGGGCT GCAAACACAT TCCCTGAGCA	240
	TCCCTTGCTG ATACAGCTTC TTTATATTTA TATCCTACTG GATGGTAGCA TATTGCTAAG	300
	GTTTCTGTGA CTCGTCTCA AGGGAATGTA AGYTTTATGG CATTGAAACA TTTAGGAAAA	360
20	AAAAAGATGT TTAAGAGAAT TAATAGAGCC GTAGTCTGTA TTAGGATGTG TGTCATATGT	420
	GTGTTCTATA AACTAAGCAT CGGTGGGTTT AGAGTGTTAA AGTGTGAGCA CATTCTCTCT	480
25	CCTTTTGTCT CTCAGGCTAA CATGAGAGAA AATAGAAAAG TCTTGGCTGT GGGGATTGGA	540
	AGCTCAGGGG GCCAAATGTC CTTGCCAGAT CCTTAGAGCA TTACTTTGAC TCCTAAAAAT	600
	AGTAGTGAT GTTATTGAT GGCTTTTGTT TCCATAGTTC CATCACTGAC AAAACTGTCA	660
30	ATACTGTTGA TGGAGCAGCA GCATAGCCTA GAGTGATGCA TTCTTACCCA GAGGTGGCAA	720
	TAGGAGAGGG TCCATGTAAA TAGGACGAGG TAGACAGTGC ATGATTGTAG GAGAAGGGTT	780
35	GAAGGGAGGA CATGATTCCA AAAAAGATCG TTCTCAATGT GTCGTCTGAC TCAACCAGCT	840
	GGCAGATTAC ACTTGCCAAG TCGTTCCCTT TCCTTCTAAG TCAGTTGGCT CCATATTCAC	900
	TTGAATATGC CTCGTGTTGG GCAAAGCAAG ATACCTCCAC TTAACCTTTA TCCAAGGAAG	960
40	CTCTTGGTGT CCTCTTGGTC ATAAAGTTGT CTCCTACCTA ACCCAGTTT ACCAAATGGA	1020
	AGTAAAAGGG GACAACTAT GGAAGATGGA CTCCATGCCA TTGCAGTCAG CCACCATCT	1080
45	CTTTTCCATA TAAGGAGCCC CATTACATAA GCTACGGGTG AGGTGGAAC AGCTATGTTT	1140
	CATAATTTC AAGAGTGTGAC CACCCTGCTC TAGTCATCAT CATGGATGA ATCCAGTTGA	1200
	CTCTTTGGCA AAAGGGTGAT ACTTTTCACT AAAAATGCCT ACTCTTCCTG TTGATGTTCC	1260
50	TTTTCTGTTT TTACCTTGTC CAATTTCAC ACTAGTCATT TTTTATTTT TTTAGAGGAT	1320
	CAGATTTTAG CGCTGGAAAA TGAGTTCAAA AATTTTCAGT TAATGTCATA AGGATGTTGG	1380
55	GATACAGAGA TTTTTTTTTT CCTTGGAAAC AAATGGACTG GGAAGAAACA CAGCATGGCT	1440
	TTGCTCTGAG TTTCAATCTG ATGATTATGA CCATGGAAGA TAGTCTTATG TAAAGGTTAA	1500
	ATGGTGTTTA CAAGTGGATA GATAAGGCGG AGATGGTGAG AAGCCGGGTT TTCTCTATGC	1560
60	TAAATGTGTC TACTAAGAGC AGCACTTCCT ACTAGCTAAG CACAATCATA GCCCCACCGT	1620

5 GATGAGCTGC TAGTCTGAAT AACATTCCCT GACTTAGGGA AAGGCACACA AAAACATATA 1680
 AAGAATATGT CTATTTTCAT ATGTGTGATA CTGACAGAGC CATGGTATTC CTAAAATATA 1740
 GGTTCCTCTT TTTTCTGTGTA TTCTTAGCAA ATTGCATTTA TTCACTACAT TACAAACCAT 1800
 CACTGATGTA TCCAAAATAG CACACATAGT TCAGTATGAA AATAAGAGAA TAAAATCTGT 1860
 10 TATAAGCAAG TGATTTAGGT ATTTCTTTT GTGTTTATGC ATTATCTGAC TATATTAAAA 1920
 CCTGTTTTTC TATTTACCTT CTATCAGTTT TCTCTACCAA TTATGTTTTT TCAATGCTCT 1980
 ATAAGAATGA ATATGGAAAT TATATTCTT TTTTCTGTAA AAGAGTTGCA ACTACTTTAT 2040
 15 TATATTTAGA AATCCAATAA ACTTCTTATT ACATTTAAAA AAAAAAAAAA AAAACTCGAA 2100

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(2) INFORMATION FOR SEQ ID NO: 172:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1930 base pairs
 25 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 172:

CCTTTGAMTG TGGTCCCGGG TGCNGATTGG CAGCGCCTCC GCCGCGGCTC GTGGTTGTCC 60
 CGCCATGGCA CTGTCGCGGG GGCTGCCCGG GGAGCTGGCT GAGGCGGTGG CCGGGGGCCG 120
 35 GGTGCTGGTG GTGGGGGCGG GCGGCATCGG CTGCGAGCTC CTCAAGAATC TCGTGCTCAC 180
 CGGTTTCTCC CACATCGACC TGATTGATCT GGATACTATT GATGTAAGCA ACCTCAACAG 240
 ACAGTTTTTG TTTCAAAAGA AACATGTTGG AAGATCAAAG GCACAGGTTG CCAAGGAAAG 300
 40 TGTACTGCAG TTTTACCCGA AAGCTAATAT CGTTGCCTAC CATGACAGCA TCATGAACCC 360
 TGACTATAAT GTGGAATTTT TCCGACAGTT TATACTGGTT ATGAATGCTT TAGATAACAG 420
 45 AGCTGCCCCG AACCATGTTA ATAGAATGTG CCTGGCAGCT GATGTTCCCTC TTATTGAAAG 480
 TGGAACAGCT GGGTATCTTG GACAAGTAAC TACTATCAA AAGGGTGTGA CCGAGTGTTA 540
 TGAGTGTCAT CCTAAGCCGA CCCAGAGAAC CTTTCTGGC TGTACAATTC GTAACACACC 600
 50 TTCAGAACCT ATACATTGCA TCGTTTGGGC AAAGTACTTG TTCAACCAGT TGTTTGGGGA 660
 AGAAGATGCT GATCAAGAAG TATCTCCTGA CAGAGCTGAC CCTGAAGCTG CCTGGGAACC 720
 55 AACGGAAGCC GAAGCCAGAG CTAGAGCATC TAATGAAGAT GGTGACATTA AACGTATTTT 780
 TACTAAGGAA TGGGCTAAAT CAACTGGATA TGATCCAGTT AAACTTTTTA CCAAGCTTTT 840
 TAAAGATGAC ATCAGGTATC TGTGACAAT GGACAACTA TGGCGGAAAA GGAAACCTCC 900
 60

	AGTTCGGTTG GACTGGGCTG AAGTACAAAG TCAAGGAGAA GAAACGAATG CATCAGATCA	960
	ACAGAATGAA CCCAGTTAG GCCTGAAAGA CCAGCAGGTT CTAGATGTAA AGAGCTATGC	1020
5	ACGTCTTTT TCAAAGAGCA TCGAGACTTT GAGAGTTCAT TTAGCAGAAA AGGGGGATGG	1080
	AGCTGAGCTC ATATGGGATA AGGATGACCC ATCTGCAATG GATTTTGTCA CCTCTGCTGC	1140
10	AAACCTCAGG ATGCATATTT TCACTATGAA TATGAAGAGT AGATTTGATA TCAAATCAAT	1200
	GGCAGGGAAC ATTATTCCTG CTATTGCTAC TACTAATGCA GTAAITGCTG GGTGATAGT	1260
	ATTGGAAGGA TTGAAGATTT TATCAGGAAA AATAGACCAG TGCAGAACAA TTTTMTTGAA	1320
15	TAAACAACCA AACCCAAGAA AGAAGCTTCT TGTGCCTTGT GCACTGGATC CTCCCAACCC	1380
	CAATGTGTAT GTATGTGCCA GCAAGCCAGA GGTGACTGTG CGGCTGAATG TCCATAAAGT	1440
20	GACTGTTCTC ACCTTACAAG ACAAGATAGT GAAAGAAAAA TTTGCTATGG TAGCACCAGA	1500
	TGTCCAAATT GAAGATGGGA AAGGAACAAT CCTAATATCT TCCGAAGAGG GAGAGACGGA	1560
	AGCTAATAAT CACAAGAAGT TGTCAGAATT TGGAAATTAGA AATGGCAGCC GGCTTCAAGC	1620
25	AGATGACTTC CTCCAGGACT ATACTTTATT GATCAACATC CTTCATAGTG AAGACCTAGG	1680
	AAAGGACGTT GAATTTGAAG TTGTTGGTGA TGCCCCGGAA AAAGTGGGS CCAAACAAGC	1740
30	TGAAGATGCT GCCAAAAGCA TAACCAATGG GCAGTGATGA TGGGAGCTTC AGCCCTCCAC	1800
	CTYCACAGCT TCAAGGAGGC AAGATGGACG TYTCYCATAG TTGATYCGGR TGAAGAAGRT	1860
	TCTCCAATAA TTGCCCGACG TTCATTGAAG GAAGGAGGAG GAGGCCCGCC AAGAGGGGAA	1920
35	TTTAGGNTTG	1930

40 (2) INFORMATION FOR SEQ ID NO: 173:

(i) SEQUENCE CHARACTERISTICS:

- 45 (A) LENGTH: 1509 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 173:

50	GGCCCTGGCC TCTGGGCTGA GGCTTGCTAG GGA CTGGGG TGGCTCTAAG GGGCAGGGAT	60
	AGGGCTGGGG AGCGCCGGCC TGTGGCCCTG ACCAGCCCTT TCTCGTGCRC GTTCCACCCC	120
	GATGCAGGTG GTCACGTGCT TGACGCGGA CAGTACCTG ACGCACTGCT TCCTCCAGCA	180
55	CCTCATGGTC GTGCTGTCCT CTCTGGAACG CACGCCCTCG CCGGAGCCTG TTGACAAGGA	240
	CTTCTACTCC GAGTTTGGGA ACAAGACCAC AGGGAAGATG GAGAACTACG AGCTGATCCA	300
60	CTCTAGTCGC GTCAAGTTTA CCTACCCAG TGAGGAGGAG ATTGGGGACC TGACGTTTAC	360

	TGTGGCCCAA AAGATGGCTG AGCCAGAGAA GGCCCCAGCC CTCAGCATCC TGCTGTACGT	420
5	GCAGGCCCTC CAGGTGGGCA TGCCACCCCC TGGGTGCTGC AGGGGCCCCC TGGGCCCCAA	480
	GACACTCTCG CTCACCAGCT CCGAGATCTT CCTCTGGAT GAGGACTGTG TCCACTACCC	540
	ACTGCCCGAG TTTGCCAAAG AGCCGCCGCA GAGAGACAGG TACCGGCTGG ACGATGGCCG	600
10	CCGCGTCCGG GACCTGGACC GAGTGCTCAT GGGCTACCAG ACCTACCCGC AGCCCTCACC	660
	CTCGTCTTCG ATGACGTGCA AGGTCATGAC CTCATGGGCA GTGTACCCCT GGACCACITT	720
15	GGGGAGGTGC CAGGTGGCCC GGCTAGAGCC AGCCAGGGCC GTGAAGTCCA GTGGCAGGTG	780
	TTTGTCCTCA GTGCTGAGAG CAGAGAGAAG CTCATCTCGC TGTGGCTCG CCAGTGGGAG	840
	GCCCTGTGTG GCGGTGAGCT GCCTGTGAG CTACCCGGCT AGCCAGGCC ACAGCCAGCC	900
20	TGTCGTGTCC AGCCTGACGC CTAAGGGG AGGGCAGCAG GCTTTTGTGT TCTCTAAAAA	960
	TGTTTTATCC TCCCTTTGGT ACCTTAATTT GACTGTCCCTC GCAGAGAATG TGAACATGTG	1020
25	TGTGTGTGTG GTTAATTCTT TCTCATGTTG GGAGTGAGAA TGCCGGGCCC CTCAGGGCTG	1080
	TCGGTGTGCT GTCAGCCTCC CACAGGTGGT ACAGCCGTGC ACACCAAGTGT CGTGTCTGCT	1140
	GMTGTGGGAC CGTGTGTAAC ACGTGACACT GTGGGTCTGA CTTTCTCTTC TACACGTCCT	1200
30	TTCTTGAAGT GTCGAGTCCA GTCCTTTGTT GCTGTGCTG TTGCTGTTGC TGTGTGTTT	1260
	GGCATCTTGC TGCTAATCCT GAGGCTGGTA GCAGAATGCA CATTGGAAGC TCCCACCCCA	1320
35	TATTGTCTTT CAAAGTGGAG GTCTCCCTG ATCCAGACAA GTGGGAGAGC CCGTGGGGGC	1380
	AGGGGACCTG GAGCTGCCAG CACCAAGCGT GATTCTCTGT GCCTGTATTC TCTATTCCAA	1440
	TAAAGCAGAG TTTGACACCG TCAAAAAAAA AAAAAAAAAA AAAAAAAAAA ATTNCTGCGG	1500
40	CCTCAAGGG	1509

45 (2) INFORMATION FOR SEQ ID NO: 174:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3173 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 174:

55	TCGACCCAS GCGTCCGTGC TTTTCCACAG AAGGTAGAC CCTGAAAGAG ATGGCTCAGC	60
	ACCACCTATG GATCTTGCTC CTTTGCCTGC AAACCTGGCC GGAAGCAGCT GGAAAAGACT	120
60	CAGAAATCTT CACAGTGAAT GGGATTCTGG GAGAGTCAGT CACTTTCCCT GTAAATATCC	180

	AAGAACCACG GCAAGTTAAA ATCATTGCTT GGACTTCTAA AACATCTGTT GCTTATGTAA	240
	CACCAGGAGA CTCAGAAACA GCACCCGTAG TTA CTGTGAC CCACAGAAAT TATTATGAAC	300
5	GGATACATGC CTTAGGTCCG AACTACAATC TGGTCATTAG CGATCTGAGG ATGGAAGACG	360
	CAGGAGACTA CAAAGCAGAC ATAAATACAC AGGCTGATCC CTACACCACC ACCAAGCGCT	420
10	ACAACTGCA AATCTATCGT CGGCTTGGGA AACCAAAAAT TACACAGAGT TTAATGGCAT	480
	CTGTGAACAG CACCTGTAAT GTCACACTGA CATGCTCTGT AGAGAAAGAA GAAAAGAATG	540
	TGACATACAA TTGGAGTCCC CTGGGAGAAG AGGGTAATGT CCTTCAAATC TTCCAGACTC	600
15	CTGAGGACCA AGAGCTGACT TACACGTGTA CAGCCCAGAA CCCTGTCAGC AACAAITCTG	660
	ACTCCATCTC TGCCCGGCAG CTCGTGTCAG ACATCGCAAT GGGCTTCCGT ACTCACCACA	720
20	CCGGTTGCT GAGCGTGCTG GCTATGTTCT TTCTGCTTGT TCTCATTCTG TCTTCAGTGT	780
	TTTTGTTCG TTGTMTCAAG AGAAGACAAG ATGCTGCCTC AAAGAAAACC ATATACACAT	840
	ATATCATGGC TTCAAGGAAC ACCCAGCCAG CAGAGTCCAG AATCTATGAT GAAATCCTGC	900
25	AGTCCAAGGT GCTTCCCTCC AAGGAAGAGC CAGTGAACAC AGTTTATTCC GAAGTGCAGT	960
	TTGCTGATAA GATGGGGAAG GCCAGCACAC AGGACAGTAA ACCTCCTGGG ACTTCAAGCT	1020
30	ATGAAATTGT GATCTAGGCT GCTGGGCTGA ATTCTCCCTC TGGAACTGA GTTACAACCA	1080
	CCAATACTGG CAGGTTCCCT GGATCCAGAT CTCTCTGCC CAACTCTTAC TGGGAGATTG	1140
	CAAACCTGCC CATCTCAGCC TGTAAGCAAA GCAGGAAACC TTCTGCTGGG CATAGCTTGT	1200
35	GCCTAAATGG ACAAATGGAT GCATACCCCT CCTGAAATGA CTCCTTCTG AATGAATGAC	1260
	AAAGCAGGTT ACCTAGTATA GTTTTCCCAA ACTTCTTCCC ATCATAGCAC ATGTAGAAAA	1320
40	TAATATTTT ATGGCACACT GGGATAAACA AGCAAGATTG CTCACTTCTG GAAGCTGCAT	1380
	ATGACTAGAG GCCTCTGTG ACTGGAGGTA ACAACCTGC CCAGTAACTG TGGGAGAAGG	1440
	GGATCAATAT TTGTCACACC TGTAATAGGC CATGGCACAC CAGCCAAGAT GCTCTGCTCA	1500
45	CAGTCAGTAT GTGTGAAGAT CCCTGGTGCG TGGCCTTCAC CACGCATCTT GAGCAAATTA	1560
	GGAAAAATGTA CCCTTCGCTT GAGGCAGATG CAGCCCTTCC CCCGAGTGCA TGGCTTGGAG	1620
50	AGCAGAATGT GGGCTGCATA TAAGCACACT CATCCCTTTG TCTGGGAATC TTTGTGCAGG	1680
	GCATAACAGG CTTAGTAAGT CCAAACACAG ATGACAGTGC TGTGTGGGTC TCTGTGCAGG	1740
	TGTGTGGCTCT CAGCCATGTA GACACACTCT CCAAATGGAG TGTGTGAAAA TGTTCCTTCT	1800
55	GCAGGTCTA GAGACTGCTG GGACACTTTT CTGGAGTGC TACTTCAGAA GCCTTATAGG	1860
	ATTTCTTTTC TGGCCAAGAT TTCTTCTGT ATCACTCCAA GCAGCCTCAG CAGAAGAAGC	1920
60	AGCCATGCCC AGTATTCCCA CTCTCCAAA GGAAGTGACC AGCTTATATT TCTCACACTT	1980

	CTGGGGA	ACT	GGGTATA	ATC	CAACCAT	CAA	AATAGA	AAGAC	CTTGCA	AAGAA	GCAGAG	TCAT	2040
	TCTCCAG	AAG	GAACTT	GGGA	GATGAT	GGTG	CAGATG	ATGA	AACTGG	GTTC	ATCCCAG	TTC	2100
5	CAAAGAC	TCA	GAGAACT	AGA	GTTTAAG	CTG	AGGCAG	AGTG	CCGCCAC	CCCT	GGCATG	CCCC	2160
	ACAAAC	CAGAT	CACCAG	CCAG	CTTACAC	AGG	CATTAA	CTCT	CCTCAAT	GAG	GAAGAAT	CAT	2220
	TCACAA	CTGA	GCAAGAC	ATT	CATATG	ATCA	TTTAAG	GAA	TGTTTCC	CTT	ATGTGT	TAGC	2280
10	AAGTATA	ATC	GGCTAA	CTCC	TAAATCC	CAA	TGAATAG	TCC	TAGGCT	GGAC	AGCAAT	GGGC	2340
	TGCAATT	AGG	CAGATA	AAGA	CATCAG	TCCC	AGTAAAT	GAA	TCCATAG	ACT	CATCTAG	CAC	2400
15	CAACTAC	CAT	TAGCACT	ATG	TTAGGAG	CTG	CAAGGCC	CCCA	AAGTAGA	AAGA	TGTGCAT	AAAT	2460
	GTCTGCT	CTT	GTGTAG	CTCA	GGAGACA	AAT	CCAGCAC	AGA	CACTAC	AGTT	AACGCT	GAA	2520
	TGCAGCT	GCA	AGTAAT	AGCA	TGAACAG	TCA	GAAAAAT	TACC	TTATGAG	GGG	GCAGGG	CTGA	2580
20	AGCTGGG	CCT	TGAAGG	ATGG	ATGAAAT	TTG	GATAGAG	AAT	GAGGAAG	ACA	GAGGGC	CTCC	2640
	AAGTGAG	GAG	AGCATG	AAAA	ATGAGC	AGG	GCCTGG	ATCA	GTGGGT	GTA	TTCAGAG	CAC	2700
25	CTCTCC	AGAT	GCACCAT	GCA	TGCTCAC	AGT	CCCTTGC	CTA	TGTGTG	GCAG	AGTGTCC	AG	2760
	CCAGATG	TGT	GCCCCAC	CCC	CATGTCC	ATT	TACATGT	CTT	TCAATG	CCCA	CCTCAAA	AGG	2820
	TACCTCT	TCT	GTAAAG	CTTT	CCCTGG	TATC	AGGAAT	CAAA	ATTAAT	CAGG	GATCTTT	TCA	2880
30	CACTGCT	GTT	TTTTCCT	CTT	TGGTCCT	TCT	ATCACTA	AAAA	CTCATCT	CAT	TCAGCC	TAC	2940
	AGCATA	ACTA	ATTATT	TGTT	TTCTCA	CTA	CATTGT	TACAT	GTGGGA	ATTA	CAGATAA	ACG	3000
35	GAAGCCK	GCT	GGGTG	GTTG	CTCACG	CCTG	TAATCCC	AAC	ACTTTG	GGAG	GCCAAGG	CAG	3060
	GCGGATC	ACC	TGAGGT	CAGG	ARTTCG	AGAT	TARTCT	GGCC	AACATG	GTGA	AACCCCAT	TNT	3120
40	N	TACTAAA	AAAA	TACGAA	ATTA	GCCAGG	TGTG	GTGGC	ACACA	TCTGTAG	TCC	CAG	3173

45 (2) INFORMATION FOR SEQ ID NO: 175:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 991 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 175:

55	AAATTCG	GCA	CAGCTG	AGAG	GAGACAC	AAG	GAGCAG	CCCCG	CAAGCAC	CAA	GTGAGAG	GCA	60
	TGAAGT	TACA	GTGTGT	TTCC	CTTTGG	CTCC	TGGGTAC	AAT	ACTGAT	ATTG	TGCTCAG	TAG	120
	ACAACCA	CGG	TCTCAG	GAGA	TGTCTG	ATT	CCACAG	ACAT	GCACCAT	TATA	GAAGAG	AGTT	180
60	TCCAAGA	AAAT	CAAAAG	AGCC	ATCCAAG	CTA	AGGACAC	CCTT	CCCAAAT	GTC	ACTATC	CTGT	240

	CCACATTGGA GACTCTGCAG ATCATTAAGC CCTTAGATGT GTGCTGCGTG ACCAAGAACC	300
5	TCCTGGCGTT CTACGTGGAC AGGGTGTTC AAGATCATCA GGAGCCAAAC CCCAAAATCT	360
	TGAGAAAAAT CAGCAGCATT GCCAACTCTT TCCTCTACAT GCAGAAAACT CTGCGGCAAT	420
	GTCAGGAACA GAGGCAGTGT CACTGCAGGC AGGAAGCCAC CAATGCCACC AGAGTCATCC	480
10	ATGACAAC TAATCAGCTG GAGGTCCACG CTGCTGCCAT TAAATCCCTG GGAGAGCTCG	540
	ACGTCTTTCT AGCCTGGATT AATAAGAATC ATGAAGTAAT GTCCTCAGCT TGATGACAAG	600
15	GAACCTGTAT AGTGATCCAG GGATGAACAC CCCCTGTGCG GTTTACTGTG GGAGACAGCC	660
	CACCTTGAAG GCGAAGGAGA TGGGAAGGC CCCTTGACG TGAAAGTCCC ACTGGCTGGC	720
	CTCAGGCTGT CTTATTCCGC TTGAAAATAG CCAAAAAGTC TACTGTGGTA TTTGTAATAA	780
20	ACTCTATCTG CTGAAAGGGC CTGCAGGCCA TCCTGGGAGT AAAGGGCTGC CTTCCCATCT	840
	AATTTATTGT GAAGTCATAT AGTCCATGTC TGTGATGTGA GCCAAGTGAT ATCCTGTAGT	900
25	ACACATTGTA CTGAGTGGTT TTTCTGAATA AATTCCATAT TTTACCTAAA AAAAAAAAAA	960
	AAAAACTCGA GGGGGGGCCC GTACCCAATT T	991

30

(2) INFORMATION FOR SEQ ID NO: 176:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1290 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

35

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 176:

40

	ACAGCCCTCT TCGGAGCTG AGCCCGGCTC TCCTCACTCA CCTCAACCCC CAGGCGGCC	60
	CTCCACAGG CCCCTCTCCT GCTGGACGG CTCTGCTGGT CTCCCCGTCC CCTGGAGAAG	120
45	AACAAGGCCA TGGGTGGCC CCTGCTGCTG CCCCTRCTGC YCCTGCTGCW GCCGCCAGCA	180
	TTTCTGCAGC CTRGTGGCTC CACAGGATCT GGTCCAAGCT ACCTTTATGG GGTCACTCAA	240
50	CCAAAACACC TCTCAGCTC CATGGGTGGC TCTGTGAAA TCCCTTCTC CTTCTATTAC	300
	CCCTGGGAGT TAGCCAYAGY TCCCRACGTG AGAATATCCT GGAGACGGGG CCACTTCCAC	360
	GGGCACTCCT TCTACAGCAC AAGGCCGCTT TCATTTCACA AGGATTATGT GAACCGGCTC	420
55	TTTCTGAACT GGACAGAGG TCAGGAGAGC GGCTTCCTCA GGATCTCAAA CCTGCGGAAG	480
	GAGGACCACT CTGTGTATTT CTGCCGAGTC GAGCTGGACA CCCGGAGATC AGGGAGGCAG	540
60	CAGTTGCAGT CCATCAAGGG GACCAAACTC ACCATCACCC AGGCTGTAC AACCACCACC	600

ACCTGGAGGC CCAGCAGCAC AACCACCATA GCCGGCCTCA GGGTCACAGA AAGCAAAGGG 660
 CACTCAGAAT CATGGCACCT AAGTCTGGAC ACTGCCATCA GGGTTGCATT GGCTGTGCGT 720
 5 GTGCTCAAAA CTGTCATTTT GGGACTGCTG TGCCTCCTCC TCTGTGGTGG AGGAGAAGGA 780
 AAGGTAGCAG GCGCCAAGC AGTGACTTCT GACCAACAGA GTGTGGGGAG AAGGGATGTG 840
 10 TATTAGCCCC GGAGGACGTG ATGTGAGACC CGCTGTGTAG TCCTCCACAC TCGTTCCTCA 900
 TTGGCAAGAT ACATGGAGAG CACCCTGAGG ACCTTTAAAA GGCAAAGCCG CAAGGCAGAA 960
 GGAGGCTGGG TCCCTGAATC ACCGACTGGA GGAGAGTTAC CTACAAGAGC CTTTCATCCAG 1020
 15 GAGCATCCAC ACTGCAATGA TATAGGAATG AGGTCTGAAC TCCACTGAAT TAAACCACTG 1080
 GCATTTGGGG GCTGTITYATT ATAGCAGTGC AAAGAGTTCC TTTATCCTCC CCAAGGATGG 1140
 AAAATACAAT TTATTTTGCT TACCATACAC CCCTTTTCTC CTCGTCCACA TTTTCCAATC 1200
 20 TGTATGGTGG CTGCTCTCTA TGGCAGAAGG TTTTGGGGAA TAAATAGCGT GANATGNTNC 1260
 TGACTNAAAA AAAAAAAAAA AAAAATCGA 1290

25

(2) INFORMATION FOR SEQ ID NO: 177:

30

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2290 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 177:

TGGGGCCCCCT TTTGGATGCT CTGGGTGTTT TTGCCAAGAG TTACAGGATG TCAAGTGTGG 60
 40 GGAGCTCAGC ACCCTTGCTG TGGACCAGTG AAGGCTGTTC CAGACCAGGT GCTTCCAGAC 120
 ATTTCCAGGC TCCAGGAGAG AGGCTGGGAG CCCCCACAGA AAGCACAGGA AAATGCAAAA 180
 45 AAAAAACAGT CTTTTTTTTT TTTTGTCTTT TTATTATGAA AACAAAACAA ATGCCCCAGG 240
 AGAAGGGTCC ATGATTACCA GAAACATCAA AGAGTACTTT CTACCATTTT TATCTGTGTG 300
 TGTGTAGGCC AGCATTGCAA TAAACAAGCT AACTACTTTC CATTGGACTC ATTTTCAGTA 360
 50 ACTGACATTT ACAGGAATAT ACTAGAAACG GCACTAAAAA GTTTAAGAAA AGTTACGGTA 420
 AACTTGCATG CACATCATAC AGAAAAGTAA CATTTTAAAT ATAAAAAGA AAAACTTCCT 480
 GGAAGCATTA TGCCAGTATT AAGGAACAGT GCTACTCTGG ATGTGACAAA TTCTGTATGT 540
 55 GGGTGTTACT CTTTCCCAA AGACTGTCTAG AGGCGTGAGT GCTGCAAAAG AACAAACA 600
 AAAACAAACA CACAAAAAAA TGTGTCTTAC AGTTTGTAAAG CAAGATGACA CTGCCCCAACA 660
 60 CAAAGAGGGG TCTGGAGTTC AGTTCACGCC CGAAGCCTGC CCCCTCGGCC TCCAGGGGTC 720

	ATTCAGAGTG TTCTCAAATC CAATTCCGAC ACACGACTTG TCACTACTCC TCTCCCCTTG	780
5	AAAAAAGCAT GTTAGAAGCT GCCCTACAGG TCTCAGCAGT GGGACAATCT AATTGAATCA	840
	CCGCAGCCTT CTAATACAGA AGAAACGGAC GTGACTGTCA CCTCAGCCC GCCAGCAAGG	900
	GCGCTGAGGA AGTCATTAAT CCTTCGAAAC TCTGAAAAGA AACCAGTGTT GAAGTCTGGA	960
10	CAGAAAGCCT TAAAAAAGTG ACAGCACCAA TGCAGCTGCT CAGTGTACCC NCCGTGGGCT	1020
	GTCAGGGTCA GTGCTTCTT TCTAGATGAA AGGAGCAGAG GCGAGCCGAC GCCACCGTCA	1080
15	CAGAGAACCA GCCGAGAAGG AAAGGCCCCA CGATGCTCCC TGTGCGCTGC CCCACAGCC	1140
	GGCCGCTCCC CCGACGGCTC ACACAGGCAG CACCTCACTG CCCTGTGGCT GGAGGGGCAT	1200
	TGCAAGGAGC GCGCCCGACG CCCAGGCACC CCCGGCTTAG GGTGTACGTA TCACCCAGCC	1260
20	CTGTGCTGGC AGCAGGTTAC CAACCAGCCT GCGTGAAGAC CTGTCAACTG TCGTGTGTGA	1320
	ATTCCTTAAA TTCGGTTTAA ATAGTCCATT AAAGATCTGT TTAGAAAATA CCTTTGAAAA	1380
25	CGAGGGTAAC TTTAAAAAAT GGAACTTTC AAATCCATTT ATATTTTAT TATAAACAAA	1440
	ACTTAATTAA AAGTTTAACA AACTGGCTGA AACTCACCA AGTGTACAGC TCACCAGCAA	1500
	TTTAAAAAAT GATAATTTAC CAGCATCTCC TCATCAGAGT TCCCTCTCCA GTAAGGGTAT	1560
30	ACCTACATCT GTAAGGGTCA GTGGA CTCTG AATCAATTTT ATGTTTGT TTAAATCACC	1620
	GTGTATTAGG ATACTAATGA TAGTCCCTAT ATCCATCCAG AAATGCTGGC AGAAAGCACT	1680
35	GGCCACCATA CAGGACAGAC CACACCACAG CTCCATACCC AGCGTCTGCC TGGAGGCTCC	1740
	CCCACGCTGA GGTCCGGGAG AATGCCTGGT TTCAGTCATT TCCGGACTAA CTGTGACAAC	1800
	GCGTGAGCAG GGAGCACCGT GCGAGTCTCC GGGAGGGAAT CCTCTGGGG CCCAGAGACT	1860
40	CCTCCACCCC TGGGGAGGCG AGACAGGCTC GGGARGGCCT GGCCAGGCCA CTGGAGGCTG	1920
	GCAGGGAGCA GGCATGTCCA CCCGCAAGCC TGGGAGGCTA ACTCTGGCAT TCCTGGCCGG	1980
45	AGCCGCCATG CTCATTGGTG GGCCAGTTTG GGACATCCCC GTACTCAAAG ACCATATGGC	2040
	AGCCTCTGGG AAAACAAAAC CAAAACATCA CCTCTATTA AACTCTGTAT ATTATTATTT	2100
	TTTACAATAG AAAGTTAAAA ATCAAGACTT AGATTTACTA TACATTTTTT CTCTCAGATT	2160
50	ACAAAGTTTA TATTATATAA CTGGGGTCC CTAAATTGAT TTCTTTTAAA ACAGTCTTAA	2220
	AGAGACCAGA AGTGAATACA AAAGAACTAA ACAAATAAAA AAATTAGAAT GTGCTGTAGC	2280
55	TGAAAGCTGT	2290

(2) INFORMATION FOR SEQ ID NO: 178:

60

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 549 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 178:

GGCACGAGCC ATGCCTGGCC TCTCCTTGAT TCTTACAGTC ACTTGTGTGG CTGTTTCTGA 60
 CTCAGCAGCT ACCTGCATTG TGGCCAAAGG ATGACCTATT CCTTCTCAGG AGGGCAAAAA 120
 TGTGGAATAG TGTCTGTCCA TGCCCTCTCT CATGGGCTAC CACCTCTGCC ACCGTGGTTA 180
 ATCAGTAACA ACCAGGAGAG AAGCTGCTGG AACTGACCTC TGGGAACTCC CTGGGATGGT 240
 TTGGTGCAGG AATGTAGTAG GCATACACGT GGTGCGTGG ATCTGGGCCC TCCTGATGTG 300
 AGTAGAGAGG TAAAAGGCCA CCATCTCCTT GACCTCTGGG GAACTCATCC ACAAAGAAGA 360
 TGTTTCCAAG ATGCTTCTGA AGATTGCCTA AAAATAGCCG GTTCCACCC CCGTGAATGC 420
 ATCCATTCTA GAATGCTCCT TCACCAGGAC CAGAGAACTG ATTTACAGAA GTGACATGAA 480
 AACATTCCAT CCCAGAATTT GCAGTAGCTC AAATTAAGTT TCTAGCTATT AAAAAGAAAA 540
 AAAAAAAAAA 549

(2) INFORMATION FOR SEQ ID NO: 179:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1509 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 179:

GGCACGAGGG CTCATTTCATT CCGCGCCGGG CCTGCCAGAC ACCTGCGCCC TTCTGCAGCC 60
 GCGCGCCGCA TCCGCGCCGG CAGCCCCCAG CATGTCGGGC CCAGACGTCG AGACGCCGTC 120
 CGCCATCCAG ATCTGCCGGA TCATGCGGCC AGATGATGCC AACGTGGCCG GCAATGTCCA 180
 CGGGGGGACC ATCTGAAGA TGATCGAGGA GGCAGGCGCC ATCATCAGCA CCCGGCATTG 240
 CAACAGCCAG AACGGGGAGC GCTGTGTGGC CGCCCTGGCT CGTGTGAGC GCACCGACTT 300
 CCTGTCTCCC ATGTGCATCG GTGAGGTGGC GCATGTCAGC GCGGAGATCA CCTACACCTC 360
 CAAGCACTCT GTGGAGGTGC AGGTCAACGT GATGTCCGAA AACATCCTCA CAGGTGCCAA 420
 AAAGCTGACC AATAAGGCCA CCCTGTGGTA TGTGCCCTG TCGCTGAAGA ATGTGGACAA 480
 GGTCTCGAG GTGCCTCTG TTGTGTATT CCGGCANGAG CAGGAGGAGG AGGGCCGGAA 540
 GCGGTATGAA GCCCAGAAGC TGGAGCGCAT GGAGACCAAG TGGAGGAACG GGGACATCGT 600

CCAGCCAGTC CTCAACCCAG AGCCGAACAC TGTCAGCTAC AGCCAGTCCA GCTTGATCCA 660
 CCTGGTGGGG CCTTCAGACT GCACCTTGCA CGGCTTTGTG CACGGAGGTG TGACCATGAA 720
 5 GCTCATGGAT GAGGTCGCCG GGATCGTGGC TGCACGCCAC TGCAAGACCA ACATCGTCAC 780
 AGCTTCCGTG GACGCCATTA ATTTTCATGA CAAGATCAGA AAAGGCTGCG TCATCACCAT 840
 10 CTCGGGACGC ATGACCTTCA CGAGCAATAA GTCCATGGAG ATCGAGGTGT TGGTGGACGC 900
 CGACCTGTGT GTGGACAGCT CTCAGAAGCG CTACCGGGCC GCCAGTGCCT TCTTCACCTA 960
 CGTGTGCTG AGCCAGGAAG GCAGGTGCTT GCCTGTGCCC CAGCTGGTGC CCGAGACCGA 1020
 15 GGACGAGAAG AAGCGCTTTG AGGAAGGCAA AGGGCGGTAC CTGCAGATGA AGGCGAAGCR 1080
 ACAGGGCCAC GCGGASCTC AGCCCTAGAC TCCCTCCTCC TGCCACTGGT GCCTCGAGTA 1140
 20 GCCATGGCAA CGGGCCAGT GTCCAGTCAC TTAGAAGTTC CCCCCTTGGC CAAAAACCCA 1200
 ATTCACATTG AGAGCTGGTG TTGTCTGAAG TTTTCGTATC ACAGTGTTAA CCTGTACTCT 1260
 CTCCTGCAAA CCTACACACC AAAGCTTTAT TTATATCATT CCAGTATCAA TGCTACACAG 1320
 25 TGTGTGCCG AGCGCCGGA GCGCTTGGC AGAAACCTC GGAATGCTT CCGAGCACGC 1380
 TGTAGGTAT GGAAGAACC CAGCACCCT AATAAGCTG CTGCTTGGCT GGAAAAAAAA 1440
 30 AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA 1500
 AGAAAAAN 1509

35

(2) INFORMATION FOR SEQ ID NO: 180:

(i) SEQUENCE CHARACTERISTICS:
 40 (A) LENGTH: 1316 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 180:

AGCTGTATCA TAGGAAAGAT GGCCACACCG GCGGTACCAG TAAGTGCTCC TCCGGCCACG 60
 CCAACCCAG TCCCGCGGC GGGCCAGCC TCAGTTCCAG CGCCAACGCC AGCACCGGCT 120
 50 GCGGCTCCGG TTCCCGCTGC GGCTCCAGCC TGCATCCTCA GACCTTGGG CAGCAGCGGC 180
 TGCAACTGCG GCTCCTGGCC AGACCCCGGC CTCAGCGCAA NTCCAGCGCA GACCCAGCG 240
 55 CCCGCTCTGC CTGGTCTGTC TCTTCCAGG CCTTCCCCG GCGGCCGCT GGTGAGGCTG 300
 CACCCAGTCA TTTTGGCCTC CATTTGTGGAC AGCTACGAGA GACGCAACGA GGGTGCTGCC 360
 CGAGTTATCG GGACCTGTTT GGGAAGTGTG GACAAACACT CAGTGGAGGT CACCAATTGC 420
 60

	TTTTCACTGC CGCACAATGA GTCAGAAGAT GAAGTGGCTG TTGACATGGA ATTTGCTAAG	480
	AATATGTATG AACTGCATAA AAAAGTTTCT CCAAATGAGC TCATCCTGGG CTGGTACGCT	540
5	ACGGGCCATG ACATCACAGA GCACTCTGTG CTGNATCCAT GAGTACTACA GCCGAGAGGC	600
	CCCCAACCCC ATCCACCTCA CTGTGGACAC AAGTCTCCAG AACGGCCGCA TGAGCATCAA	660
10	AGCCTACGTC AGCACTTTAA TGGGAGTCCC TGGGAGGACC ATGGGAGTGA TGTTCACGCC	720
	TCTGACAGTG AAATACGCGT ACTACGACAC TGAACGCATC GGAGTTGACC TGATCATGAA	780
	GACCTGCTTT AGCCCCAACA GAGTGATTGG ACTCTCAAGT GACTTGACGC AAGTAGGAGG	840
15	GGCATCAGCT CGCATCCAGG ATGCCCTGAG TACAGTGTG CAATATGCAG AGGATGTACT	900
	GTCTGGAAAG GTGTACAGTG ACAATACTGT GGGCCGCTTC CTGATGAGCC TGGTTAACCA	960
20	AGTACCGAAA ATAGTTCCCG ATGACTTTGA GACCATGCTC AACAGCAACA TCAATGACCT	1020
	TTTGATGGTG ACCTACCTGG CCAACCTCAC ACAGTCACAG ATTGCACTCA ATGAAAAACT	1080
	TGTAAACCTG TGAATGGACC CCAAGCAGTA CACTTGCTGG TCTAGGTATT AACCCCAGGA	1140
25	CTCAGAAGTG AAGGAGAAAT GGGTTTTTTG TGGTCTTGAG TCACACTGAG ATAGTCAGTT	1200
	GTGTGTGACT CTAATAAACG GAGCCTACCT TTTGTAAATT AAAAAAAAAA AAAAAAACCN	1260
30	SGRGGGGGGG CCCGGTCCCA TTSSCCCTTT NGTAATTCGT NITACAATCC CCNNGC	1316

35 (2) INFORMATION FOR SEQ ID NO: 181:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 777 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - 40 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 181:

45	GGCATGWKCA GACATGACTT CTATTGCCAG GCTGGTCAAG TGGCAGGGTC ATGAGGGAGA	60
	CATCGATAAG GGTGCTCCTT ATGCTCCCTG CTCTGGAATC CACCAGCGGG CTATCTGCGT	120
	TTATGGGGCT GGGGACTAGA ATTGGATGCT TCAAAACCAT CACCTGTTGG CCAACAAGTT	180
50	TGACCCAAAG GTAGATGATA ATGCTCTTCA GTGCTTAGAA GAATACCTAC GTTATAAGGG	240
	CCATTCTATT GGGACCTGAA CTTTGAAGAC CACAMTATTG AAGAGGCGTT GCTTACCYGT	300
55	TGGGGGCCAA GAGGCATGTT ACCAAACATG GYYCARGAAM YTTGGYKGGG AMCARKKKKK	360
	GKKGGGARRM CMRGGGYTTG SCAAWTCSK KGGCMWCCYT TTAGGGTAAR RRGGGCKGTW	420
	ATTAGATTGT GGGTAAAGTA GGATCTTTTG CCCTTGCAAA TTTGCTGCCT GGGTGAATGY	480
60	TGCTTGTTCC TTCTCMACCC CTAACCCTAG TAGTTCCTCC ACTAACTTTC TCACTAAGTG	540

AGAATGAGAA CTGCTGTGAT AGGGAGAGTG AAGGAGGGAT ATGTGGTAGA GCACTTGATT 600
TCAGTTGAAT GCCTGCTGGT AGCTTTTCCA TTCTGTGGAG CTGCCGTTCC TAATAATTCC 660
5 AGGTTTGGTA GCGTGGAGGA GAACTTTGAT GGAAAGAGAA CCTTCCTTC TGTACTGTTA 720
ACTTAAAAAT AAATAGCTCC TGATTCAAAG TAAAAA AAAA AAAA AAAA 777

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(2) INFORMATION FOR SEQ ID NO: 182:

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- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 791 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 182:

GGCACAGATA ACTATGTACA TGTATTCCTT AAATGTTTTT TTAAGTTTTA TATTCTTGGC 60
25 ACTGGTCTTC AAATGTGTAC ATGTGTGCCA GGGAGCAAAT GCCTTCTTGT TTCTGAAATT 120
GGTCTTTTAG ACTGTTCTTT TTTCCCATCT TCTCACCTCC TGCCCTCCT TCAGGGTACT 180
TCCGTGGCCA GAACCCCTCC AGGTCAGAGG CAGAAGAGAA GCCTCATGGG TCACAGCAGC 240
30 AGATGTGGGC TGGAGATCTA TTCATTTGGT TTTGGCTTGA ATTTTCTGRA TGGTTTACTT 300
GATCYTGGGA AAGANATATC TTGCCAGGAA AAATGATAGN CCTTGACAAT GTTGAATGAT 360
35 CCTGCACCAC CTTGAAAGAC ATTTCTAATA TGGTTTGTC GGCAAAGTGG TTAGTAGTCA 420
TTTGTGGCCT GAGGTAGAAG TCCTCAGAAA TCAGCAGACT TCACTGATAA AATGCTGACT 480
TGCCCTGGA CTGGGCTCTG TGAGAGTGGC CTTCGCACT GTGCACAGTA GGTGTGAACA 540
40 CACCACACCT ACAGGGACCA CGTGGTGGGC TGTGGACTAG CGGCCAAGCT CCCTGCAGGC 600
CCACTAATAG AATTCAGCTT TTAGCATGGG CTGTTTCATA CTGTTCTGAT GAAACTGATT 660
45 TGGTTTCTTT CCTCCATACC CCTTCGCACT TTCAGTGTTC TTGTTTAGTT TTCTGGTTT 720
TTAATTATAA CTACAAAATA AAATCTTTAG GCTATTACCC TTAGCTTAGT AAAAAAAAAA 780
AAAAAAAAACT C 791

50

(2) INFORMATION FOR SEQ ID NO: 183:

55

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1405 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

60

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 183:

5	AAATTGATTA ACAGCTTGAA AGAAGGCTCT GGTMTTGAAG GCCTAGATAG CAGCACTGCC	60
	AGTAGCATGG AGCTGGAAGA ACTTCGGCAT GAGAAAGAGA TGCAGAGGGA GGAAATACAG	120
	AAGCTGATGG GCCAGATACA TCAGCTCAGA TCCGAATTAC AGGATATGGA GGCACAGCAA	180
10	GTTAATGAAG CAGAAATCAGC AAGAGAACAG TTACAGGWTG TGCATGACCA AATAGCTGGG	240
	CAGAAAGCAT CCAAACAAGA ACTAGAGACA GAACTGGAGC GACTGAAGCA GGAGTTCCAC	300
15	TATATAGAAG AAGATCTTTA TCGAACAAAG AACACATTGC AAAGCAGAAT TAAAGATCGA	360
	GACGAAGAAA TTCAAAACT CAGGAATCAG CTTACCAATA AAACTTTAAG CAATAGCAGT	420
	CAGTCTGAGT TAGAAAATCG ACTCCATCAG CTAACAGAGA CTCTCATCCA GAAACAGACC	480
20	ATGCTGGAGA GTCTCAGCAC AGAAAAGAAC TCCCTGGTCT TTCAACTGGA GCGCCTCGAA	540
	CAGCAGATGA ACTCGCCTC TGGAAAGTAGT AGTAATGGGT CTTGATTAA TATGTCTGGA	600
25	ATTGACAATG GTGAAGGCAC TCGTCTGCGA AATGTTCTCTG TTCTTTTAA TGACACAGAA	660
	ACTAATCTGG CAGGAATGTA CGGAAAAGTT CGCAAAGCTG CTAGTTCAAT TGATCAGTTT	720
	AGTATTCGCC TGGGAATTTT TCTCCGAAGA TACCCCATAG CGCGAGTTT TGTAAATATA	780
30	TATATGGCTT TGCTTCACCT CTGGGTCATG ATTGTTCTGT TGACTTACAC ACCAGAAATG	840
	CACCACGACC AACCATATGG CAAATGAACC AAGCCCAGTT GTTGCACTGA TTGGTTGTCT	900
35	TTTCTAGAC TTGGGATCTG CAAGAAGGCC AATGCTCTAA AATTCTGAG AACAGTGCAC	960
	AAGATTATTT TATCACTACA AGCTTTTAAC TTTTAAAGTT ATTTGTACAAG TATTCTACCT	1020
	AAATCTTCCA ATTTCTTTA AATGGTAAGA GTTCTAAAA CAGACAATAA TTTAACAAGC	1080
40	TCAGCTCTGC TTTATCTGAG TTTAGTGGTC CTAATATATA TGTAAGAGAA GATGGTGGGG	1140
	TTGTTACCT CTGTACAGAC CATCTGTATG TTAGGTGACA TTGATTATGG GTTATAATCA	1200
45	GGGAACTAA TTGTATTTAG TGACAAAAAT AAAAAGTTTT TTTTATATAA TTCAGTCTGC	1260
	TTTTGGATTT TCATATATTT AACTTTGCAA AAAGATTAC TTTGTACATG TTACAGGCTT	1320
	GATTGGTGTA AATCTTTTAA TAAATACATA AATAAAAGNA AAATATGCAT TTTTCTTTTC	1380
50	TAAAAAATAA AAAAAAATAA CTCGA	1405

55 (2) INFORMATION FOR SEQ ID NO: 184:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1596 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double

60

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 184:

5	GTTCATGCACT GCGCCGGAGA ACTGTGCTCT TTGAGGCCGA CGCTAGGGGC CCGGAAGGGA	60
	AACTGCGAGG CGAAGGTGAC CGGGGACCGA GCATTTTCAGA TCTGCTCGGT AGACCTGGTG	120
	CACCACCACC ATGTTGGCTG CAAGGCTGGT GTGTCTCCGG ACACTACCTT CTAGGGTTT	180
10	CCACCCAGCT TTCACCAAGG CCTCCCCTGT TGTGAAGAAT TCCATCACGA AGAATCAATG	240
	GCTGTTAACA CTAGCAGGG AATATGCCAC CAAAACAAGA ATTGGGATCC GCGTGCGGAG	300
15	AACTGGCCAA GAACTCAAAG AGGCAGCATT GGAACCATCG ATGGAAAAA TATTTAAAAT	360
	TGATCAGATG GGAAGATGGT TTGTGCTGG AGGGGCTGCT GTTGGTCTTG GAGCATTTTG	420
	CTACTATGGC TTGGGACTGT CTAATGAGAT TGGAGCTATT GAAAAGGCTG TAATTTGGCC	480
20	TCAGTATGTC AAGGATAGAA TTCATTCCAC CTATATGTAC TTAGCAGGGA GTATTGGTTT	540
	AACAGCTTTG TCTGCCATAG CAATCAGCAG AACGCCTGTT CTCATGAACT TCATGATGAG	600
25	AGGCTCTTGG GTGACAATTG GTGTGACCTT TGCAGCCATG GTTGGAGCTG GAATGCTGGT	660
	ACGATCAATA CCATATGACC AGAGCCCAGG CCCAAAGCAT CTTGCTTGGT TGCTACATTC	720
	TGGTGTGATG GGTGCAGTGG TGGCTCCTCT GACAATATTA GGGGGTCCTC TTCTCATCAG	780
30	AGCTGCATGG TACACAGCTG GCATTGTGGG AGGCCTCTCC ACTGTGCCA TGTGTGCGCC	840
	CAGTGAAAAG TTTCTGAACA TGGGTGCACC CCTGGGAGTG GGCCTGGGTC TCGTCTTTGT	900
35	GTCTCTATTG GGATCTATGT TTCTTCCACC TACCACCGTG GCTGGTGCCA CTCCTTACTC	960
	AGTGGCAATG TACGGTGGAT TAGTTCCTTT CAGCATGPTC CTTCTGTATG ATACCCAGAA	1020
	AGTAATCAAG CGTGCAGAAG TATCACCAAT GTATGGAGTT CAAAAATATG ATCCCATTA	1080
40	CTCGATGCTG AGTATCTACA TGGATACATT AAATATATTT ATGCGAGTTG CAACTATGCT	1140
	GGCAACTGGA GGCAACAGAA AGAAATGAAG TGAATCAGCT TCTGGCTTCT CTGCTACATC	1200
45	AAATATCTTG TTTAATGGGG CAGATATGCA TTAAATAGTT TGTACAAGCA GCTTTCTGTTG	1260
	AAGTTTAGAA GATAAGAAAC ATGTCATCAT ATTTAAATGT TCCGGTAATG TGATGCCTCA	1320
	GGTCTGCCCT TTTTCTGGA GAATAAATGC AGTAATCCTC TCCCAAATAA GCACACACAT	1380
50	TTTCAATTCT CATGTTTGAG TGATTTTAAA ATGTTTGGT GAATGTGAAA ACTAAAGTTT	1440
	GTGTCATGAG AATGTAAGTC TTTTCTTAC TTTAAATTT AGTAGTTCA CTGAGTAACT	1500
55	AAAATTTAGC AAACCTGTGT TTGCATATTT TTTKGGAGTG CAGMMTAWTG TAATTARAGC	1560
	ATTCCAGTAA NAGTGTNTTT AAAGTTGNTC TATATN	1596

(2) INFORMATION FOR SEQ ID NO: 185:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2293 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 185:

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5      GCGCAGAGCC CGYACGAGCA GGACGACGAC GACAAGGGCG ACTCCAAGGA AACGCGGCTG      60
      ACCCTGATGG AGGAAGTGCT CCTGCTGGGC CTCAAGGACC GCGARGGTTA CACATCATTT      120
15     TGGAAATGACT GTATATCATC TGGATTACGT GGCTGTATGT TAATTGAATT AGCAATTGAGA      180
      GGAAGGTTAC AACTAGAGGC TTGTGGAATG AGACGTAAAA GTCTATTAAC AAGAAAGGTA      240
20     ATCTGTAAGT CAGATGCTCC AACAGGGGAT GTTCTTCTTG ATGAAGCTCT GAAGCATGTT      300
      AAGGAACTC AGCCTCCAGA AACGGTCCAG AACTGGATTG AATTACTTAG TGGTGAGACA      360
25     TGGAAATCCAT TAAAAATGCA TTATCAGTTA AGAAATGTAC GGAACGATT AGCTAAAAAC      420
      CTGGTGGAAA AGGGTGTATT GACAACAGAG AAACAGAACT TCCTACTTTT TGACATGACA      480
      ACACATCCCC TCACCAATAA CAACATTAAG CAGCGCCTCA TCAAGAAAGT ACAGGAAGCC      540
30     GTTCTTGACA AATGGGTGAA TGACCTTCAC CGCATGGACA GCGCCTTGCT GGCCCTCATT      600
      TACCTGGCTC ATGCCCTCGA CGTCTGGAG AATGCTTTTG CTCCTCTTCT GGACGAGCAG      660
35     TATGATTTGG CTACCAAGAG AGTGCGGCAG CTTCTGACT TAGACCCTGA AGTGGAATGT      720
      CTGAAGGCCA ACACCAATGA GGTCTGTGG GCGGTGGTG GCGCGTTCAC CAAGTAACTC      780
      TGCTCGGGGT GAACCATTTCT CCTTCTCTC AAGTAAACCA GTAGTTTTC TTCTGTTGAC      840
40     TTCTGGTTT CTGTAATTTG TACTTTCCCA CACTATAATT GGCTTCTGTT TTACAAAATG      900
      GTGGGTGGCT TTTTCTTTT TGTACGTGTA CAGGATTCTG CTGGTACGAG AGGCCTTCCT      960
45     CTTTCTGTTT TAAAAAAG TTTTACTGCC ATATTGGCAT TCCATTCCCT GTTGCCATCC      1020
      TCACGTGTAC CTGTTTGGG TTTCTGGTCT ACTTTGACTT TCAAAGTACC TCCAGCCTCC      1080
      TCATACGCAC AGCTTTTGGA TGACCTCAGC TTGAGTTTCT CCATATGTGC ATGTACATCT      1140
50     AGCATTTCTG CTACAGTTCA GACAGAAGTC AAAAAAGGC CTTCAACTCA CCAAAGGTAA      1200
      ATATCTGTAT CTATTAGGAC ATTTTTTACA TAGACTTCAG TTGAGATGTA TACTTAGCAA      1260
55     AATTATTTT AAATTGAAAC AGCACAGTAA ATACTTAATA TAAATGTCC CTTGGATTTT      1320
      GCTTCCCATG TAAATCTATT GTATTATTAC ACTTGTATA ATTTTAACTA TAAAGGTCCA      1380
      ATTGTTTCAC AGAGCCAGTT TGGGATGGGC TGCAATCCAT TTATGCTGTA TATAGTTTGA      1440
60     ATTATATATA AATTACCCCT TCTCTGGCC ACCCCTGCTC CCATCTTAGT ATTTTGCAAG      1500

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	ATCTAATCAG TTGTACACCT GGTGCCCCCTC GCTTGCTTCA ATCATGGTTA TTTGATGGCA	1560
5	AAATCGACCT CTTGTGCTG AAGGAGAGAG AAAAGATGTG TGTCTGATTG GTCCTGGGAT	1620
	TTTTTGAGCT GTGCCATTTA TGGTACTCTT TGCCTATGCA TCCCTTTTTT AGATTTTTTT	1680
	TAAATTTTAT CTTACTGTTT TTATAATTC TATTGGAAG AGGCTTGTGA CCAGTACCAA	1740
10	TCTTGAGTTT CTTTTTCTGT CCACAAGTAA ATTAATATCT GCTCTGAAAT GTCATTTATC	1800
	TACTCACACA TTCTTGGGA AAAAAATCAA ATGTCAGTCC TAGCAGATGT TGCATGTAAA	1860
15	TTGGTAGCAA GTAATGATTA CAACCCAGAG GATTAAGAAT TTGTAAACAG AAAGCTCTAT	1920
	GTPTTAATTT TTTATATACA ATTAGGATAA TTAGCATTGT CAGACTATAA ACCTTTGCTT	1980
	TTTAAAGTTT ATTTTACTA TTTCTTTATC ACTTTATTGT ATCATCACCA TTGGTTTCAT	2040
20	AATGTAAATA CTATATGTTG AACAAATPAA ATGTCAAAT TTTTATTAC CATAGTCCAT	2100
	GTTAATAGTG GGGCTTCAG GTGTTTAGAG ATTTTTTTTG TTGTTGTTAA CATTCATTGC	2160
25	AAAAGTACTA GATGGTGTAT AACTCTAGAG TTGAATTTTA AGGGATTCCC TAATATGTAT	2220
	ACTATCTTTT TATCTGAAGT AATAAATAA CAATGATCTT GAAAGTGCCY RAAAMAAAAA	2280
	AAAAAAAAAA AAA	2293

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(2) INFORMATION FOR SEQ ID NO: 186:

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(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1212 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 186:

	GGCACGAGGC GAGCCGGCGC ACCGTACGCT GGGACGTGTG GTTTCAGCTC GTGCGCCTCC	60
45	CCGTGGGTTT GCGACGTTTA GCGACTATTG CGCCTGCGCC ACGCCGGCTG CGAGACTGGG	120
	GCCGTGGCTG CTGGTCCCGG GTGATGCTAG GCGCTCCCT GGGCTCCAGG CTGTTGCGGG	180
50	GTGTAGGTGG GAGTCACGGA CGGTCGGGG CCCGAGGTGT CCGCGAAGGT GGCACACATG	240
	GGCGGCAGGG GAGAGCATGG CTCAGCGGAT GGTCTGGGTG GACCTGGAGA TGACAGGATT	300
	GGACATTGAG AAGGACCAGA TTATTGAGAT GGCCTGTCTG ATAAGTACT CTGATCTCAA	360
55	CATTTTGGCT GAAGTCCCTA ACCTGATTAT AAAACAACCA GATGAGTTGC TGGACAGCAT	420
	GTCAGATTGG TGTAAAGAGC ATCAGGGGAA GTCTGGCCTT ACCAAGGCAG TGAAGGAGAG	480
60	TACAATTACA TTGCAGCAGG CAGAGTATGA ATTTCTGTCC TTTGTACGAC AGCAGACTCC	540

	TCCAGGGCTC TGTCCACTTG CAGGAAATTC AGTTCATGAA GATAAGAAGT TTCTTGACAA	600
	ATACATGCCC CAGTTCATGA AACATCTTCA TTATAGAATA ATTGATGTGA GCACTGTTAA	660
5	AGAACTGTGC AGACGCTGGT ATCCAGAAGA ATATGAATTT GCACCAAAGA AGGCTGCTTC	720
	TCATAGGGCA CTTGATGACA TTAGTGAAAG CATCAAAGAG CTTCAGTTTT ACCGAAATAA	780
10	CATCTTCAAG AAAAAAATAG ATGAAAAGAA GAGGAAAATT ATAGAAAATG GGGAAAATGA	840
	GAAGACCGTG AGTTGATGCC AGTTATCATG CTGCCACTAC ATCGTTATCT GGAGGCAACT	900
	TCTGGTGGTT TTTTTCCTC ACGCTGATGG CTTGGCAGAG CACCTTCGGT TAACTTGCAT	960
15	CTCCAGATTG ATTACTCAAG CAGACAGCAC ACGAAATACT ATTTTCTCC TAATATGCTG	1020
	TTTCCATTAT GACACAGCAG CTCTTTGTA AGTACCAGGT CATGTCCATC CCTTGGTACA	1080
20	TATATGCATT TGCTTTTAAA CCATTCTTT TGTTTAAATA AATAAATAAG TAAATAAAGC	1140
	TAGTTCTATT GAAATGCAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA	1200
	AAAAAAAAAA AN	1212
25		

(2) INFORMATION FOR SEQ ID NO: 187:

30	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 1605 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
35	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 187:	
	GCTTCCGAA GTTGCTTTTG TCCAAACATC CGGGCTTCTC CTTTTTGTGT TCCGGCCGAT	60
40	CCCACCTCTC CTCGACCTTG GACGTCTACC TTCCGGAGGC CCACATCTTG CCCACTCCGC	120
	GCGCGGGGCT AGCGCGGGTT TCAGCGACGG GAGCCCTCAA GGGACATGGC AACTACAGCG	180
45	GCGCCGGCGG GCGGCGCCCG AAATGGAGCT GGCCCGGAAT GGGGAGGGTT CGAAGAAAAC	240
	ATCCAGGGCG GAGGCTCAGC TGTGATTGAC ATGGAGAACA TGGATGATAC CTCAGGCTCT	300
	AGCTTCGAGG ATATGGGTGA GCTGCATCAG CGCTGCGCG AGGAAGAAGT AGACGCTGAT	360
50	GCAGCTGATG CAGCTGCTGC TGAAGAGGAG GATGGAGAGT TCCTGGGCAT GAAGGGCTTT	420
	AAGGGACAGC TGAGCCGGCA GGTGGCAGAT CAGATGTGGC AGGCTGGGAA AAGACAAGCC	480
55	TCCAGGGCCT TCAGCTTGTA CGCCAACATC GACATCCTCA GACCTACTT TGATGTGGAG	540
	CCTGCTCAGG TGCGAACAGG GCTCCTGGAG TCCATGATCC CTATCAAGAT GGTCAACTTC	600
	CCCCAGAAAA TTGCAGGTGA ACTCTATGGA CCTCTCATGC TGGTCTTCAC TCTGGTTGCT	660
60	ATCCTACTCC ATGGGATGAA GACGTCTGAC ACTATTATCC GGGAGGGCAC CCTGATGGGC	720

	ACAGCCATTG GCACCTGCTT CGGCTACTGG CTGGGAGTCT CATCCTTCAT TTACTTCCTT	780
5	GCCTACCTGT GCAACGCCCA GATCACCATG CTGCAGATGT TGGCACTGCT GGGCTATGGC	840
	CTCTTTGGGC ATTGCATTGT CCTGTTTCATC ACCTATAATA TCCACCTCCA CGCCCTCTTC	900
	TACCTCTTCT GGCTGTTGGT GGGTGGACTG TCCACACTGC GCATGGTAGC AGTGTGGTG	960
10	TCTCGGACCG TGGGCCCCAC ACAGCGGCTG CTCCTCTGTG GCACCTGGC TGCCCTACAC	1020
	ATGCTCTTCC TGCTCTATCT GCATTTTGCC TACCACAAAG TGGTAGAGG GATCCTGGAC	1080
15	ACACTGGAGG GCCCAACAT CCGGCCATC CAGAGGGTCC CCAGAGACAT CCCTGCCATG	1140
	CTCCCTGCTG CTCGGCTTCC CACCACCGTC CTCAACGCCA CAGCCAAAGC TGTTCGGTG	1200
	ACCCTGCAGT CACACTGACC CCACCTGAAA TTCTTGCCA GTCTCTTTC CCGCAGCTGC	1260
20	AGAGAGGAGG AAGACTATTA AAGGACAGTC CTGATGACAT GTTTCGTAGA TGGGGTTTGC	1320
	AGCTGCCACT GAGCTGTAGC TCGTAAGTA CCTCCTTGAT GCMTGTGGC ACTTCTGAAA	1380
25	GGCACAAGGC CAAGAACTCC TGGCCAGGAC TGCAAGGCTC TGCAGCCAAT GCAGAAAATG	1440
	GGTCAGCTCC TTTGAGAACC CCTCCCACC TACCCCTTCC TTCTCTTTA TCTCTCCAC	1500
	ATGTCTTGC TAAATATAGA CTGGTAATT AAAATGTGA TTGAAGTCTG GAAAAAAAAA	1560
30	AAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAC TCGAG	1605

35 (2) INFORMATION FOR SEQ ID NO: 188:

(i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 1516 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 188:

45	ATTCGGCATG AGGGGGTCAC GTGGTGGCTG GGCGGGGAA ATGGCGGCTT CAGGAGAGAG	60
	CGGGACTTCA GCGGCGGAG GCAGCACC GAAGCATTT ATGACCTTCT ACAGTGAGGT	120
50	GAAACAAATA GAGAAGAGAG ACTCGTTTCT AACTTCGAAA AATCAGATTG AAAGACTGAC	180
	CCGTCTGGT TCCTCTTACT TCAATTGAA CCCATTTGAG GTTCTTCAGA TAGATCCTGA	240
	AGTTACAGAT GAAGAAATAA AAAAGAGTT TCGGCAGTTA TCCATCTTGG TGCATCCTGA	300
55	CAAAAATCAA GATGATGCTG ACAGGCACA AAAGGCTTTT GAAGCTGTGG ACAAGCTTA	360
	CAAGTTGCTA CTGGATCAGG AGCAAAAGAA GAGGGCCCTG GATGTAATTC AGGCAGGAAA	420
60	AGAATACGTG GAACACACTG TGAAAGAGCG AAAAAACAA TTAAAGAAGG AAGGAAAACC	480

	TACAATTGTA GAGGAGGATG ATCCTGAGCT GTTCAAACAA GCTGTATATA AACAGACAAT	540
	GAAACTCTTT GCAGAGCTGG AAATTAAAAG GAAAGAGAGA GAAGCCAAAG AGATGCATGA	600
5	AAGGAAACGA CAAAGGGAAG AAGAGATTGA AGCTCAAGAA AAAGCCAAAC GGGAAAGAGA	660
	GTGGCAGAAA AACTTTGAGG AAAGTCGAGA TGGTCGTGTG GACAGCTGGC GAAACTTCCA	720
	AGCCAATACG AAGGGGAAGA AAGAGAAGAA AAATCGGACC TTCTTGAGAC CACCGAAAGT	780
10	AAAAATGGAG CAACGTGAGT GACCGCCCAA GGTCACAGGC ACAGAACCTT TCCCCTGCTA	840
	TCTCCCTTCC TGCTTCGAAG GACTCATTCT TTCTCCAC TTCCACCCCA ACATAGAGTA	900
15	GTATTTGCTT TTTAGTCCAT TTGTPTTCA ATACGATTTA ATATCGATCA GAGTAATTCT	960
	TTGTACATT GAAATGAGGG GCTTGGTTTA AAAAAAGACC TTCCCTCTC CCGCCCTA	1020
	GAACAACCAG TATTAGAAGG TGCCACCAIT GGTCGTGCCT TCTCTTCCA CAGCCTGTAA	1080
20	CTCAGTGTTT TGTAATTAC TGAATGTGA TGGTTAGAAA CTTCGTGGAT AGTTTGTGGA	1140
	AATCATCCAA TTAAACATAC TGCTTAAAC AGTGTGCTG TGAATTCAGA GACAAGCCTG	1200
25	GAAGGGGCAC CTTAGGAAGC CCCTTCGCTT CAGTTGCTCG CTTCGTGGTG TGCTCCCTTC	1260
	GAAGGGCCAG ATAAGACAGG GAACACTTGT GAGCACACAG AGCAGCATCT GATGCCCTGT	1320
	GGTGTPTGGC ATGTGCCCC TGTCTACTGA CCAATCAGTG TGGCATGAGG CCCACGCCAC	1380
30	CCAAACCTTT CACTTTCCAA AGAGCTAGCC GTCTCCACC CAGTACCATG TCCTAGCCTG	1440
	TCTGCATTTG TTAGTGGTAA TATTCTTTAT GTATAATAAA TTTTATATACC CAAAAAAAAA	1500
35	AAAAAAAAAA ACTCGA	1516

40 (2) INFORMATION FOR SEQ ID NO: 189:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 681 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 189:

50	GCTCCCATGT TGCTGGCTGT CCGTACATCA CCCTGTCCCC TGCAGGAGGG GGCTACAGGC	60
	CATCTCCCTC CTGTAGGCCT CTGACTCCCC TCCACTTTTG GGCCCTCAGC TTATCTCGGG	120
	CAGGGGACCA TTGCAGCATC CTCCCTCCT CNGACTCAA GGTGCTGAGG TATAAGCCCT	180
55	GGGCCCCAGA TCCCTGRTKA CACCTTCCTG GAGAAGACTC TCAAAAGTGA CTGTATATTT	240
	GAGTTCACCA GCAATAACTC CCCACACTCG AAGCAGGTCC AAACCCMAGG ATCCCAGGGT	300
60	CCTTGGGCTC TGTTGGCACTG TCTTCCCAAG ATCCTTCCTG TTGCACAATG GGAAACCTAA	360

GAGGAAAAAG ACAGGGGCCT GCTTGCCAG CCATGCGAGG GATTCCATGC CCACCTGCCC 420
 TCTGYCTGCC TCGCTGGAAT GTGGGCCCT GCTCCCCGTC AGGTTGTGCT GTCTCTGACC 480
 5 TATGTTTACA TCCCCGAGGG GTTCTGCCT CCTCCCCACC CAGGTCAGGG TGTGGTCCAG 540
 CAGCTTGCTG TGGGGTGCTG ACATGTGTCA CCACTGCCCC CCTTGCCCC GGGGGGTCA 600
 10 TGGTCTCTC CTGGATGCTG CTCCTTGAAT YTTTTTYYT GAWAAACCYT TTAMAATTAA 660
 AAAAAAAAAA AAAAAACTCG A 681

15

(2) INFORMATION FOR SEQ ID NO: 190:

(i) SEQUENCE CHARACTERISTICS:
 20 (A) LENGTH: 1014 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 190:

GCCTCAAGCC ACGCATATGA TAATTTCTG GAACATTCAA ATTCAGTGT TCTACAGCCA 60
 GTTAGTCTAC AAACCATGTC AGCAGCACCA TCAAACCAGA GTCTGCCACT TTTGTGTCATC 120
 30 GCTGGATGAT TGCTGGGCAA AGGTGGCCTT TTAGAGCTCT TAAAAGCCCA CAAAAGGCT 180
 ATTCGTAGAG CCACAGTCAA CACATTTGGT TATATTGCAA AGGCCATTGG CCTCATGATG 240
 35 TATGGCTAC ACTTCTGAAC AACCTCAAAG TTCAAGAAAG GCAGAACAGA GTTGTACCA 300
 CTGTAGCAAT AGCTATTGTT GCAGAAACAT GTTCACCCCT TACAGTACTC CCTGCCTTAA 360
 TGAATGAATA CAGAGTTCTT GAACTGAATG TTCAAAATGG AGTGTAAAA TCGCTTTCCT 420
 40 TCTGTTTGA ATATATTGGT GAAATGGGAA AAGACTACAT TTATGCCGTA ACACCGTTAC 480
 TTGAAGATGC TTAAATGGAT AGAGACCTTG TACACAGACA GACGGCTAGT GCAGTGGTAC 540
 45 AGCACATGTC ACTTGGGGTT TATGGATTG GTTGTGAAGA TCGCTGAAT CACTTGTGA 600
 ACTATGTATG GCCCAATGTR TTTGAGACAT CTCCTCATGT AATTCAGGCA GTTATGGGAG 660
 CCTAGAGGG CCTGAGAGTT GCTATTGGAC CATGTAGAAT GTTGCAATAT TGTTTACAGG 720
 50 GTCTGTTTCA CCCAGCCCGG AAAGTCAGAG ATGTATATTG GAAAATTAC AACTCCATCT 780
 ACATGGTTC CCAGGACGCT CTCATAGCAC ATTACCCAAG AATCTACCAA CGATGATAAG 840
 55 RACACCTATA TTCGTTATGA ACTTGACTAT ATCTTATAAT TTTATGTIW ATTTKGTKT 900
 TAATGCACAS TACTTCACAC CTAAACTTG CTTTGATTG GTGATGTAA CTTTAAACA 960
 TTGCAGATCA GTGTAGGACT GGTCCATAGG GGAAGAGCTA GGAANTCCAT AGGC 1014
 60

(2) INFORMATION FOR SEQ ID NO: 191:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2779 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 191:

5	TCGCAGCAGG GTGTGTCCAG ATGGTCAGTC TCTGGTGGCT AGCCTGTCCT GACAGGGGAG	60
15	AGTTAAGCTC CCGYTCTCCA CCGTGCCGGC TGGCCAGGTG GGCTGAGGGT GACCGAGAGA	120
	CCAGAACCTG CTTGCTGGAG CTTAGTGCTC AGAGCTGGGG AGGGAGGTTT CGCCGCTCCT	180
20	CTGCTGTGAG CGCCGGCAGC CCCTCCCGGC TTCACTTCCT CCCGCAGCCC CTGCTACTGA	240
	GAAGCTCCGG GATCCAGCA GCCGCCACGC CCTGGCCTCA GCCTGCGGGG CTCCAGTCAG	300
25	GCCAACACCG ACGCGCANTG GGAGGAAGAC AGGACCCTTG ACATCTCCAT CTGCACAGAG	360
	GTCTTGCTG GACCGAGCAG CCTCCTCCTC CTAAGATGAC CTCACCTCC AGCTCTCCAG	420
	TTTTCAGGTT GGAGACATTA GATGGAGGCC AAGAAGATGG CTCTGAGGCG GACAGAGGAA	480
30	AGCTGGATTT TGGGAGCGGG CTGCCTCCCA TGGAGTCACA GTTCCAGGGC GAGGACCGGA	540
	AATTGCCCC TCAGATAAGA GTCAACCTCA ACTACCGAAA GGAACAGGT GCCAGTCAGC	600
35	CGGATCCAAA CCGATTGAC CGAGATCGGC TCTTCAATGC GGTCTCCCGG GGTGTCCCCG	660
	AGGATCTGGC TGGACTTCCA GAGTACCTGA GCAAGACCAG CAAGTACCTC ACCGACTCGG	720
	AATACACAGA GGGCTCCACA GGTAAGACGT GCCTGATGAA GGCTGTGCTG AACCTTAAGG	780
40	ACGGGGTCAA TGCTTGCAAT CTGCCACTGC TGCAGATCGA CCGGGACTCT GGCAATCCTC	840
	AGCCCCCTGGT AAATGCCCAG TGCACAGATG ACTATTACCG AGGCCACAGC GCTCTGCACA	900
45	TGCCCATTTGA GAAGAGGAGW CTGCAGTGTG TGAAGCTCCT GGTGGAGAAT GGGGCCAATG	960
	TGCATGCCCC GGTCTGCGGC GCTTCTTCCA GAAGGGCCAA GGGACTTGCT TTTATTTCGG	1020
	TGAGCTACCC CTCTYTTTGG CCGCTTGCAC CAAGCAGTGG GATGTGGTAA GCTACCTCCT	1080
50	GGAGAACCCA CACCAGCCCG CCAGCCTGCA GGCAGTGA CTCCAGGGCAA CACAGTCTTG	1140
	CATGCCCTAG TGATGATCTC GGACAATCA GCTGAGAACA TTGCACTGGT GACCAGCATG	1200
55	TATGATGGGC TCCTCCAAGC TGGGGCCCCG CTCTGCCCTA CCGTGCAGCT TGAGGACATC	1260
	CGCAACCTGC AGGATCTCAC GCCTCTGAAG CTGGCCGCCA AGGAGGGCAA GATCGAGATT	1320
	TTCAAGCACA TCCTGCAGCG GGAGTTTTC AAGACTGAGCC ACCTTTCCCG AAAGTTCACC	1380
60	GAGTGGTGCT ATGGGCCCTGT CCGGGTGTG CTGTATGACC TGGCTTCTGT GGACAGCTGT	1440

	GAGGAGAACT CAGTGCTGGA GATCATTGCC TTTCATTGCA AGAGCCCGCA CCGACACCGA	1500
5	ATGGTCGTTT TGGAGCCCCCT GAACAACTG CTGCAGGCGA AATGGGATCT GCTCATCCCC	1560
	AAGTTCCTCT TAAACTTCCT GTGTAATCTG ATCTACATGT TCATCTTCAC CGCTGTGACC	1620
	TACCATCAGC CTACCCTGAA GAAGCAGGCC GCCCCTCACC TGAAAGCGGA GGTGGAAGAC	1680
10	TCCATGCTGC TGACGGGCCA CATCCTTATC CTGCTAGGGG GGATCTACCT CCTCGTGGGC	1740
	CAGCTGTGGT ACTTCTGGCG GCGCCAGTG TTTCATCTGA TCTCGTTCAT AGACAGCTAC	1800
15	TTTGAAATCC TCTTCCTGTT CCARGCCCTG CTCACAGTGG TGTCCARGT GCTGTGTTTC	1860
	CTGGSCATCG AGTGGTACCT GCCCCTGCTT GTGTCTGCGC TGGTGTGGG CTGGCTGAAC	1920
	CTGCTTTACT ATACACGTGG CTTCACGAC ACAGGCATCT ACAGTGTCTAT GATCCAGAAG	1980
20	CCCTGGTGAG CCTGAGCCAG GANNTTGGCG CCCCGAAGCT CCTACAGGCC CCAATGCCAC	2040
	AGAGTCAGTG CAGCCCATGG AGGGACAGGA KGACGAKGGC AACGGGGCCC AGTACAGGGG	2100
25	TATCTGGAA GCCTCCTTGG AGCTCTTCAA ATTCACCATC GGCATGGGCG AGCTGGCCTT	2160
	CCAGGARCAG CTGCACTTCC GCGGCATGGT GCTGCTGCTG CTGCTGGSCT ACGTGTGCT	2220
	CACCTACATC CTGCTGCTCA ACATGCTCAT CGCCCTCATG AGCGAGACCG TCAACAGTGT	2280
30	CGCCACTGAC AGCTGGAGCA TCTGGAAGCT GCAGAAAGCC ATCTCTGTCC TGGAGATGGA	2340
	GAATGGCTAT TGGTGGTGCA GGAAGAAGCA GCGGGCAGGT GTGATGCTGA CCGTTGGCAC	2400
35	TAAGCCAGAT GGCAGCCCSG ATGAGCGCTG GTGCTTCAGG GTGGAGGAGG TGAAGTGGC	2460
	TTTCATGGAG CAGACGCTGC CTACGCTGTG TGAGGACCCG TCAGGGGCAG GTGTCCCTCG	2520
	AACTCTCGAG AACCTGTGCC TGGCTTCCCC TCCCAAGGAG GATGAGGATG GTGCCTCTGA	2580
40	GGAAACTAT GTGCCCCTCC AGCTCCTCCA GTCCAAGTGA TGGCCAGAT GCAGCAGGAG	2640
	GCCAGAGGAC AGAGCAGAGG ATCTTTCCAA CCACATCTGC TGGCTCTGGG GTCCCACTGA	2700
45	ATTCTGGTGG CAAATATATA TTTTCACTAA CTCAAAAAAA AAAAAAAAAA AAAAAAAAAA	2760
	AAAAAAAAAA AAAAAAGGC	2779

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(2) INFORMATION FOR SEQ ID NO: 192:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1923 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

55

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 192:

	ACCCGCTCCG CTCGCTCCG CTCGGCCCCG CGCGCCCCGT CAACATGATC CGCTGCGGCC	60
	TGGCCTGCGA GCGCTGCCG TGGATCCTGC CCTGCTCCT ACTCAGCGCC ATCGCCTTCG	120
5	ACATCATCGC GCTGGCCGGC CGCGGCTGGT TGCAGTCTAG CGACCACGGC CAGACGTCTT	180
	CGCTGTGGTG GAAATGCTCC CAAGAGGGCG GCGGCAGCGG GTCTTACGAG GAGGGCTGTC	240
10	AGAGCCTCAT GGAGTACGCG TGGGGTAGAG CAGCGGCTGC CATGCTCTTC TGTGGCTTCA	300
	TCATCTGGT GATCTGTTTC ATCTCTCCT TCTTCGCCCT CTGTGGACCC CAGATGCTTG	360
	TCTTCTGAG AGTGATTGGA GGTCTCCTTG CCTTGGCTGC TGTGTTCCAG ATCATCTCCC	420
15	TGGTAATTTA CCCCCTGAAG TACACCCAGA CCTTCACCCT TCATGCCAAC CSTGCTGTCA	480
	CTTACATCTA TAACTGGCC TACGGCTTTG GGTGGGCAGC CACGATTATC CTGATYGGCT	540
20	GTGCCTTCTT CTCTGCTGC CTCCTCAACT ACGAAGATGA CCTTCTGGGC AATGCCAAGC	600
	CCAGGTACTT CTACACATCT GCCTAACTTG GGAATGAATG TGGGAGAAAA TCGCTGCTGC	660
	TGAGATGGAC TCCAGAAGAA GAACTGTTT CTCCAGGCGA CTTTGAACCC ATTTTGTGGC	720
25	AGTGTTCATA TTATTAACT AGTCAAAAAT GCTAAAATAA TTTGGGAGAA AATATTTTTT	780
	AAGTAGTGT ATAGTTTCAT GTTTATCTTT TATTATGTTT TGTGAAGTTG TGTCTTTTCA	840
30	CTAATTACCT AACTATGCC AATATTTCTT TATATCTATC CATAACATTT ATACTACATT	900
	TGTAAGAGAA TATGCACGTG AAACCTAACA CTTTATAAGG TAAAAATGAG GTTTCCAAGA	960
	TTTAATAATC TGATCAAGTT CTGTATTATT CCAAATAGAA TGGACTCGGT CTGTTAAGGG	1020
35	CTAAGGAGAA GAGGAAGATA AGGTTAAAG TTGTTAATGA CCAAACATTC TAAAAGAAAT	1080
	GCAAAAAAA AGTTTATTTT CAAGCCTTCG AACTATTTAA GGAAAGCAA ATCATTTCTT	1140
40	AAATGCATAT CATTTGTGAG AATTCTCAT TAATATCCTG AATCATTCAT TTCAGCTAAG	1200
	GCTTCATGTT GACTCGATAT GTCATCTAGG AAAGTACTAT TTCATGGTCC AAACCTGTTG	1260
	CCATAGTTGG TAAGGCTTTC CTTTAAGTGT GAAATATTTA GATGAAATTT TCTCTTTTAA	1320
45	AGTTCTTTAT AGGGTTAGGG TGTGGGAAAA TGCTATATTA ATAAATCTGT AGTGTTTGT	1380
	GTTTATATGT TCAGAACCAG AGTAGACTGG ATTGAAAGAT GGACTGGGTC TAAITTTATCA	1440
50	TGACTGATAG ATCTGGTTAA GTTGTGTAGT AAAGCATTAG GAGGGTCATT CTTGTCACAA	1500
	AAGTGCCACT AAAACAGCCT CAGGAGAATA AATGACTTGC TTTTCTAAAT CTCAGGTTTA	1560
	TCTGGGCTCT ATCATATAGA CAGGCTTCTG ATAGTTTGCA ACTGTAAGCA GAAACCTACA	1620
55	TATAGTTAAA ATCCTGGTCT TTCTTGGTAA ACAGATTTTA AATGTCTGAT ATAAAACATG	1680
	CCACAGGAGA ATTCTGGGAT TTGAGTTTCT CTGAATAGCA TATATATGAT GCATCGGATA	1740
60	GGTCATTATG ATTTTTTACC ATTTGACTT ACATAATGAA AACCAATTCA TTTTAAATAT	1800

CAGATTATTA TTTTGTAAAGT TGTGGAAAAA GCTAATTGTA GTTTTCATTA TGAAGTTTTC 1860
 CCAATAAACC AGGTATTCTA AAAAAAAAAA AAAAAAACTN GAGGGGGGGC CCGGTACCCA 1920
 5 ATT 1923

10 (2) INFORMATION FOR SEQ ID NO: 193:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2346 base pairs
 (B) TYPE: nucleic acid
 15 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 193:

20 AGGCTCAGGG GGACACTCTC AAAATTACAC AGCTTTTAAC AGGTGGCAGA ATGGGGGTTC 60
 AGACCCAGAT CTGGGTTCAA GTCACATCATG GTGTGATTGC GGCATTCCCTT CCCGCATCTG 120
 25 GGCCTTGCCA TCTCTCTCTC CGAGTGGACA TGGAGAGGAC GGGGGCCCAG CAGCTGGATG 180
 GCTGCAGGGG ATCAAGTCTT CTCTGGGGCT GGGCACGTAN AAGAGCATGT GGCTGGTGGG 240
 CGGCATGCCT GGCTCCTCAC CTGGCAGTCT GCCTGCCCTG CTAACCGGCT GTCTCTTGTT 300
 30 CCCCTAGTGC CCTCGGCTAG CATGACCCGC CTGATGCGWT SCCGCACAGC CTCTGGTTCC 360
 AGCGTCATTC TCTGGATGGC ACCCGCAGCC GCTCCACAC CAGCGAGGGC ACCCGAAGCC 420
 GCTCCACAC CAGCGAGGGC ACCCGCAGCC GCTCGCACAC CAGCGAGGGG GCCCACCTGG 480
 35 ACATCACCCC CAACTCGGGT GCTGCTGGGA ACAGNGCCGG GCCCAAGTCC ATGGAGGTCT 540
 CCTGCTAGGC GGCCTGCCCA GCTGCCGCC CCGGACTCTG ATCTCTGTAG TGGCCCCCTC 600
 40 CTCCCCGCC CCTTPTCGCC CCCTGCCTGC CATACTGCGC CTAATCTGGT ATTAATCCAA 660
 AGCTTATTTT GTAAGAGTGA GCTCTGGTGG AGACAAATGA GGTCTATTAC GTGGGTGCCC 720
 TCTCCAAAGG CGGGGTGGCG GTGGACCAA GGAAGGAAGC AAGCATCTCC GCATCGCATC 780
 45 CTCTTCCATT AACCAGTGGC CGGTTGCCAC TCTCTCCCC TCCCTCAGAG ACACAAACT 840
 GCCAAAAACA AGACGCGTAC AGCACACACT TCACAAAGCC AAGCCTAGGC CGCCCTGAGC 900
 50 ATCTTGGTTC AAACGGGTGC CTGGTCAGAA GGCCAGCCGC CCACTTCCCG TTTCTCTTT 960
 AACTGAGGAG AAGCTGATCC AGTTTCGGG AACAAAATCC TTTTCTCATT TGGGGAGGGG 1020
 GGTAATAGTG ACATGCAGGC ACCTCTTTTA AACAGGCAA ACAGGAAGGG GGAAAAGGTG 1080
 55 GGATTCATGT CGAGGCTAGA GGCATTTGGA ACAACAAATC TACGTAGTTA ACTTGAAGAA 1140
 ACCGATTTTT AAAGTTGGTG CATCTAGAAA GCTTTGAATG CAGAAGCAA CAAGCTTGAT 1200
 60 TTTTCTAGCA TCCTCTTAAT GTGCAGCAA AGCAGGCRAC AAAATCTCCT GGCTTTACAG 1260

	ACAAAAATAT TTCAGCAAAC GTTGGGCATC ATGGTTTITG AAGGCTTTAG TTCTGCTTTC	1320
5	TGCCTCTCCT CCACAGCCCC AACCTCCAC CCCTGATACA TGAGCCAGTG ATTATTCTTG	1380
	TTCAGGGAGA AGATCATTTA GATTGTGTTT GCATTCTTA GAATGGAGGG CAACATTCCA	1440
	CAGCTGCCCT GGCTGTGATG AGTGTCTTG CAGGGGCCGG AGTAGGAGCA CTGGGGTGGG	1500
10	GGCGGAATG GGGTACTCG ATGTAAGGA TTCCTTGTG TTGTGTTGAG ATCCAGTGCA	1560
	GTTGTGATTT CTGTGGATCC CAGCTTGGTT CCAGGAATTT TGTGTGATTG GCTTAAATCC	1620
15	AGTTTTCAT CTTCGACAGC TGGGCTGGAA CGTGAATCA GTAGCTGAAC CTGTCTGACC	1680
	CGGTACGTT CTGTGATCCT CAGAACTCTT TGCTCTGTG GGGGTGGGG TGGGAATCA	1740
	CGTGGGAGC GGTGGCTGAG AAAATGTAAG GATTCTGGAA TACATATTCC ATGGGACTTT	1800
20	CCTTCCCTCT CCTGCTTCCT CTPTTCTGC TCCCTAACCT TTCGCCGAAT GGGGCAGCAC	1860
	CACTGACGTT TCTGGGCGGC CAGTCCGGCT GCCAGTTCC TGTACTACTG CCTTGTACTT	1920
25	TTCATTTTGG CTCACCGTGG ATTTTCTCAT AGGAAGTTG GTCAGAGTGA ATTGAATATT	1980
	GTAAGTCAGC CACTGGGACC CGAGGATTTT TGGGACCCCG CAGTTGGGAG GAGGAAGTAG	2040
	TCCAGCCTTC CAGGTGGCGT GAGAGGCAAT GACTCGTTAC CTGCCGCCA TCACCTTGA	2100
30	GGCCTTCCCT GGCCTTGAGT AGAAAAGTCG GGGATCGGG CAAGAGAGGC TGAGTACGGA	2160
	TGGGAACTA TTGTGCACAA GTCTTCCAG AGGAGTTTCT TAATGAGATA TTTGTATTTA	2220
35	TTTCCAGACC AATAAATTTG TAACTTTGCA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA	2280
	AAAAAAAAA AAAAAAACT CGAGGGGGC CCGTACCCAA TTCGCCGTAT ATGATCGTAA	2340
	ACAATC	2346
40		

(2) INFORMATION FOR SEQ ID NO: 194:

- 45 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 3054 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 194:

	TATCTGAACC ACCCTTTATT CTACATATGA TAGGCAGCAC TGAAATATCC TAACCCCTA	60
55	AGCTCMAGGT GCCCTGTGGN ACGAGCAACT GGAATATAGC AGGGCTGGG TCTGTCTTCC	120
	TGGTCATAGG CTCACTCTTT CCCCCAAATC TTCCTCTGGA GCTTTGCAGC CAAGGTGCTA	180
60	AAAGGAATAG GTAGGAGACC TCTTCTATCT AATCCTTAAA AGCATAATGT TGAACATTCA	240

	TTCAACAGCT GATGCCCTAT AACCCCTGCC TGGATTTCCTT CCTATTAGGC TATAAGAAGT	300
	AGCAAGATCT TTACATAATT CAGAGTGGTT TCATTGCCTT CCTACCCCTCT CTAATGGCCC	360
5	CTCCATTAT TTGACTAAAG CATCACACAG TGGCACTAGC ATTATACCAA GAGTATGAGA	420
	AATACAGTGC TTTATGGCTC TAACATTACT GCCTTCAGTA TCAAGGCTGC CTGGAGAAAG	480
10	GATGGCAGCC TCAGGGCTTC CTTATGTCTT CCACCACAAG AGCTCCTTGA TGAAGGTCAT	540
	CTTTTCCCC TATCCTGTTT TTCCCTCCC CGCTCCTAAT GGTACGTGGG TACCCAGGCT	600
	GGTCTTGGG CTAGGTAGTG GGGACCAAGT TCATTACCTC CCTATCAGTT CTAGCATAGT	660
15	AAACTACGGT ACCAGTGTTA GTGGGAAGAG CTGGGTTTTC CTAGTATACC CACTGCATCC	720
	TACTCCTACC TGGTCAACCC GCTGCTTCCA GGTATGGGAC CTGCTAAGTG TGAATTACC	780
20	TGATAAGGGA GAGGGAAATA CAAGGAGGGC CTCTGGTGT TCTGGCCTCA GCCAGCTGCC	840
	CACAAGCCAT AAACCAATAA AACAAGAATA CTGAGTCAGT TTTTATCTG GGTCTCTTC	900
	ATTCCCACTG CACTTGGTGC TGCTTTGGCT GACTGGGAAC ACCCCATAAC TACAGAGTCT	960
25	GACAGGAAGA CTGGAGACTG*TCCACTTCTA GCTCGGAAT TACTGTGTAA ATAAACTTTC	1020
	AGAACTGCTA CCATGAAGTG AAAATGCCAC ATTTTGCTTT ATAATTCTTA CCCATGTTGG	1080
30	GAAAACTGG CTTTTTCCCA GCCCTTTCCA GGGCATAAAA CTCACCCCT TCGATAGCAA	1140
	GTCCCATCAG CCTATTATTT TTTTAAAGAA AACTTGCACT TGTTTTCTT TTTACAGTTA	1200
	CTTCCTTCCT GCCCCAAAT TATAACTCT AAGTGTA AAAAGTCTTA ACAACAGCTT	1260
35	CTTGCTTGTA AAAATATGTA TTATACATCT GTATTTTAA ATCTGCTCC TGAAAAATGA	1320
	CTGTCCCAT CTCCACTCAC TGCATTGGG GCCTTTCCCA TGGTCTGCA TGTCTTTTAT	1380
40	CATTCAGGC CAGTGGACAG AGGGAGAAGG GAGAACAGG GTCGCCAACA CTTGTGTTGC	1440
	TTTCTGACTG ATCCTGAACA AGAAAGAGTA AACTGAGGC GCTCGCTCCC ATGCACAACT	1500
	CTCCAAAACA CTTATCCTCC TGCAAGAGTG GGCTTTCCAG GGTCTTACT GGAAGCAGT	1560
45	TAAGCCCCCT CCTCACCCT TCCTTTTTC TTTCTTACT CCTTTGGCTT CAAAGGATTT	1620
	TGGAAAAGAA ACAATATGCT TTCACTCAT TTTCAATTC TAAATTGCA GGGGATACTG	1680
50	AAAAATACGG CAGGTGGCTT AAGCTGCTG TAAAGTTGAG GGGAGAGGAA ATCTTAAGAT	1740
	TACAAGATAA AAAACGAAT CCCTAAACAA AAAGAACAAT AGAACTGGTC TTCCATTTTG	1800
	CCACCTTTC TGTTCATGAC AGCTACTAAC CTGGAGACAG TAACATTTCA TTAACCAAAG	1860
55	AAAGTGGGTC ACCTGACCTC TGAAGAGCTG AGTACTCAG CCACTCCAAT CACCCTACAA	1920
	GATGCCAAGG AGGTCCAGG AAGTCCAGCT CCTTAACTG ACGCTAGNCA ATAAACCTGG	1980
60	GCAAGTGAGG CAAGAGAAAT GAGGAAGAAT CCATCTGTGA GGTGACAGGC AAGGATGAAA	2040

	GACAAAGAAG GAAAAGAGTA TCAAAGGCAG AAAGGAGATC ATTTAGTTGG GTCTGAAAGG	2100
	AAAAGTCTTT GCTATCCGAC ATGTACTGCT AGTACCTGTA AGCATTTTAG GTCCCAGAAT	2160
5	GGAAAAAAA ATCAGCTATT GGTAATATAA TAATGTCCCT TCCCTGGAGT CAGTTTTTTT	2220
	AAAAAGTTAA CTCCTAGTTT TTACTTGTTT AATTCTAAAA GAGAAGGGAG CTGAGGCCAT	2280
10	TCCCTGTAGG AGTAAAGATA AAAGGATAGG AAAAGATTCA AAGCTCTAAT AGAGTCACAG	2340
	CTTTCCCAAG TATAAACCTT AAAATTAAGA AGTACAATAA GCAGAGGTGG AAAATGATCT	2400
	AGTTCTCGAT AGCTACCCAC AGAGCAAGTG ATTTATAAAT TTGAAATCCA AACTACTTTC	2460
15	TTAATATCAC TTGGTCTCC ATTTTCCCA GGACAGGAAA TATGTCCCCC CCTAACTTTC	2520
	TTGCTTCAAA AATTAAAATC CAGCATCCCA AGATCATTCT ACAAGTAATT TTGCACAGAC	2580
20	ATCTCTCAC CCCAGTGCCT GTCTGGAGCT CACCCAAGGT CACCAAACAA CTTGGTTGTG	2640
	AACCNACTG CCTTAACCTT CTGGGGGAGG GGGATTAGCT AGACTAGGAG ACCAGAAGTG	2700
	AATGGGAAAG GGTGAGGACT TCACAATGTT GGCCTGTCAG AGCTTGATTA GAAGCCAAGA	2760
25	CAGTGCAGC AAAGGAAGAC TTGCCCCAGG AAAAACCTGT GGGTTGTGCT AATTCTGTC	2820
	CAGAAAATAG GGTGGACAGA AGCTTGTTGG GTGCATGGAG GAATTGGGAC CTGGTTATGT	2880
30	TGTTATCTC GGACTGTGAA TTTTGGTGAT GTAAACAGA ATATTCTGTA AACCTAATGT	2940
	CTGTATAAAT AATGAGCGTT AACACAGTAA AATATTCAAT AAGAAGTCAA AAAAAAAAAA	3000
	AAAAAACTCG AGGGGGGGCC CGGTACCCAA TTTNCCAAAT AGAGATNGTA TTAC	3054
35		

(2) INFORMATION FOR SEQ ID NO: 195:

- 40 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 907 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear
- 45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 195:

	GGCAGAGCTC GTGGCCGNAA CTTTTTCTGC TCCTGGCTGC CACCTACTGG CTGGCCGCGG	60
50	CCCTGGCCTG GGCCTGCACC AGCCTGCGNG CGGGCTCCCA CAGCAGCCCC CTTCCAAGCA	120
	GCGTCCCCAC ACCCGGCACC TTCTGCGGGA ACGTGTCTGC CGTGCCGGGG ACCATATGGA	180
55	CGGAAGGCTT TGTGCTCACC TACAAGCTGG GTGAGCAGGG TGCCAGCAGC CTGTTGATCC	240
	TCTTGGCTCC TGCTGGAGCA CGAGCGGCGT TTCTGCTCCC GAGTTGGGAC TGTGGAATGG	300
	TGTGGGTGCT GTGGTCTGCT CCATCGCTGG CTCTCCCTG GGTGGGACCT TGCTGGCCAA	360
60	GCACTGAAAA CTGCTGCCTC TGTGAGGTCG GTGCTGCGCT TCCGCTCGG GGGCCTAGCC	420

5 TGTCAGACTG CCTTGGTCTT CCACCTTGA CACCTGGGG GCCAGCATGG ACGCTGGCAC 480
 AATCTTGAGA GGGTCAGCCT TGCTGAGCCT ATGTCTGCAG CACTTCTTGG GARGCCTGGT 540
 CACCACAGTC ACCTTCACTG GGAATGATGC GCTGCAGCCA GCTGGCCCCC AGGGCCTTGC 600
 AGGCCACACA CTACAGCCTT CTGGCCACGC TGGAGCTGCT GGGGAAGCTG CTGCTGGGCA 660
 10 CTTTGGSCGG AGGGCCTGGC TGATGGGTTG GGGCCACATC CCTGCTTCTT GCTCCTGCTC 720
 ATCCTCTCTG CCTTTCCTGT TCTGTACCTG GACCTAGCAC CCAGCACCTT TCTCTGAGCT 780
 GAGTGGCTGG AGTGGTCAAT AAAGCCACAT GTGCTGTGG CCCAAAAAA AAAAAAAA 840
 15 AAAAAAAA AAAAAAAGT GAGGGGGGC CCGTACCCA AATCGCCGA TATGATCGTA 900
 AACAATC 907

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(2) INFORMATION FOR SEQ ID NO: 196:

25

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1290 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 196:

GGCACGAGGA GGGACAGGA GTGGCAAGG GGAAGAAGCA GCTTATTGA CTAACCAGCC 60
 35 CCTCTGTGGT CCACCAGCGT CTGGCTTGG TGGAGGGCT CTCAATCAGC AGGGCCCCAG 120
 KAGGGCAAGA AGAAGTGGG CAAAGCCTGG CGCTCGGCCG CGGTCGGGC AGCTTTGCMA 180
 TCTGGAGCCA CGCTCTCTCC AGGCCATGCT CTTGAACCTT GGAAATGTCA ACCGGAGCCC 240
 40 TTAACACCAG CCCTCCAGCA TCTAATAGAC TTGAATCTAC TCTAAACGAA TATTTAATCC 300
 AACCTCAACT ACATTGTAGC TCAGTCCAAC GACTAACCTT GAAATGGGGG TGTTCAGCC 360
 45 TTCAGCGAGA TGGCCAAGCG GTCCCTGGG GGCTGTGGCA GCGGGCTTAT CTTTCTCTGT 420
 TGCCAACCTT GCCGTCGAC CTCTCCGCC CCCATGCGGT GACCCCGTCC GTGTCTGTGT 480
 CTGTCCATAC GTGTGAGTCC AGCTAAAAAG ACAAACAGA ACCCGTGGGC CCAGCTCGGA 540
 50 AGGTGCGTGG AGAAGGCTCC GACGTCTCCG AAGTGCAGCC CTTGGGATGG CATTCGTTG 600
 TGTGCCTTAT TCCTGGAGAA TCTGTATACG GCTCGCCTAT AAGAAATATA GCCTCTTCAT 660
 55 GCTGTATTAA AAGGACTTTT AAAAGCAAAA AAAAAAAA AAAAACTCGA GGGGGGGCCC 720
 GGTACCCAAT TCGCCAATA GTGAGTCGTA TTACAATTCA CTGGCCGTC STTTTAACAA 780
 60 CGTCGTGAAC TGGGAAAACC CTGGCGTTTA CCCAACTTAA TCGCCTTGCA GCACATCCCC 840

CTTTCGCCAG CTGGCGTTAA TAGCGAAAAA NGCCCGCACC CGAATCGCCC TTCCCAACAG 900
 TTTGCGCAGC CCTGAATGGC GAAATGGCAA ATTGTAAGCG TTTAATATTT TKKTTAAAAT 960
 5 TCCNCGTTWA AWTMTTGTGTT TAAATCARCT CAATTTTMTT AACCCAATAA GSCCGAAATC 1020
 CGGCAATCC CCYTTATTAA TTCCAAAAA ATAAACCSAA AAWGGGTTTG AATTTTTKT 1080
 10 TTCCCACTT TTGGAAACAA AWTYCCCCCT TTTTAAAAA GTTGAACCC CCAMCCYTCC 1140
 AAAGGGGAAA AAACSYTTT YTGCGGGGNA ANGGGGCCCC CNTACTTTNA ACAYCCCCC 1200
 CCAAWCAATT TTTTGGGGG GTCCCNAAAG GTCCCCCTAA AANCTTTTTC CGGAACCCNA 1260
 15 AGGGGANCCC CCCATTTAAA ATTTTNGGTN 1290

20 (2) INFORMATION FOR SEQ ID NO: 197:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1020 base pairs

(B) TYPE: nucleic acid

25 (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 197:

30 GGTGTGCGTG GATGGTCGTG TAGGTGAGTT TTACCAAGGA TTATGGTAAC AAATGAGTGA 60
 GACCTCTATG GAGAAAATAT TGAAGNNCAT TAAAGAAGAC CTCATANTAG GAGAGAATGT 120
 35 SCITTGAGG ATTGTATATG AGCTTTTACA GTATTCATTT TTCAACTCAA GGCAATGGCT 180
 TTCTACACCA ACTCTAATCC ATAAACGGGT CTTATGACAT CTATGAAGTA GTAGCAAGAC 240
 ATGCTTAGTG TGTATTTCTC TCTTTGAGAC ACTGTAATTT CTACCAGAAA TTTCAGAGC 300
 40 ATTATGTAGG TAGAAAAAAA TGCAAGCAAG CTGTTAAGA TCTTGATCC CATTATATAG 360
 TATGTATAGC TGAATCTGT AATTCAATCA CTTTTCTCT TTTATCCTCT AACCAAAAA 420
 45 TTGTTTAATT TTGCATCCA AATGTTTTTA ATCTTTGTAT ATTTTTTAAA AAYCCTTTTC 480
 TCCTCATCAT TGCCTTTTTT GTGGTGTAA ATAGACTTAC TTGCACTTG AAGATGAGTT 540
 ACTCCTGTG ATCTTACAAA TATGTGATAT GGTAATTTTC ATAACAGATG TCAGTTTGA 600
 50 ACCAAGAATT GGTGATTTGT TTATAAGAAA AAAACTGGCT TCATTTCTGT GAAATTGCTC 660
 TTTGAAAATT TCTTTTACA CGTGAAGCC AACTGAGATA CCGTATGGT GTTGATTTCT 720
 55 TTCAATGATG CTTACCATCT ATTTTAGCCA CTGAGCCTTT TATTATTTGT CTATTTGTAA 780
 AGTTTATTTG TCTTAACTCA TTTAATAAAT ATACTGTTA TCTGTTCTG AATGGGGACT 840
 GAACCTTTTG GATATTGATA TTGATTTGAA AATATTTTGG AATTTTCTT ACTTGAAATT 900
 60 TTAGAAATCT AATKGAAAT TCTATAATGT ACTGAAAGTA WGGTTGTGTA CAGTGAKCAC 960

TCTCTAATAA TATGATGCT TGCCTTAAAN GAGGNGGGAC ATGTCCCACT TTCCACCACG 1020

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(2) INFORMATION FOR SEQ ID NO: 198:

- 10 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 524 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 198:

AATTCCCGAA GCTGAGGGTT GTGTGCCNTC GGGCGAGCCA AGTCTTTTGA CCGGACCCCTT 60
CCCGGCGCAG AAGANCTGAA GTTGATTGTA GAGCCTGTCT TTGGGGTTTA GCCGAGCTGC 120
20 TCGGGCCTTY GTCGCCGCC AGGACACAAG YTACTTGCAA CGGGGCGGCG CCTGGCTTAT 180
GATGTTCTTC AACCCAGGGG CGGCCTCTGC CCTCTACTCG TGCCAGGCC ACTTGCCAGG 240
25 CAGGAGCCCT CCCCAAGCCT TCAGGGCTGC TCGGAGTCAC CTGTTGGAAT GGAATAAAG 300
GACCCTTGTC TGGGAACAGG TGCTCCAAAC ACCCTGCTGC TGGCTGCCAG GCAGGCCCTC 360
TGGAAGGGAA GGGGCAGGAC TCATCAGGAC CTCCCTGGAC CTTGCAGGGC AGGCAGTTGG 420
30 CCCGAGCCA AGCATTTGGC TCTGCTTGCC CCAAGGGGAC AGGAAGCCTC TTGGGCCTCT 480
TCCCTTCCTG GACAAGGCC CCTGCTTTG CCTCACATAA ACTG 524

35

(2) INFORMATION FOR SEQ ID NO: 199:

- 40 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 332 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
45 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 199:

GTGATACAAG GAAGGGTGAT CATCATCTGT CACCATGCAA TTCCTGCTCA CAGCCTTTCT 60
50 GTTGGTGCCA CTCTGGCTC TTTGTGATGT CCCATATCC CTAGGCTTCT CCCCTCCTA 120
GAAGGGCTTC TTGATAGATT AGAAAATAAG AATGAGTGAC ATTTCCTATG TGCATATAAG 180
AAGGAGCCAC AAGACATGTC TTTTAAATAA AAGGACAGTG TCCATCCTTT TAGCTGCCGA 240
55 ATAGAACCTT GGTCTCATCC TCCTGGAGCT AGGSCCTAAA ACAGCTTCTG TGTTTCTSAT 300
TKGTCTCART GTTTTGCCAA GGTTTTATTC GG 332

60

(2) INFORMATION FOR SEQ ID NO: 200:

- 5 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 376 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
10 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 200:

CCAGGGAAGC CCCARGCCTG TCCTGAATTG ACATCAGTGC TTCCCTGAAC TGCTCCCCC 60
15 ACCCCTGGGC ATTATCCAG GAAACTTATG TTTTCTAGAA GCTAAGCAGC TGCTGGGACT 120
CAGGGACTGG TGCAGGTAGG CTGAGTGCCA GCTCAGTCTC AGAAGGTCTC TGAAGATCTG 180
GACTGAGGAC CYTGCTACTC CCCAAGCCAG AGCCCATCAG CCAGGCCTGC TGTGAGCCAC 240
20 CTGCCTGTGG AGTGCTGAGC TCAACCAAAG GCTGGCAAGC TCTGGGCCTC ATTTAAGGGA 300
TTCTGATGAG CCGATGGGCC CTGGAGGCAG CCCATTAAAG CATCTGGCTC GTTTTGGAA 360
25 AAAAAAAAAA AAAAAG 376

30 (2) INFORMATION FOR SEQ ID NO: 201:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1192 base pairs
35 (B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 201:

40 CCCAGTATAT TTCTATAACA TTTATTTAG TGAAGTTATA ATGTTTCTTT GTATTAAATT 60
ATTAGATTAT ATCTTTAGAT AATATTGTTA CTNAATTAGT AGGTAATATA TATTTTATTC 120
AAAAATAAAT TGTGCATCTA ATGTCTACCA ATTAATGTAC TTGTAGATGT ATCTTATCTT 180
45 AACTTGAGTC TTTGCTGCCC CTAATGAGGT GTGAAGGACT CTTCTCCCTT GGGGAAGTTT 240
TTCTTTTTC A GGAGGGAGGA GGGCTTTCCC AGGTAATGTG TCTAGAGTGT TGGCAGAAR 300
50 AATCTGGGAC CACACCACAC CAGTTCTCTC CTTAATCCAC GTCATTTGCC TTCTATCCCA 360
GCTATGTTTC CAGTGTCTTC TGGGTGTTTC CAAGAGCAAC AAGAAAYGAA TAAATCTCTG 420
KTGAGTTGTT TATTTGTTCT TCACTTTGTT TTACACTGTA WTTTCTGAGT TTATGGGTGT 480
55 CTGTGAATTA AAAAGGAAAA GTRGAAATAA GTAAACTCA GGTGAAGGA AATATACATA 540
AATAAGATAA AGCTGACCTG TAGATATARR CAGGTTATAA RAGCTTAGAG TTGTCTAAGT 600
60 TGRGTGCAAA KTTTCCTCTG ATCTTTCTGA TGCCGARACA AAAAAGGCAG TCATGTTTGT 660

WATGTGATTG GAATGGAACC CGARAAGAGA GCAYGCTGTG TTCTTGGGGA CAGGAAAGCT 720
5 TGYGTGCACC AAGTCTKAAC CACCACCTTC ATGGGACATA GRTTATGTGC TGGAACATAT 780
TTCACACCGG CCTGGCAGTA AACACTTGTA GTGTTGTGCA GTGGAAACGG TCATCTCCG 840
CTAAAGCAGC GCGTGTGTG CAGCGGAAAT GGTTCATCTGC TGCTAAAACA CAGCTTCCAT 900
10 CGTAATGTAT GCTCCTTACT CAAAGAGTGT GGTCCCAAAC AGCCTTTGGG AGTCCTCCT 960
TGATTCATGG ATGAAACCTG GAACATCTTG AGGACTGAGT TAACCATAGG TCCTTAAATA 1020
ACTCTCCACA CGTTTTTCTT AGTTTATCTC TACATGCAGG GTGTGCAGCA GCCTGTTCAA 1080
15 AGTCATATTT TCTGGGAAAT ATTTCCAGTG TTTATTTGCA CTTTAGCCCA CTCTGTGTAG 1140
CCTTATTTCT TCTAAACTCA CCATTAATCT GAATAATAGT CAAATTTAGG GG 1192
20

(2) INFORMATION FOR SEQ ID NO: 202:

25 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 589 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
30 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 202:

ATCTTGGGCT ATCTTTGACA GGGGATTCCTT GCAAGTTGAT GCTTTCTACA AGTGAATATA 60
35 GTCAGTCCCC AAAGATGGAG AGCTTGAGTT CTCACAGAAT TGATGAAGAT GGAGAAAACA 120
CACAGATTGA GGATACGGAA CCCATGTCTC CAGTTCTCAA TTCTAAATTT GTTCCTGCTG 180
AAAATGATAG TATCCTGATG AATCCAGCAC AGGATGGTGA AGTACAAC TGTCAGAAATG 240
40 ATGACAAAAC AAAGGGAGAT GATACAGACA CCMGGGATGA CATTAGTATT TTAGCCACTG 300
GTTGCAAGGG CAGAGAAGAA ACGGTAGCAG AAGATGTTTG TATTGATCTC ACTTGTGATT 360
45 CGGGGAGTCA GGCAGTTCCG TCACCAGCTA CTCGATCTGA GGCACCTTCT AGTGTGTTAG 420
ATCAGGAGGA AGCTATGGAA ATTAAAGAAC ACCATCCAGA GGAGGGGTCT TCAGGGTCTG 480
AGGTGGAAGA AATCCCTGAG ACACCTTGTG AAAGTCAAGG AGAGGAACTC AAAGAAGAAA 540
50 ATATGGAGAG TGTTCGTTG CACCTTCTC TGA CTGAAAC TCAGTCCCA 589

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(2) INFORMATION FOR SEQ ID NO: 203:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 847 base pairs
60 (B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 203:

5
GGCACGAGCG CAAGCTGCTG GCCGCCATCA ACGCGTTCCG CCAGGTGCGG CTGAAACACC 60
GGAAGCTCCG GGAACAAGTG AACTCCATGG TGGACATCTC CAAGATGCAC ATGATCCTGT 120
10 ATGACCTGCA GCAGAACTCTG AGCAGCTCAC ACCGGGCCCT GGAGAAACAG ATTGACACGC 180
TGGCGGGGAA GCTGGATGCC CTGACTGAGC TGCTTAGCAC TGCCCTGGGG CCGAGCAGCT 240
TCCAGAACCC AGCCAGCAGT CCAAGTAGCT GGACCCACGA GGAGGAACCA GGCTACTTTC 300
15 CCCAGTACTG AGTGGTGGAC ATCGTCTCTG CCACTCCTGA CCAGCCTGAA CAAAGCACCT 360
CAAGTGCAAG GACCAAAGGG GGCCTGGCTT GGATGGGTG GCTTGCTGAT GGCTGCTGGA 420
20 GGGGACGCTG GCTAAAGTGG GGAGGCCTTG GCCCACCTGA GGCCCCAGGT GGAACATGG 480
TCACCCCCAC TCTGCATACC CTCATCAAAA AACTCTCAC TATGCTGCTA TGGACGACCT 540
CCAGCTCTCA GTTACAAGTG CAGGCGACTG GAGGCAGGAC TCTTGGGTCC CTGGGAAAGA 600
25 GGGTACTAGG GGCCCGGATC CAGGATTCTG GGAGGCTTCA GTTACCGCTG GCCGAGCTGA 660
AGAACTGGGT ATGAGGCTGG GCGGGGCTG GAGGTGGCGC CCCCTGGTGG GACAACAAAG 720
30 AGGACACCAT TTTTCCAGAG CTGCAGAGAG CACCTGGTGG GGAGGAAGAA GTGTAACTCA 780
CCAGCTCTG CTCTTATCTT TGTAATAAAT GTTAAAGCCA GAAAAAAAAA AAAAAAAAAA 840
AAAAAAAA 847
35

(2) INFORMATION FOR SEQ ID NO: 204:

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(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 852 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

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(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 204:

50 ACAAACATAC TCGCAGGAAG GAGTCTCATG CTGCCCGCAG CATCAGCGCA ACNCNTGGCC 60
GCCATCAACG CGTTCGCCA GGTGCGGCTG AAACACCGGA AGCTCCGGGA ACAAGTGAAC 120
TCCATGGTGG ACATCTCCAA GATGCACATG ATCCTGTATG ACCTGCAGCA GAATCTGAGC 180
55 AGCTCACACC GGGCCCTGGA GAAACAGATT GACACGCTGG CGGGGAAGCT GGATGCCCTG 240
ACTGAGCTGC TTAGCACTGC CCTGGGGCCG AGGCAGCTTC CAGAACCAG CCAGCAGTCC 300
AAGTAGCTGG ACCCACGNAG GAGGAACCAG GCTACTTTCC CCAGTACTGA GGTGGTGGAC 360
60

ATNCGTCTCT TGCCACTCCN TGNACCCAGC CCTGAACAAA GCACCTCAAG TGCAAGGACC 420
 AAAGGGGGCC CTGGCTTGA GTGGGTGGC TTGCTGATGG CTGCTGGAGG GGACGCTGGC 480
 5 TAAAGTGGGK AGGCCTTGGC CCACCTGAGG CCCCAGGTGG GAACATGGTC ACCCCCACTC 540
 TGCATACCCT CATCAAAAAC ACTCTCACTA TGCTGCTATG GACGACCTCC AGCTCTCAGT 600
 10 TACAAGTGCA GGCAGCTGA GGCAGGACTC CTGGGTCCCT GGGAAAGAGG GTACTAGGGG 660
 CCCGGATCCA GGATTCTGGG AGGCTTCAGT TACCGCTGGC CGAGCTGAAG AACTGGGTAT 720
 GAGGCTGGGG CGGGGCTGGA GGTGGCGCCC CCTGGTGGGA CAACAAAGAG GACACCATTT 780
 15 TTCCAGAGCT GCAGAGAGCA CCTGGTGGGG AGGAAGAAGT GTAACCTACC AGCCTCTGCT 840
 CTTATCTTTG TA 852

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(2) INFORMATION FOR SEQ ID NO: 205:

25 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1354 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 205:

GATTCCGCAC GAGGCTTGCT GGAGCAGGAG AAGTCTCTRG CCGGCTGGGC ACTGGTGCTG 60
 GCASGARCTG GCATTGGACT CATGGTGCTG CATGCAGAGA TGCTGTGGTT CGGGGGGTGC 120
 35 TCGGCTGTCA ATGCCACTGG GCACCTTTCA GACACACTTT GGCTGATCCC CATCACATTC 180
 CTGACCATCG GCTATGGTGA CGTGGTGCCG GGCACCATGT GGGCAAGAT CGTYTGCCCTG 240
 40 TGCACTGGAG TCATGGGTGT CTGCTGCACA GCCCTGCTGG TGGCCGTGGT GGCCCGGAAG 300
 CTGGAGTTTA ACAAGGCAGA GAAGCACGTG CACAACCTCA TGATGGATAT CCAGTATACC 360
 AAAGAGATGA AGGAGTCCGC TGCCCGAGTG CTACAAGAAG CCTGGATGTT CTACAAACAT 420
 45 ACTCGCAGGA AGGAGTCTCA TGCTGCCCCG AGGCATCAGC GCAANCTGCT GGCCGCCATC 480
 AACGCGTTCC GCCAGGTGCG GCTGAAACAC CGGAAGCTCC GGAACAAGT GAACTCCATG 540
 50 GTGGACATCT CCAAGATGCA CATGATCCTG TATGACCTGC AGCAGAATCT GAGCAGCTCA 600
 CACCGGGCCC TGGAGAAACA GATTGACACG CTGGCGGGGA AGCTGGATGC CCTGACTGAG 660
 CTGCTTAGCA CTGCCCTGGG GCCGAGGCAG CTTCCAGAAC CCAGCCAGCA GTCCAAGTAG 720
 55 CTGGACCCAC GAGGAGGAAC CAGGCTACTT TCCCCAGTAC TGAGGTGGTG GACATCGTCT 780
 CTGCCACTCC TGNACCCAGC CCTGAACAAA GCACCTCAAG TGCAAGGACC AAAGGGGGCC 840
 60 CTGGCTTGA GTGGGTGGC TTGCTGATGG CTGCTGGAGG GGACGCTGGC TAAAGTGGGK 900

AGGCCTTGGC CCACCTGAGG CCCAGGTGG GAACATGGTC ACCCCCACTC TGCATACCTT 960
 CATCAAAAAC ACTCTCACTA TGCTGCTATG GACGACCTCC AGCTCTCAGT TACAAGTGCA 1020
 5 GCGGACTGGA GGCAGGACTC YTGCGTCCCT GGGAAAGAGG GYACTAGGGG CCCGGATCCA 1080
 GGATTCTGGG AGGCTTCAGT TACCGCTGGC CGAGCTGAAG AACTGGGTAT GAGGCTGGGG 1140
 10 CGGGGCTGGA GGTGGCGCCC CCTGGTGGGA CAACAAAGAG GACACCATT TCCAGAGCT 1200
 GCAGAGAGCA CCTGGTGGGG AGGAAGAAGT GTAACCTACC AGCCTCTGCT CTTATCTTTG 1260
 TAATAAATGT TAAAGCCAGA AAAAAATAAA AAAAAAAAAA AAAAAACTCG AGGGGGGCCC 1320
 15 AGACCCAATC TCCCTATAGT AAGNCGCCNN ANAN 1354

20

(2) INFORMATION FOR SEQ ID NO: 206:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1378 base pairs
 25 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 206:

30 TCCCCAGGTG CACAGCCAGG GCCCTCCTGT CTGCAGGAGA ATTCACAGCT GGTGTGGGAC 60
 TCAGCCCCCTA GNCCATTCAA AGCCTTAATG TTGTAATCAT ATCTTACGTG TTGAAGACCT 120
 35 GACTGGAGAA ACAAATGTG CAATAACGYG AATTTTATCT TAGAGATCTG TGCAGCCTAT 180
 TTCTGTCAACA AAAGTTATAT TGTCTAATAA GAGAAGTCTT AATGGCCTCT GTGAATAATG 240
 TAACTCCAGT TACACGGTGA CTTTAAATAG CATACAGTGA TTTGATGAAA GGACGTCAAA 300
 40 CAATGTGGCG ATGTCGTGGA AAGTTATCTT TCCCGCTCTT TGCTGTGGTC ATGTGTCTT 360
 GCAGAAAGGA TGGCCCTGAT GCAGCAGCAG CGCCAGCTGT ANATAAAAAA TAATTCACAC 420
 45 TATCAGACTA GCAAGGCACT AGAAGTGGAA AAGACCACAG AAAACAAAGA ATCCAACCTT 480
 TTCATCTTAC AGGTGAACAA ACTGTGATGA TGCACATGTA TGTGTTTGTG AAGCTGTGAG 540
 CACCGTAACA AAATGTAAAT TGCCATTAT TAGGAAGTGC TGGTGGCAGT GAAGAAGCAC 600
 50 CCAGGCCACT TGACTCCAG TCTGGTGCCC TGTCTACACC AGACAACACA GGAGCTGGGT 660
 CAGATTCCCC TCAGCTGCTT AACAAAGTTC CTCGAACAGA AAGTGCTTAC AAAGCTGCCT 720
 55 TCTCGGATAC TGAAAGGTCG AGTTTCTGA ACTGCACGTA TTTTATTGCA GTTGAAAAAA 780
 AAAAAAGCT ATTCCAAAGA TTTCAAGCTG TTCTGAGACA TCTTCTGATG GCTTTACTTC 840
 CTGAGAGGCA ATGTTTTTAC TTTATGCATA ATTCATTGTT GCCAAGGAAT AAAGTGAAGA 900
 60

AACAGCACCT TTTAATATAT AGGTCTCTCT GGAAGAGACC TAAATTAGAA AGAGAAAAC 960
 GTGACAATTT TCATATCTTC ATTCTTAAAA AACACTAATC TTAAC TAACA AAAGTTCTTT 1020
 5 TGAGAATAAG TTACACACAA TGGCCACAGC AGTTTGCTTT TAATAGTATA GTGCCTATAC 1080
 TCATGTAATC GGT TACTC TACTGCCCTTT AAAAAAAAA ACCAGCATAT TTATTGAAAA 1140
 10 CATGAGACAG GATTATAGTG CCTTAACCGA TATATTTTGT GACTTAAAA ATACATTTAA 1200
 AACTGCTCTT CTGCTCTAGT ACCATGCTTA GTGCAATGA TTATTTCTAT GTACAACTGA 1260
 TGCTGTCTCT TATTTTAATA AATTTATCAG AGTGAAAAA AAAAAAAAA AAAAAAAAA 1320
 15 AAAAAAAAA AAAAAAAAA AAAAAAAAA AAAAAAAAA AAAAAAGAA NAAAAANA 1378

20 (2) INFORMATION FOR SEQ ID NO: 207:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1166 base pairs
 (B) TYPE: nucleic acid
 25 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 207:

30 AANCCACTGC ANTTTAAACC CCTCCCTC CAAGAAAGTT CACAACCGGC CATGGATGAC 60
 CCTCATTTTA GATGGGCCNC AATATTAAAG ATGGACTGRG GMCCCARAG ACTGACCCTT 120
 35 GAAAGGGGGA CTCAGAAGAA AGATCCTGA CATTGCCMAA CATGCTGGGC TTGTCCAACA 180
 CAGTGATGCG GCTCATCGAG AARCGGCTT TCCMAGGACA AGTACTTTAT GATAGGTGGG 240
 ATGCTGCTGA CCTGTGTGGT CATGTTCTC GTGGTGCACT ACCTGACATG AGCCAGCCAC 300
 40 GCTCAGTGGC TGAACAGCAT TCCCACAGCC TGCAAGTGTG TGTGTGTGTG AAAGAGAGAG 360
 GGGGCCAGA GGCCGCTTT TGAAATGTTT GCCTGTCTGA ACTGTGAAGA CACTTGGGAG 420
 TGATTGTGGT CTAATTTCCA ACCTGCTCTG TTTTCTGTGA CATCTTGGAG GGGGAGCTAG 480
 45 TGCCAMCACC ATGCGCGGTG CTTAGGAAAT GAAAGAAGTC CCGGTCTGT CTCTCTCACT 540
 CTCGCTCTCA MTGGGGGAGG GAAAGAATGG CTTTGGTGGC TTGTTCACA CAGCTGATGC 600
 50 GTGSCCTGGG AAGGTGTCCA CAGTGAGCCC TGTGTGCAGG ACTGTCCACN ACGGTTTACA 660
 CCTGTCAACC ATCAGGCTT TCTGGCTCCT GATAGGTGG AGCAAAAGTG GAAAGGAAAG 720
 GAAAGAGGCY TTTTCTCACA GCCATTATAT TAAATAGTAG GTCGATTCAC ATCTCGTGC 780
 55 TCCTGGCCAC CCTCCCTGT GCCTCAGTGA CATGTAGATG ACTGACTGCC AATACTTGTG 840
 ACCATTCCCT GGAAGCAGCT ACCTAGGGGA AACAAGATGT AGTGCTATTG CCGATAACAA 900
 60 GTAAGATTTT CCACACTACA GCTGGGTGTT TCTCTTTTCT AAAGTGAGGC CAGTGTATT 960

TCCCGGGAGT GTTCAGTCTT GACCCTAGTC ACTGATTTT TCTAGTTGTT AATAGAGTGG 1020
 5 TTGGGCTTTT AAGGTTTACA GACTGTGGGC TTGGGCACCT GCGCCCAGGG STTTTGTGGG 1080
 GGCCTTTGCC CCTTAGRAAA GTAGCTTTTA GGGGCAAAGA TTTGTGATT TTCCCCATTA 1140
 CAGTCTTCAG CTCNAGGGTT TTAAAA 1166

10

(2) INFORMATION FOR SEQ ID NO: 208:

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(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 697 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 208:

TACTTCTAGG ATTATAAGGA ATTAACATTG AGATGACATT TCCATTTGAG AAGGAAAATA 60
 25 GTTGCTTTCA GTGCCCTTTA TTTGATTCTT GGAGAGAGCA GACTGCGACS AACATTCAAC 120
 CCCAGCGCTG ATATGACAGT AATCCTCAGA GGCAGAGCCC AGCACAAAAC AGCAATGCTA 180
 30 GAAAGTTACA ATTGGAAAGT TTCCTGCCAG CTCGGGAAT GACACTGCAA AGCTGATGCC 240
 AGAAACTGCC AGRGTAATTC TCCTCATTAC TGCTCTACCC ACCCACTTTC AGCTCCCCAA 300
 ATTAAGTAGT GCAGTTGACT AATCTCTTTT ACCTTTATCA TTTARGGTGA RGCATTGCAC 360
 35 AAAAAGTCTC GACTTTGCCA TATAAGGGCT GTGGTCTCTT GTGGTCCCTT GGATAAGAGG 420
 CATCACCATT ATCTGGAAAC ATGCAGTAAA TGCAGATINT TCATCTTCTC CCCAGACCTC 480
 CTGAGTTAGA AATTCAACAAG TTCTCCAGGT GATCTCATAC ATGCTAAAGT TTGAGAACCA 540
 40 TTGAGTAAAG TTAATGCATT AAGAAGAGAT TAGATAGGGA TGGTGGCGTA TCTTCCTACA 600
 GTTTCCTGT TAACAAGAAA GTCAGAGGTC AGTTGATCAG ACATTAGATT ATTTATGCT 660
 45 AAAACTAAAA AAAATTAAAA AAAACTGGAG GGGGGCC 697

50

(2) INFORMATION FOR SEQ ID NO: 209:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 932 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 209:

60 CGTGAGTCAC CTCTCTATAG TGGGCGTGGC CGAGGCCGGG GTGACCCTGC CGAAGCCTCC 60

5 GCTGCCAGAA ACCATGTTCA AGGTAATTAA AAGGTCCGTG GGGCCAGCCA GCCTGAGCTT 120
 GCTCACCTTC AAAGTCTATG CAGCACCAAA AAAGGACTCA CCTCCCAAAA ATTCCGTGAA 180
 GGTGATGAG CTTTCACTCT ACTCAGTTCC TGAGGGTCAA TCGAAGTATG TGGAGGAGGC 240
 AAGGAGCCAG CTTGAAGAAA GCATCTCACA GTCCTGACAC TATTGCGAGC CATACACAAC 300
 10 CTGGTGTGAG GAAACGTACT CCCAACTAA GCCCAAGATG CAAAGTTTGG TTCAATGGGG 360
 GTTAGACAGC TATGACTATC TCCAAAATGC ACCTCCTGGA TTTTTCCTGA GACTTGGTGT 420
 TATTGGTTTT GCTGGCCTTA TTGGACTCCT TTTGGCTAGA GGTTCAAAAA TAAAGAAGCT 480
 15 AGTGTATCCG CCTGGTTTCA TGGGATTAGC TGCCTCCCTC TATTATCCAC AACCAAGCCAT 540
 CGTGTTCGCC CAGGTCAGTG GGGAGAGATT ATATGACTGG GGTTCACGAG GATATATAGT 600
 20 CATAGAAGAT TTGTGGAAGG AGAACTTTCA AAAGCCAGGA AATGTGAAGA ATTCACCTGG 660
 AACTAAGTAG AAACTYCAT GYTCTGCCAT CTTAATCAGT TATRGGTAAA CATTTGGAAC 720
 TCCATAGAAT AAATCAGTAT TTCTACAGAA AAATGGCATA GAAGTCAGTA TTGAATGTAT 780
 25 TAAATTGGCT TTCTTCTTCA GGAAAACTA GACCAGACCT CTGTTATCTT CTGTGAAATC 840
 ATCTTACAAG CAACTAACC TGAATCCCT TCACCTAGAG ATAATGTACA AGCCTTAGAA 900
 30 CTCCTCATTC TCATGTTGCT ATTTATGTAC CT 932

35 (2) INFORMATION FOR SEQ ID NO: 210:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 661 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 210:

45 GTCATTCTTT AAATAAAAGC TTTCCTGTTT AAAGCTTTTC AAAGGAGCAG ACCACCTTGA 60
 AGATTCCCC TAGGGTTGAT ATGTGTCTAA TTCATTTTAT AAAAATTATT CTGTCTTCA 120
 TTTTAAAGCT TTGGCTATAT AGTCAGAAAT GTCCTAAATA ACAAATATT TTGTATTAA 180
 50 TTTAGGAAG ACTAAAGGA AGAAAAATGA AAATCAGTC TTTATGTAAG CTCCAAGGAT 240
 ATTAGGCTT AAAGGCTTT TCTAGTTTAA TGAGAAATTTG TACTACTGAT TTTTATATAT 300
 55 TCCTGTTTTT GAGATGAACA GATCTCTGGG GAAATTGTTG AGTTACAATG GCATTTCACT 360
 GTGATCCCTC TCAAGCTCAG ATCAGTTCTA TAACCCAATG ACAACCTGTC TCTTTGGTTT 420
 ACTGTCCTGT GAAATGTCAG CTCAAGTTTC CCAGAAGTCG TGTGTTTATG ATGAGTCAGA 480
 60

GTGCTTTTCC TCGGTGGGAC AGTTGCTGGC CCTCTTAATT TTGGTGTATG TGCTTCCAAG 540
 TATCTAAACC TCCAGTCTGA TCTGTATATG CTATCCTAAC TGTTAATGT ATTATGATT 600
 5 ATGTTGATTA TCTTGCTTGA AGGTTTCATAC TTTTCAATTT GATAGAAATA AAGTTTTTTT 660
 C 661

10

(2) INFORMATION FOR SEQ ID NO: 211:

15 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 592 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 211:

GAAACTGACA TTGTTAAACA CACTAAAACA GAAGTACTTA CCTCTGAAG ATTTAATATA 60
 TAATGGTTGA CATGATACAT GTACATGAAT GGAATGACCA GATGCTTATG GTCTACATTT 120
 25 TCCTTTATCC TGTTAGTATT ACCTTCCTTA ATCTTTGTTC CTTAACATGC TAAATTCCTC 180
 TTCAGTGTIT ATTTTCTAGT GACAGAATGC TAACATTTCT TACACCCTGG CAGAAGGGAG 240
 30 AGAAATGTGT TTTGGGGTGG GTAACATAAT TTTTGAGTGA AATATCATAA GATGAGAATG 300
 GAAAGAGGGA GACACAAAGA GTTATAACAA AAAACAATG GTTTTTTTAG CCATTTGACT 360
 GGCTCTTTAA ATAGTCTACA AGACATTCAC GTTNAACATC ACTTTTAGTG AAATAAAATG 420
 35 TGCCATACTA GTATGTGCTT CAAAAGGGCA AATGTGCTTT AGTGCCCTAA GGCTAAATTT 480
 TGGTCATTG ACATCAGAGA TGTTGTAAGT ATTGCACITTA ATACGCACCT ATTTCTCAAT 540
 40 AGTGNATTTT TTTTGGCTAG CATTTNCTTT ACCACTAACC TTGTTGGATA GC 592

45 (2) INFORMATION FOR SEQ ID NO: 212:

50 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 938 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 212:

55 TGGAGTGGCT TTCCAGCTGA ATGAATCCTA TGTCTGCGT GCAGGTGGTT GGTMTTCAAT 60
 GTTCTTSC TAATTTTTTCC TATGGCTCT TGGGAGTTN CTTGTPTGC TCCTGTGTTT 120
 60 GCCCAGCTTT AATAAAACCA GGCGCAAACA AAAACCATAG CATCTGAAA CAATAGGGGG 180

	CCCACATGG ACCCAGTATG TCACTTTAAT GGACTTCAAG AAAAAATCTG AATGGGAAAA	240
	TGACACTAGG AATGTATACT CCACACATTT TATGCCATAT AATGGTGTGT TTTCTTAATT	300
5	TTGTTTCTMG TGGCGAAATG TGGCTTTCAA ATTAAATGM CCTTTTCTTC TTKGAACTT	360
	TTTGTTTKGA CTGTATAAT TAAGGGTTTG GAAAGATTCA TAATTMTGAG AGAGGTTTGC	420
	AACCAGGAGA TACAAAGAAG TCTCAGTAGT AATCTTGTTC ATGTGCTTTT ACAGCCAGCT	480
10	ACATTTAAGR ATGTATTAGT TACAGAAATT ATATGTCTGT GTATGTGTCT CTA CTCAATA	540
	AAGTACATGC CTCCACATAA TGCGGTGCTG TCCATCTCGG CAAATACTGG CCAAGTCCCT	600
15	TTATGACAGG CACACAGAAA CCATAGCATG GTCTGGCTTT CAGAAAATGC CTCTCATCTT	660
	TCCTGGAACC TTATTTTGCT AAATGTCTGT TTTCTTGTGA TTTGTGTAC CTCACAGCAC	720
	CATGTGACC ATGGTGATGC CTCATTGCA TGATATGTAC CTTGTGTTTA ATGTGAAATA	780
20	CATTTTCATT GAAGAGTCTG ATGACTTGCT AGCGTTTAT TTTTCTGTA AGCTCAATGT	840
	GCTGAAACCA AACCAGGCTT TTA AAAACCT GTGTAGAAGA AAACCAAAA ATCCTGTGTG	900
25	GGTGTCTTTT CCCTGTCAAA CTCATTAAAA ATTCCTTT	938

30 (2) INFORMATION FOR SEQ ID NO: 213:

(i) SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH: 1079 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 213:

40	AGCCTGCCGG GAGAGTGGTG GCATCTRARA GGCTGGTCGT GGACTGTGGT TGGGGGAGGT	60
	GGGAGCTGTT TTAACCGTGT GCCCCCTCTC CTGTGCKGC GTGGGCATCC CCCGGGCAG	120
	TGGAACGCGG GCGTCTCTCC AGCTTCCGAG TCCAGCCAGC CTGGGCGCGG GCGCGCCCC	180
45	CGAGACACCC GAGGAGTCCG TTCTTCCCTG GTTACGTGGA CTGTGGAGCT GGTCTCTTGT	240
	GGCTCAGCGC CGTGCGGAGG TTGAAGCGTA CCTGCGGAGG TCGCACCAGG GCGGTGAGGA	300
50	GGAGGAGGAA GGGCATGAGC CGAGCTTGAG GAATCCGTGY TCCAACTCT ACACTCAAGG	360
	RTGCMCTGCG CAACTCTGGT GCGATGGGC TGGGGCAGAT GTCCCTGGAG TTCTACCAGA	420
	AGAAGAAGTC TCGCTGGCCA TTCTCAGACG AGTGCATCCC ATGGGAAGTG TGGACGGTCA	480
55	AGGTGCATGT GGTAGCCCTG GCCACGAGC AGGAGCGGCA GATCTGCCGG GAGAAGGTGG	540
	GTGAGAAACT CTGCGAGAAG ATCATCAACA TCGTGGAGGT GATGAATCGG CATGAGTACT	600
60	TGCCCCAAGAT GCCCACACAG TCGGAGGTGG ATAACGTGTT TGACACAGGC TTGCGGGACG	660

5 TGCAGCCCTA CCTGTACAAG ATCTCCTTCC AGATCACTGA TGCCCTGGGC ACCTCAGTCA 720
CCACCACCAT GCGCAGGCTC ATCAAAGACA CCCTTGCCCT CTGAGCGTCG CTGGATCTCT 780
GGGAGCTCCT TGATGGCTCC CAGACCTTGG CTTTTGGGAA TTGCACTTTT GGGCCTTTGG 840
GCTCTGGAAC CTGCTCTGGG TCATTTGGTGA GACTTGGAAG GGGCAGCCCC CGCTGGCTTC 900
10 TTGGTTTGT GGTGCCAGC CTCAGGTCAT CCTTTAATC TTTGCTGACG GTTCAGTCCT 960
GCCTCTACTG TCTCTCCATA GCCCTGGTGG GTCCCCCTT CTTTCTCCAC TGTACAGAAG 1020
AGCCACCACT GGGATGGGA ATAAAGTTGA GAACATGAGT TTGGCTGAA AAAAAAAAAA 1079
15

20 (2) INFORMATION FOR SEQ ID NO: 214:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 3791 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
25 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 214:
30 TGAAGCAGGC GCTCTTGGCT CGGCGCGGCC CGCTGCAATC CGTGGAGGAA CGCGCCGCCG 60
AGCCACCATC ATGCTTGGC ACTTACAGGA AGGCTTCGGC TGCCTGGTCA CCAACCGATT 120
CGACCAGTTA TTTGACGACG AATCGGACCC CTTCGAGGTG CTGAAGGCAG CAGAGAACAA 180
35 GAAAAAAGAA GCCGGCGGG GCGCGTTGG GGGCCCTGGG GCCAAGAGCG CATCAGGGCC 240
GCGGCCCAGA CCAACTCCAA CGCGGCAGGC AAACAGCTGC GCAAGGAGTC CCAGAAAGAC 300
CGCAAGAACC CGCTGCCCC CAGCGTTGGC GTGGTTGACA AGAAAGAGGA GACGCAGCCG 360
40 CCCGTGGCGC TTAAAGAAAG AAGGAATAAG ACGAGTTGGA AGAAGACCTG ATCAACAACT 420
TCAGGTGAA GGGAAATAA TTGATAGAAG ACCAGAAAGG CGACCACCTC GTGAACGAAG 480
45 ATTCGAAAAG CCACTTGAAG AAAAGGGTGA AGGAGGCGAA TTTTCAGTTG ATAGACCGAT 540
TATTGACCGA CCTATTGAG GTCGTGGTGG TCTTGAAGA GGTGAGGGG GCGTGGACG 600
TGGAATGGC CGAGGAGATG GATTTGATTC TCGTGGCAA CGTGAATTG ATAGGCATAG 660
50 TGGAAGTGAT AGATCTTCTT TTTCACATTA CAGTGGCCTG AAGCACGAGG ACAAACGTGG 720
AGGTAGCGGA TCTCACAAC GGGGAACGT CAAAGACGAA TTAAGTACT TGGATCAATC 780
55 AAATGTGACT GAGGAAACAC CTGAAGGTGA AGAACATCAT CCAGTGGCAG AACTGAAAA 840
TAAGGAGAAT GAAGTTGAAG AGGTAAAGA GGAGGTCCA AAAGAGATGA CTTTGGATGA 900
GTGGAAGGCT ATTCAAAATA AGGACCGGC AAAAGTAGAA TTTAATATCC GAAAACCAA 960
60

	TGAAGGTGCT GATGGGCAGT GGAAGAAGGG ATTTGTTCTT CATAAATCAA AGAGTGAAGA	1020
	GGCTCATGCT GAAGATTGCG TTATGGACCA TCATTTCCGG AAGCCAGCAA ATGATATAAC	1080
5	GTCTCAGCTG GAGATCAATT TTGGAGACCT TGGCCGCCA GGACGTGGCG GCAGGGGAGG	1140
	ACGAGGTGGA CGTGGGCGTG GTGGGCGCCC AAACCGTGGC AGCAGGACCG ACAAGTCAAG	1200
10	TGCTTCTGCT CCTGATGTGG ATGACCCAGA GGCATTCCCA GCTCTGGCTT AACTGGATGC	1260
	CATAAGACAA CCCTGGTTCC TTTGTGAACC CTCTGTTC AAGCTTTTGC ATGCTTAAGG	1320
	ATTCCAAACG ACTAAGAAAT TAAAAAATAA AAGACTGTCA TTCATACCAT TCACACCTAA	1380
15	AGACTGAATT TTATCTGTTT TAAAAATGAA CTCTCCCGC TACACAGAAG TAACAAATAT	1440
	GGTAGTCAGT TTTGTATTTA GAAATGTATT GGTAGCAGGG ATGTTTTCAT AATTTTCAGA	1500
20	GATTATGCAT TCTTCATGAA TACTTTTGTA TTGCTGCTTG CAAATATGCA TTTCCAAACT	1560
	TGAAATATAG GTGTGAACAG TGTGTACCAG TTAAAGCTT TCACTTCATT TGTGTTTTTT	1620
	AATTAAGGAT TTAGAAGTTC CCCCAATTAC AAACGTGTTT TAAATATTGG ACATACTGGT	1680
25	TTTAATACCT GCTTTGCATA TTCACACATG GTCAACTGGG ACATGTTAAA CTTTGATTTG	1740
	TCAAATTTTA TGCTGTGTGG AATACTAACT ATATGTATTT TAACTTAGTT TTAATATTTT	1800
30	CATTTTGGG GAAAAATCTT TTTTCACTTC TCATGATAGC TGTATATAT ATATGCTAAA	1860
	TCTTTATATA CAGAAATATC AGTACTTGAA CAAATTCAAA GCACATTGGG TTTATTAACC	1920
	CTTGCTCCTT GCATGGCTCA TTAGGTTCAA ATTATAACTG ATTTACATTT TCAGCTATAT	1980
35	TTACTTTTTA AATGCTGAG TTTCCCATTT TAAAACTAA ACTAGACATC TTAATTGGTG	2040
	AAAGTGTGTT AAACACTTA TTGTTGGTAG GCACATCGTG TCAAGTGAAG TAGTTTATA	2100
40	GGTATGGGTT TTTTCTCCCC CTTCAACAGG GTGGGTGGAA TAAGTTGATT TGGCCAATGT	2160
	GTAATATTTA AACTGTCTG TAAAAAAGT GTCTGGCCAT TTGGTATGAT TTCTGTGTGT	2220
	GAAAGGTCCC AAAATCAAAA TGGTACATCC ATAATCAGCC ACCATTTAAC CCTTCCTTGT	2280
45	TCTAAAACAA AAACCAAAGG GCGCTGGTGT GTAGGTGAG GTGGGGGAGT ATTTTAATTT	2340
	TTGGAATTTG GGAAGCAGAC AGCTTTACTT TGTAAGGTTG GAACAGCAGC ACTATACATG	2400
50	AAATATAAAC CAAAAACCTT TACTGTTTCT AAATTCCTA GATGCTATT ATTTGGTTGT	2460
	AAGTTGAGTA TTCCACAGAA AGTGGTAATT ATCTCTTCTC TCTTCCTCCA TTAGAAAAAT	2520
	AGGTAAATAA TGGATTCCCTA TAATGGGAGC ATCACCCTT ATTAACACAC ACATAGAATG	2580
55	ATGAATTAAA AAAGTTTCTT AGGATTGTCT TTTATCTGTC CACATTTATT GATAAACAGT	2640
	GAAGGAATTT TTAATAAATT TTTAAGAATT GTTTGTCACG TCATTTTATG AAATGTTCTA	2700
60	CCTGTATATG GTAATGTCCA GTTTTAAAAA TATTGGACAT CTTCAATCTT AAACATTTCT	2760

	ATTTAGCTGA TTGGTTCTCA CATATACTTC TAAAAGAAAC TTTTATGTTA TAAGAGTTAC	2820
	TTTTTGATA AGATTATTA ATCTCAGTTA CCTACTATTC TGACATTTTA GGAAGGAGGT	2880
5	AATGTMTT AATGATGGAT AAACCTGTGC TGGTGTMTG GATCTTATGA TGCTGAGCAT	2940
	GTCTGCACT GGTGCTAATG TCTAATATAA TTTTATATTT ACACACATAC GTGCTACCCA	3000
10	GAGATTAATT TAGTCCATAT GAACTATTGA CCCATTGTTC ATTGAGACAG CAACATACGC	3060
	ACTCCTAAAT CAGTGTGTTT AGACTTTTCA AGTATCTAAC TCATTTCCTAA ACATGTACCA	3120
	TGTTTTATAA ACCTCTTGAT TTCCAGCAAC ATACTATAGA AAACACCTGC TACTCAAAAC	3180
15	ACAACTTCTC AGTGTCATCC ATTGCTGTGC TGAGAGACAA CATAGCAATA TCTGGTATGT	3240
	TGCAAGCTTT CAAGATAGCC TGAACCTAAA AAGTTGGTGC ATTAGTTGTA TCTGATGGAT	3300
20	ATAAATTGTC CTCCTAGTTC ACTTTGTGTC AAGAGCTAAA ACTGTGAACC TAACTTTCTC	3360
	TTATTGGTGG GTAATAACTG AAAATAAAGA TTTATTTTCA TGCTCACTTC TTAAAAGTCA	3420
	TAAAAACAAT CAAATAGGRT CATGTTTATT GTCATGTGTT TCCTGGKTTT TGACCTGTGT	3480
25	GCACACCCCT GTGTGTTTAT AATTTTAA TGAATTTTA TATGGGGTTT TTATTTGCTA	3540
	AAAACCAGGC TGTGAATCA CATTTGGGAA GGGTACTTAT CTTAATGACT AATGACTTAA	3600
30	TTGGGAAAGT TGAATTCCTG TAAATACAA AATCCAAGGA CTTCTTGGGA TTTAATCTAA	3660
	TTGTCACTTC NTTAGGCAGA TNCATTTTTT TGGATAATGG AAAGTTAAGC ATACCGAATG	3720
	CTACTTTTGG TTGACAAACG GGCCTAATAG TCCGGGGGGA AATCCCTAAC NGGTAAGGNT	3780
35	CCCAAGTATG G	3791

40 (2) INFORMATION FOR SEQ ID NO: 215:

(i) SEQUENCE CHARACTERISTICS:

- 45 (A) LENGTH: 1334 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 215:

50	CAGTGCTCGC TCCTGCTCGG GCGCTGCGG CCCCAGGCGT CGCCATGACC AGTGAGCTGG	60
	ACATCTTCGT GGGGAACAGA CCCTTATCGA CGAGGACGTG TATCGCCTCT GGCTCGATGG	120
55	TTACTCGGTG ACCGACGCGG TGGCCCTGCG GGTGCGCTCG GGAATCCTGG AGCAGACTGG	180
	CGCCACGGCA GCGGTGCTNC AGAGCGACAC CATGGACCAT TACCGCACCT TCCACATGCT	240
	CGAGCGGCTG CTGCATGCGC CGCCCAAGCT ACTGCACCAG YTCATCTTCC AGATTCCGCC	300
60	CTCCCGGCAG GCACTACTCA TCGAGAGGTA CTATGCCTTT RATGAGGCCT TTGTTCCGGA	360

	GGTGTCTGGC AAGAAGCTGT CCAAAGGCAC CAAGAAAGAC CTGGATGACA TCAGCACCAA	420
5	AACAGGCATC ACCCTCAAGA GCTGCCGGAG ACAGTTTGAC AACTTTAAAC GGGTCTTCAA	480
	GGTGGTAGAG GAAATGCGG GCTCCCTGGT GGACAATATT CAGCAACACT TCCTCCTCTC	540
	TGACCGGTTG GCCAGGGACT ATGCAGCCAT CGTCTTCTTT GCTAACAACC GCTTTGAGAC	600
10	AGGGAAGAAA AACTGCAGT ATCTGAGCTT CGTGACTTT GCCTTCTGCG CTGAGCTCAT	660
	GATCCAAAAC TGGACCCCTG GAGCCGTCGA CTCACAGATG GATGACATGG ACATGGACTT	720
15	AGACAAGGAA TTTCTCCAGG ACTTGAAGGA GCTCAAGGTG CTAGTGGCTG ACAAGGACCT	780
	TCTGGACCTG CACAAGAGCC TGGTGTGCAC TGCTCTCCGG GGAAAGCTGG GCGTCTTCTC	840
	TGAGATGGAA GCCAACTTCA AGAACCTGTC CCGGGGCTG GTGAACGTGG CCGCCAAGCT	900
20	GACCCACAAT AAAGATGTCA GAGACCTGTT TGTGGACCTC GTGGAGAAGT TTGTGGAACC	960
	CTGCCGCTCC GACCACTGGC CACTCAGCGA CGTGCGGTTT TTCTGAATC AGTATTCAGC	1020
25	GTCTGTCCAC TCCCTCGATG GCTTCCGACA CCAGGCCTCT GGGACCGCTA CATGGGCACC	1080
	CTCCGCGGCT GCCTCCTGCG CCTGTATCAT GACTGAGGTG CCTCCCAACG CTCCGCCCAC	1140
	GCTGACAATA AAGTTGCTCT GAGTTTGGAG ACTGGTCTCT GCTCCGGGGA GCAAGTGGGG	1200
30	GGCGTCAGA TGTGCCTGTG TCTGTCTCTG AGCACCTGGT GTCCGTGTAC AAGGATGGAT	1260
	GTGTNCNGTG GCTCCTTGGG AACTGAGACA TATCTCAGGG AATGGTGTCT GTGCTCAGCC	1320
35	CATCCACCAG AAGA	1334

(2) INFORMATION FOR SEQ ID NO: 216:

40

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1511 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

45

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 216:

50	GTGGCGGGGA TGCTGCGAGG GGGTCTCTTG CCCAGGCGG GCCGGCTGCC TACCTCCAG	60
	ACTGTCCGCT ATGCGTCCAA GGCTGTTACC CGCCACCGTC GTGTGATGCA CTTTCAGCGG	120
	CAGAAGCTGA TGGCTGTGAC TGAATATATC CCCCCGAAAC CAGCCATCCA CCCATCATGC	180
55	CTGCCATCTC CTCCAGCCC CCCACAGGAG GAGATAGGCC TCATCAGGCT TCTCCGCCGG	240
	GAGATAGCAG CAGTTTTCCT GGACAACCGA ATGATAGCCG TCTGCCAGAA TGTGGCTCTG	300
60	AGTGCAGAGG ACAAGCTTCT TATGCGACAC CAGCTGCGGA AACACAAGAT CCTGATGAAG	360

	RTCTTCCCCA ACCAGGTCCT GAAGCCCTTC CTGGAGGATT CCAAGTACCA AAATCTGCTG	420
	CCCCTTTTTG TGGGGCACAA CATGCTGCTG GTCAGTGAAG AGCCCAAGGT CAAGGAGATG	480
5	GTACGGATCT TAAGGACTGT GCCATTCCCTG CCGCTGCTAG GTGGCTGCAT TGATGACACC	540
	ATCCTCAGCA GGCAGGGCTT TATCAACTAC TCCAAGCTCC CCAGCCTGCC CCTGGTGCAG	600
10	GGGAGCTTG TAGGAGGCCT CACCTGCCTC ACAGCCCAGA CCCACTCCCT GCTCCAGCAC	660
	CAGCCCCCTC AGCTGACCAC CCTGTTGGAC CAGTACATCA GAGAGCAACG CGAGAAGGAT	720
	TCTGTCATGT CGGCCAATGG GAAGCCAGAT CCTGACACTG TTCGGACTC GTAGCCAGCC	780
15	TGTTTAGCCA GCCCTGCGCA TAAATACACT CTGCGTTATT GGCTGTGCTC TCCTCAATGG	840
	GACATGTGGA AGAACTTGGG GTCGGGGAGT GTGTTTGTC CTTGGTTTTC ACTAGTAATG	900
20	ATATTGTCAG GTATAGGGCC ACTTGAGAT GCAGAGGATT CCATTTCAGA TGTCAGTCAC	960
	CGGCTTCGTC CTTAGTTTTC CCAACTTGGG ACGTGATAGG AGCAAAGTCT CTCCATTCTC	1020
	CAGGTCCAAG GCAGAGATCC TGAAAAGATA GGGCTATTGT CCCCTGCCTC CTTGGTCACT	1080
25	GCCTCTTGCT GCACGGGCTC CTGAGCCACC CCCTTGGGGC ACAACCTGCC ACTGCCACAG	1140
	TAGCTCAACC AAGCAGTTGT GCTGAGAATG GCACCTGGTG AGAGCCTGCT GTGTGCCAGG	1200
30	CTTTGTGCTG AGTGCTGTAC ATGTATTAGT TCCTTTACTG CTGACCACAT TGTACCCATT	1260
	TCACAGAGAA GGAGCAGAGA AATTAAAGTG CTTGCTCAAG GTCATGCAGT TAGTAAGTGG	1320
	CAGAACAGGG ACTTGAACCA AGCCCTCTGC TCTGAAGACC GCGTCCTGAA TTTCTTCACT	1380
35	AGAGCTTCCT CATCAGGTTA CCCAGAAGTG GGTCCCATCC ACCATCCAGG TGTGCTTGGA	1440
	TGTTAGTTCT CCACCCTCGA GGTGTACGCT GTGAAAAGTT TGGGAGCACT GCTTTATAAT	1500
40	AAAATGAAAT A	1511

45 (2) INFORMATION FOR SEQ ID NO: 217:

- 50 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 642 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 217:

55	AGGCCTTACT TTTCCTCCCA CAAAGGAGTC GCAGCCACGC TAGCTCTGAC TTGCCACTGT	60
	GACAAAGTTC ACGTAGCAGG TCTAGGCAAA GACTGGGCAA TTGAGCAGAG GAGACGGACC	120
	TGTGAGTCTG ACCRYGAGSC GGRCCCTTC ACCTTGGCTG GGCTGGTCCT GGTCCCTTAGG	180
60	TTTTGTGAGG TTGTCCTTGT TTGGATCCCT CAACTAGGTG ATAAGCACTG GAGGGGGATG	240

ACCCGCCTTG GACGTGTTTC TTAAACCTCA TCCATATAAT AGGGCCGTGG GATGGTTGTA 300
 GAGGTAAAGC AGGATGATGG TGTTTTAAGA CCAGAGCTTG GGACCAGGGC TCCTACACCT 360
 5 AATTTTCTCT CCTGGTAGCT GAACAAAGGT CTAAATTAGC TTAACAAAAG AACAGGCTGC 420
 CGTCAGCCAG AGTTCTGAAG GCCATGCTTT CAGTTTCCCT TGTGACAAT TGCTCTCCAG 480
 10 TTCTTATGAA AGCACAGAGC CTTAGGGGGC CTGGCCACAG AACACAACCA TCTTAGGCCT 540
 GAGCTGTGAA CAGCAGGGGG TTGTGTGTCT GTTCTGTTTC TCTGCTTGCC GAACTTTCTC 600
 AATAAACCTT ATTTCTTATT TTATATTAC GTNGGTGCTG GG 642
 15

20 (2) INFORMATION FOR SEQ ID NO: 218:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1241 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 25 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 218:

GGTCCCACTG TTCCATTTTA TGCTAATAGA TTCCATTCTA GGGCCCAGCC GTCTCTTGAC 60
 30 TGATGGTGT CCCTTTAACC CTTGGCATGT ATAATAGAAT TTTGGTGAAT GAAAGAACCC 120
 AAATAGGCCA GATAGTCCCC CCAGGCCCTG ATATCCATAA AAGGCTTGGG AATGCATTAT 180
 35 GTAATGTGCC TTAGTCTTTT TGTGTTTTAA GAAAAAACA ACAAGATGGG CTCAGATGGA 240
 TGCCTACGTA AAAATGGTTC CTAGCTGTGT ACTCATAACT TTTCTTTGAA TTGAGTAGTG 300
 AAAGGAAGGA GGAGGAAAGG AAATTAAATG TCCTTCTAGT ATTCTCTGGA CTCAAGTCTG 360
 40 ACATATGRGA TAATAACCTA TATTGAAATG CCAAGAATTG TATCTGAAAC AAGRGAACAG 420
 TTTGACACAT TTATCATGCC TTCATATTAC ATATTAACTG AAACCAATTA ATAAACATAT 480
 45 GAAATATCCA TTGCACAAGG CAAAGGCACC TAAACCTTTT GTTCTTTTTC CTACATAGCA 540
 GAAATTGATT TTTTTTTTAT TTTTTTAGGG GAACCTATAT AATTATGACC CAGTGATGTC 600
 TTTTGGTGAC TTAAGCTTAT GAATTCAGGT TACAATGAG TTGATTCTAG ATGGTTACTA 660
 50 CCTTGAAAAG GATGTTGGTG CCTTATGTGA CAGGAGCCAG AGCCTGCTGG GAATAAACAA 720
 AGCAGATTCA TGCCAACACC AACTCGTAGC TTTAGTGGCA GATGGGAGTG GTCACAGACT 780
 55 CCCAAATGT GGGGCTTTGG ATTTCCACAC CATCCACGT GTGTGTCATC TTCTCTTTTC 840
 ACACTCTTGA TGATAATTG AAAATGRTGA AATCACCTCT GAATTTGCCT ATAGCATGAG 900
 CACATTCTTA TGACAACATA ACAAATAGTT CATAATGTGA ATATTAGAAA CTGTTACAGC 960
 60

CTGCAGTTAC CATAATTTTC CATGTTTGTG GAATTGATAT TGAAATAGCA GGGCTAAGGA 1020
 ATTACTGGCA AGTTTTFAGCC TGTGGGTAAT ACCTTAGGGT TATTTAAATA TTTGTAATTT 1080
 5 TATTTAAATG TTCATGAATG TTTGAAAGGA ACAAATTAT CAGGGATGGC TCTTTGCCAT 1140
 GGGTCTTATT TTCACCTCT TTTCTGTAAG AAAAAAGAAC AATGCTTAA TGTATTTTAA 1200
 10 AAGTTTTTGG TATAGTTTCT AATTCCAATT TTAATAAAG T 1241

(2) INFORMATION FOR SEQ ID NO: 219:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1080 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 219:

TGTTTATGTG ACCTAAAACA TACACACATG CACACACACA TACATATCCA TTCATTCAAT 60
 25 CATCAAGTG GTGTTCCAG TGTCTGTGTG TCACTGTTTA TGCAGTTTCC ATTTCCCAAT 120
 GAATTATGAG TGGAGGGCAA CTTTCTAAC CAGATTGTCT TTTCAGAACA AAGACCKGGG 180
 30 RATTGAGGAA GAGTTTGAA AGAGGGAGAG GCAAGGAAAG AGAGCTTTAA ATTGAAAGGT 240
 TAATTTCTTA AGAGGAACCT GGGCTGAATG ACTACAGTGT TATACCTCTC AATCTTTGCA 300
 GGTGGGCATG GAACACTGCT TGTATCACTC TGTGCACGGT ATAAATCCAT ATATCCACAA 360
 35 AAACACACAT CCATCCATCA ACATATACAT GGTTTGGGAT GAGCAGGTCA ATAGTTTGA 420
 GAGGGAGTTT GTTCCTTTT TTTCTCATT ATACTCTTAA ATTGTTGTCA GTTATCAAAC 480
 40 AAACAAACAG AAAAATTGTT TGGGAAAAAC CTTGCATACG CCTTTTCTAT CMAGTGCTTT 540
 AAAATATAGA CTAAATACAC ACATCCTGCC AGTTTTTCT TACAGTGACA GTATCCTTAC 600
 CTGCCATTTA ATATTAGCCT CGTATTTTTC TCACGTATAT TTACCTGTGA CTTGTATTTG 660
 45 TTATTTAAAC AGGAAAAAA ACATTCAAAA AAAGAAAAAT TAACTGTAGC GCTTCATTAT 720
 ACTATTATAT TATTATTATT ATTGTGACAT TTTGGAATAC TGTGAAGTTT TATCTCTTGC 780
 50 ATATACTTTA TACGGAAGTA TTACGCCTTA AAAATACGAA AATAAATTTT ACAAGGTTTC 840
 TGTMTTGTGT GGAAGAGTAA TTGATGTGTC TAAGAAATGAT GPTTGTMTTT TTGGGGTTTT 900
 TGTGTMTTTT TTTTAAATG TTACCAGCAC TTTTMTTGTG AGTTTCACTT TCCGAGGTAT 960
 55 TGTACAAGTT CACACTGTTT GTGAAGTTTG AATATGAAGG AATAATTAAA AAAAAAAAAA 1020
 AAACNCGGG GGGGGCCCG TCCATTGNN CCCAAGGGG CGTTACGGG GTCACGGCCG 1080
 60

(2) INFORMATION FOR SEQ ID NO: 220:

- 5 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1258 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 220:

TGAATTGAGG GCTTAAAGAT AAACATATGG GRITGGAGTT GTGTGTCCAT AGGGTTTCAC 60
 15 TGCCCTATTG ATTGAGTTT ATCCCTATTA ATTTTTTACA GTGAAATTTT ATTAAAGTAT 120
 AATGTACATA TATTTTCAGT GGATTTTGCT CTGAAGGTTT TCCAGTGGTC TGA CTACGAG 180
 ATAGTGC GGC TTCAGCTGTG GGATATTGCA GGGCAGGAGC GCTTCACCTC TATGACACGA 240
 20 TTGTATTATC GGGATGCCTC TGCCCTGTGTT ATTATGTTTG ACGTTACCAA TGCCACTACC 300
 TTCAGCAACA GCCAGAGGTG GAAACAGGAC CTAGACAGCA AGCTCACACT ACCCAATGGA 360
 25 GAGCCGGTGC CTTGCCTGCT CTTGGCCAAC AAGTGTGATC TGTCCCTTG GGCAGTGAGC 420
 CGGGASCAGA TTGACCGGTT CAGTAAAGAG AACGGTTTCA CAGGTTGGAC AGAAACATCA 480
 GTCAAGGAGA AAAAAATAT TAATGAGGCT ATGAGAGTCC TCATTGAAAA GATGATGAGA 540
 30 AATTCCACAG AAGATATCAT GTCTTTGTCC ACCCAAGGGG ACTACATCAA TCTACAAACC 600
 AAGTCCTCCA GCTGGTCCTG CTGCTAGTAG TGTITGGYTT ATTTTCCATC CCAGTTCTGG 660
 35 GAGGTCTTTT AAGTCTCTC CCTTTGGTTG CCCACCTGAC MATTTTATTA AGTACATTTG 720
 AATTGTCTCC TGA CTACTGT CCAGTAAGGA GGCCCATGT CACTTAGAAA AGACACCTGG 780
 AACCCAKGTG CATTTCTGCA TCTCCTGGAT TAGCCTTTSA CATGTTGCTG RCTCACATTA 840
 40 GTGCCAGTTA GTGCCCTCGG TGTAAGATCT TCTCATCAGC CCTCAATTG TGATCCGAA 900
 TTTTGTGAGA AGGATKAGAA ATCAGCACCT GCGTTTITAGA GATCATAATT CTCACCTACT 960
 45 TCTGAGCTTA TTTTCCATT TGATATTCAT TGATATCATG ACTTCCAATT GAGAGGAAAA 1020
 TGAGATCAAA TGTCAATTCC CAAATTTCTT GTAGCCGTT GTTTCAGATT CTTTCTGTCT 1080
 TGAATGTAA ACATCTGATT CTGGAATGCA GAAGGAGGGG TCTGGGCATC TGTGGATTTT 1140
 50 TGGCTACTAG AAGTGTCCA GAAGTCACTG TATTTTTGAA ACTTCTAAG TCATAATTAA 1200
 GTTTCCTTG TCTTGGGCAT CAAGANTAGT TCCAATTTTT TGGGCCGGG CAGGGTGG 1258

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(2) INFORMATION FOR SEQ ID NO: 221:

- 60 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1693 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 221:

	CACAATATAT GAAATAGTAC CCTCTAAAAA AGAGAAAAAA AAAATCAGGC GGTCAAACCTT	60
10	AGAGCAACAT TGTCTTATTA AAGCATAGTT TATTTCACTA GAAAAAATTT AATATCAAGG	120
	ACTATTACAT ACTTCATTAC TAGGAAGTTC TTTTAAAAAT GACACTTAAA ACAATCACTG	180
15	AAAACCTGAT CCACATCACA CCCTGTTTAT TTTCCCTAAA CATCTTGGAA GCCTAAGCTT	240
	CTGAGAATCA TGTGGCAAGT GTGATGGGCA GTAAAAATACC AGAGAAGATG TTTAGTAGCA	300
	ATTAAAGGCT GTTTGCACCT TTAAGGACCA GCTGGGCTGT AGTGATTCTT GGGGCCAGAG	360
20	TGGCATTATG TTTTACAAA ATAATGACAT ATGTCACATG TTTGCATGTT TGTTTGCTTG	420
	TTGAATTTTT GAACAGCCAG TTGACCAATC ATAGAAAGTA TTAATTTCTT TCATATGGTT	480
25	TTTGGTTCAC TGGCTTAAGA GGTTCCTCAG AATATCTATG GCCACAGCAG CATACCAGTT	540
	TCCATCCTAA TAGGAATGAA ATTAATTTTG TATCTACTGA TAACAGAATC TGGGTCACAT	600
	GAAAAAAAT CATTTTATCC GTCTTTTAAG TATATGTTTA AAATAATAAT TTATGIGTCT	660
30	GCATATTGCA GAACAGCTCT GAGAGCAACA GTTCCCATT AACTCTTTCT GACCAATAGT	720
	GCTGGCACCG TTGCTTCCTC TTTGGGAAGA GGAAAGGGTG TGTGAACATG GCTAACCAATC	780
35	TTCAAATACC CAAATGTGA TAGCATAAAT AAAGTATTTA TTTTATGCCT CAGTATATTA	840
	TTATTTAATT TTTTAGGTAA TGCCTATCTC TTGGTCTATT AAGGAAAGAA GCAATCAGTA	900
	GAGAATTCAG GATAGTTTGT TTAAATTTCT TGCAGATTAC ATGTTTTTAC AGTGGCCTGC	960
40	TATGTAGGAA AGGTATTTCT CYATACAACT TGTTTTAACC TTTGAGAACA TTGACAGAAA	1020
	TTATGCAATG GTTTGTTGAG ATACGGACTT GATGGTGCTG TTTAATCAGT TTGCTTCCAA	1080
45	AGTGGCCTAC TCAAGAGGCC CTAAGACTGG TAGAAATTAA AAGGATTTCA AAAACTTTCT	1140
	ATTCCTTTCT TAAACCTACC AGCAAACTAG GATTGTGATA GCAATGAATG GTATGATGAA	1200
	GAAAGTTTGA CCAAAATTTGT TTTTGTGTTG TTGTTGTGTT TTTGAATTTG AAATCAATTCT	1260
50	TATFCCCTTT AAGAAATGTT ATGTATGAGT GTGAAGATCC TAGCGAACCT ATGCTCAGAT	1320
	ATTCATCGTA AGTCTCCCTT CACCTGTTAC AGAGTTTCAG ATCGGTCACCT GATAGTATGT	1380
55	ATTTCTTTAG TAAGAATGTG TTAAAATTAC AATGATCTTT TAAAAAGATG ATGCAGTTCT	1440
	GTATTTATTG TGCTGTGCTT GGTCTTAAGT GGAGCCAATT AAACAAGTTT CATATGTATT	1500
	TTTCCAGTGT TGAATCTCAC AACTGTACT TTGAAAATTT CCTTCCATCC TGAATAACGA	1560
60	ATAGAAGAGG CCATATATAT TGCCTCCTTA TCCTTGAGAT TTCCTACCT TTATGTTAAA	1620

AGTTGTGTAT AATGTGTAAA ATCTGTGAAA GAATAAAAAG TGGATTTAAJ TTAAAAAAA 1680

AAAAAAAAA AAA 1693

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(2) INFORMATION FOR SEQ ID NO: 222:

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(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1196 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 222:

ACGCGTGGGT CGACCCACGC GTCGCGGACN TGGCGTGGTG GGGAAAGGAG AAGGATTTGT 60

20

AAACCCCGGA GCGAGGTCTT GCTTACCCGA GGCCGCTGCT GTGCGGAGAC CCCCGGGTGA 120

AGCCACCGTC ATCATGTCTG ACCAGGAGGC AAAACCTTCA ACTGAGGACT TGGGGGATAA 180

25

GAAGGAAGGT GAATATATTA AACTCAAAGT CATTTGGACAG GATAGCAGTG AGATTCACTT 240

CAAAGTGAAA ATGACAACAC ATCTCAAGAA ACTCAAGAA TCATACTGTC AAAGACAGGG 300

TGTTCCAATG AATTCACCTA GGTTCCTCTT TGAGGGTCAG AGAATTGCTG ATAATCATAC 360

30

TCCAAAGAA CTGGGAATGG AGGAAGAAGA TGTGATTGAA GTTTATCAGG AACAAACGGG 420

GGGTCAATCA ACAGTTTAGA TATTCTTTTT ATTTTTTTTC TTTTCCCTCA ATCCTTTTTT 480

35

ATTTTTAAAA ATAGTTCTTT TGTAATGTGG TGTTCAAAC GGAATTGAAA ACTGGCACCC 540

CATCTCTTTG AACATCTGG TAATTTGAAT TCTAGTGCTC ATTATTCATT ATTGTTTGTT 600

40

TTCATGTGTC TGATTTTGGG TGATCAAGCC TCAGTCCCTC TCATATTACC CTCTCCTTTT 660

TAAAAATTAC GTGTGCACAG AGAGGTCACC TTTTTCAGGA CATTCATTT TCAGGCTTGT 720

GGTGATAAAT AAGATCGACC AATGCAAGTG TTCATAATGA CTTTCCAATT GGCCCTGATG 780

45

TTCTAGCATG TGATTACTTC ACTCCTGGAC TGTGACTTTC AGTGGGAGAT GGAAGTTTTT 840

CAGAGAACTG AACTGTGGAA AAATGACCTT TCCTTAACTT GAAGCTACTT TTAAAATTG 900

AGGGTCTGGA CCAAAAGAAG AGGAATATCA GGTGAAGTC AAGATGACAG ATAAGGTGAG 960

50

AGTAATGACT AACTCCAAAG ATGGCTTCAC TGAAGAAAAG GCATTTTAAG ATTTTTTAAA 1020

AATCTTGTC GAAGATCCCA GAAAAGTTCT AATTTTCATT AGCAATTAAT AAAGCTATAC 1080

55

ATGCAGAAAT GAATACAACA GAACACTGCT CTTTTTGATT TTATTTGTAC TTTTGGCCT 1140

GGGATATGGG TTTTAAATGG ACATTGTCTG TACCAGCTTC ATTAAAATAA ACAATA 1196

60

(2) INFORMATION FOR SEQ ID NO: 223:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1791 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 223:

5 TCAGGGAGGT GGCAGGAAAG GCTTGGAACA GCTGCCGGAG TGACGGAGCG GCGGCCCCGC 60
 CCGGTTGCGC TGGAGGTCGA AGCTTCCAGG TAGCGGCCCG CAGAGCCTGA CCCAGGCTCT 120
 15 GGACATCCTG AGCCCAAGTC CCCCACTC AGTGCACTGA TGAGTGCGGA AGTGAAGGTG 180
 ACAGGGCAGA ACCAGGAGCA ATTCTGCTC CTAGCCAAGT CGGCCAAGGG GGCAGCGCTG 240
 20 GCCCACTCA TCCATCAGGT GCTGGAGGCC CCTGGTGTCT ACGTGTITGG AGAACTGCTG 300
 GACATGCCCA ATGTTAGAGA GCTGGCTGAG AGTGACTTTG CCTCTACCTT CCGGCTGCTC 360
 25 ACAGTGTITG CTTATGGGAC ATACGCTGAC TACTTAGCTG AAGCCCGGAA TCTTCCTCCA 420
 CTAACAGAGG CTCAGAAGAA TAAGCTTCGA CACCTCTCAG TTGTCACCCT GGCTGCTAAA 480
 GTAAAGTGTA TCCCATATGC AGTGTGCTG GAGGTCTTGC CCTGCCGAAT GTGCGGCAGC 540
 30 TGGAAGACCT TGTGATTGAG GCTGTGTATG CTGACGTGCT TCGTGGCTCC CTGGACCAGC 600
 GCAACCAGCG GCTCGAGGTT GACTACAGCA TCGGGCGGGA CATCCAGCGC CAGGACCTCA 660
 35 GTGCCATTGC CCGAACCTG CAGGAATGGT GTGTGGGCTG TRAGGTCTG CTGTCAGGCA 720
 TTGAGGAGCA GGTGAGCCGT GCCAACCAAC ACAAGGAGCA GCAGCTGGGC CTGAAGCAGC 780
 AGATTGAGAG TGAGGTGCC AACCTTAAAA AAACCATTAA AGTTACGACG GCAGCAGCAG 840
 40 CCGCAGCCAC ATCTCAGGAC CCTGAGCAAC ACCTGACTGA GCTGAGGGAA CCAGCTCCTG 900
 GCACCAACCA GCGCCASCCA GCAAGAAAGC CTCAAAGGGC AAGGGGCTCC GAGGAGCGC 960
 45 CAAGATTTGG TCCAAGTCGA ATTGAAAGRA CTGTCGTTTC CTCCCTGGGG ATGTGGGGTC 1020
 CCAGCTGCCT GCCTGCCTCT TAGGAGTCCT CAGAGAGCCT TCTGTGCCCC TGGCCAGCTG 1080
 ATAATCCTAG GTTCATGACC CTTCACTCC CCTAACCCCA AACATAGATC ACACCTTCTC 1140
 50 TAGGGAGGAG KCAAAATGTAG GTCATGTTT TGTGGTACT TTCTGTTTT TGTGACTTCA 1200
 TGTGTTCCAT TGCTCCCCGC TGCCATGCTC TCTCCCTTGT TTCCTAAGA GCTCAGCATC 1260
 55 TGTCCCTGTT CATTACATGT CATTGAGTAG GTGGGTAGCC CTGATGGGGG TCGCTCTGTC 1320
 TGGAGCATAA CCCACAGGCG TTTTCTGTC CACCCCATCC CTGCATGCCT GATCCCCAGT 1380
 TCCTATACCC TACCCCTGAC CTATTGAGCA GCCTCTGAAG AGCCATAGGG CCCCCACCTT 1440
 60 TACTCACACC CTGAGAATTC TGGGAGCCAG TCTGCCATGC CAGGAGTCAC TGGACATGTT 1500

CATCCTAGAA TCCTGTCACA CTACAGTCAT TTCCTTTCTCT CTCTCTGGCC CTGGGTCTCT 1560
 5 GCGAATGCTG CTGCTTCAAC CCCAGAGCCT AAGAATGGCA GCCGTTTCTT AACATGTTGA 1620
 GAGATGATTC TTTCTTGGCC CTGGCCATCT CGGGAAGCTT GATGGCAATC CTGGAAGGGT 1680
 TTAATCTCCT TTTGTGAGTT TGGTGGGAA GGAAGGGTA TATAGATTGT ATTAAAAAA 1740
 10 AAAAGGTATA TATGCATATA TCTATATATA ATATGACGCA GAAATAAATC T 1791

15 (2) INFORMATION FOR SEQ ID NO: 224:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2517 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 224:

25 ACACTAGTGG ATCAAAGAA TTCGGCACAG CGGCACAGCA TTGTGAGCT TTTCTGTGTG 60
 TGTGGGGCCC TCAAGCGAGC TCGACTGGTC CATCCTGGGG TAGCGASGTG GTGTTTGTGA 120
 AAAAGGACGA TGCCATCACC GCATAYAAGA AGTACAACAA CCGGTGTCTG GACGGGCAGC 180
 30 CGATGAAGTG CAACCTTCAC ATGAATGGGA ATGTTATCAC CTCAGACCAG CCCATCCTGC 240
 TCGGGCTGAG TGACAGCCCA TCAATGAAAA AGGAGAGCGA GCTGCCTCGC AGGGTGAAC 300
 35 CTGCCTCCTC CTCAACCCC CCTGCCGAAG TGGACCCTGA CACCATCCTG AAGGCACTCT 360
 TCAAGTCTTC AGGGGCCTCT KTGACCACGC AGCCACAGA WTTCAAAATC AAGCTTTGAG 420
 CAGGGGAGTR AGGCAGCCAG AAGTGGGGGC AGAGGAGGGT GGCTCTGTTT CCCCAAGGCA 480
 40 AAGCTTATGA CCAATGGGCC ATCGGACTGG AGACCCCTGA TTGTGGGAAG GGTGCCAGG 540
 GATAAAGAGC TTCTCACTG GATGGGACCC GCCTTTCTGT GTTGTGTTCT GCCCTGTGCT 600
 45 CTCTCTCTA CGTTAACGTT TCCTGTAGTA TGTTCCTCA TCTCATCGCC AAGGTAGGCT 660
 TGTGTTTTTT AGTGTGTGCC TCCCCGAGCC TCAGCCCCAA GCTGATTTCT TATCTGGAAA 720
 TGGTACACTG AATTCTCTGG GTGGCTTTCT TGTGGCCCCA TGGGATGCAG CGTGGGGGCT 780
 50 GTCTGAAGGA CCCTGCTTTT TCCAGGGGCC GAGGGGCTGC CTTTCCTTTG TGTGTATTAA 840
 GCTTTTCAAA CAATGGAGGG GATGGAGAGC CCTGGTGTCC TGACGGGAGC CAGGTCGGCC 900
 55 TGAGAGCTGT GCCGCTCCTC TGTCTGTGCA GTGGAGGTGC CTGGGTGGGG AGCAGGTCTC 960
 AGGCCTCTTG TCCTCTCCCC AGTGGCTCCA GGCTCACTA GTGGCAAGGG CAGGATGAGG 1020
 CTGACCGCT GGAAGAGTC TATCTAAGCT CTGGCTTGG AGTCCCGTGT CGTCTCCRCC 1080
 60

	CAGAGGAAGT TCTCCAGAGT TCACCTTTCC CTTTTCCTTG AGTTGTGCTG AATGCCCCAC	1140
	CCCAGCTCTC TTTCCCTTCT GGGTGTCTTT GCTGGGAGGG GGCTGTGTTG TGAGCCCTCC	1200
5	CGGTTCAC CTCGCCTGGC ACTTAACCAC ACCCTGGTTT TGTGTAGCCG CCAGCTCTCT	1260
	TCTGGTTGGG CCTTTGAAAG GCTCAGCCTC CCATTGTGCA GTGCTTGGGT TTGGAGCTTA	1320
10	TTTGAATGGA AGAGGTCAGT TTGTTCTGG CTCTCCATT TGGCCTCAG TTGTCTACAG	1380
	GACAGTGGTC AGGGATGCCT GGAGGCATAT ATCCAGCTGC CACCAAGGGG CACTGTTTGT	1440
	TCCCACTTAT GTGAGTGACC CCATCCATCC ATGACCAGAG GATTATTTTC CTGCCTTGGC	1500
15	AGAGGAGGAG GAGTCAAGGG AGCAGGGCAG CTCTACCAGG CAAGGTGTTT CCCAGCATA	1560
	GGCGCAGACA GTTGGGACGA AACTTCAGAG CCCAGGCAGT CCCTGAATGA CCAGGCCAGT	1620
20	GTTGTCACTG AGTGGTCCCC TGCTGGTTGG GAGTGAAGAG AATCCAGGCT GGCAGAGCTG	1680
	GAGCCAGTTG GGGAGCACGG TTCTGGGAGC TCTGCAAAAT CAGTAGCAAG TGCTGAAAA	1740
	GGCACATGCC GAAGATACTC AAGAGCTCCC AAGATTTGCT TGAGGCTAGC CCAGTGAAAA	1800
25	AAACCAGAGA CTCATGTTTC CAGGGTCAG TCTGTCAGGC AGGAAGGACC CAGGATTGA	1860
	ACCCAGCTTC AGTGTGCAGG CTCTGAGGCT GCCCAGGACG GGAAAGTCCA AGGAAGGGGC	1920
30	CTGGTGGTGC TCCACTTGCA GTTCTTTAAA GAATGCTGCT TTTTATCTC CTAACCCTTT	1980
	CAAGTGGGTG CAGACTTCTC GTTAGCAGCT GGAAGACATT CCTCCACAC TTTTCCCTTC	2040
	CTGGCCCAAG AGAGCATCCA GAAGGCAGTA GGACCTGGT TTTCAAGTAC TGGGAGCCGG	2100
35	GGGCTCACTG CTTGCACTGT GCTTAGGGTA GGGATGGTAA ATATCCTCCC TGCACTGGCTT	2160
	TATCCTCCCT CTCATCCCAA AGCAGGTATC TTCTGGTTGT CACAGAGTTT CATTGAGTCC	2220
40	AGCTGCAGCC ACGTGGCCAT CTGGAGCTGG TGCTATAGGT GACCATCTGG TACATTGAGG	2280
	GGACCTGTTT GCCTCCTCCA CTCTATAAGC AGTCATCTTG GGAGACCGGG AGGAGAAGGT	2340
	GGTGGGCTAG TCCTGTGTCC TCCTCCACTT CCCATGCCTC TATGTTACCC ATCTGTGTCT	2400
45	CCTGTGCAGA AGGAGAGGAA GGGGCATTAA GAGATGAAG GTGATTATGT ATTACTTATC	2460
	CATTCTGAA TAAACATTTG TTATTCCTAA AAAAAAAAAA AAAAAACTCG AGGGGGG	2517

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(2) INFORMATION FOR SEQ ID NO: 225:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 2424 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 225:

	TTGTANCTAA TCGAGGATPG ATTCTAATGA CAGAGTCTTT CAACACTTTG CACATGATGT	60
5	ATCACGAAGC TACAGCTTGC CATGTGACTG GAGATTTAGT AGAACTTCTG TCAATATTTT	120
	TTTCGGTTTT GAAGTCTACA CGCCCTTATC TTCAGAGAAA AGATGTGAAA CAAGCATTAA	180
	TCCAGTGCCA GGAGCGAATT GAATTTGCCC ATAAACTGTT AACTCTTCTT AATTCCTATA	240
10	GTCTCCAGA ACTTAGAAAT GCCTGTATAG ATGTCTCAA GGAAC TTGTA CTTTGTAGTC	300
	CCCATGATTT TYTTCATACT CTGGTCCCT TTCTACAACA CAACCATTTGT ACTTACCATC	360
15	ACAGTAATAT ACCAATGTCT CTTGGACCTT ATTTCCCTTG TCRAGAAAAT ATCAAGCTAA	420
	TAGGAGGGAA AAGCAATATT CGGCCTCCGC GCCCTGAACT CAATATGTGC CTCTTGCCCA	480
	CAATGGTGGA AACCAGTAAG GGCAAAGATG ACGTTTATGA TCGTATGCTG CTAGACTACT	540
20	TCTTTTCTTA TCATCAGTTC ATCCATCTAT TATGCCGAGT TGCAATCAAC TGTGAAAAAT	600
	TTACTGAAAC ATTAGTTAAG CTGAGTGTCC TAGTTGCCTA TGAAGGTTTG CCACTTCATC	660
25	TTGCACGTGTT CCCCAAAC TTGACTGAGC TATGCCAGAC TCAGTCTGCT ATGTCAAAAA	720
	ACTGCATCAA GCTTTTGTGT GAAGATCCTG TTTTCGCAGA ATATATTAAA TGTATCCTAA	780
	TGGATGAAAG AACTTTTTTA AACACAACA TTGTCTACAC GTTCATGACA CATTTCTTTC	840
30	TAAAGTTCA AAGTCAAGTG TTTTCTGAAG CAAACTGTGC CAATTTGATC AGCACTCTTA	900
	TTACAAACTT GATAAGCCAG TATCAGAACC TACAGTCTGA TTTCTCCAAC CGAGTTGAAA	960
35	TTTCCAAAGC AAGTGCTTCT TTAAATGGGG ACCTGAGGGC ACTCGCTTTG CTCCTGTCAG	1020
	TACACACTCC CAAACAGTTA AACCAGCTC TAATTCCAAC TCTGCAAGAG CTTTAAAGCA	1080
	AATGCAGGAC TTGTCTGCAA CAGAGAACT CACTCCAAGA GCAAGAAGCC AAAGAAAGAA	1140
40	AAACTAAAGA TGATGAAGGA GCAACTCCCA TTAAAAGGCG GCGTGTAGC AGTGATGAGG	1200
	AGCACACTGT AGACAGCTGC ATCAGTGACA TGAAAACAGA AACCAGGGAG GTCTTGACCC	1260
45	CAACGAGCAC TTCTGACAAT GAGACCAGAG ACTCCTCAAT TATTGATCCA GGAAC TGAGC	1320
	AAGATCTTCC TTCCCTGAA AATAGTTCTG TTAAAGAATA CCGAATGGAA GTTCCATCTT	1380
	CGTTTTCAGA AGACATGTCA AATATCAGGT CACAGCATGC AGAAGAACAG TCCAACAATG	1440
50	GTAGATATGA CGATTGTAAA GAATTTAAAG ACCTCCACTG TTCCAAGGAT TCTACCCTAG	1500
	CCGAGGAAGA ATCTGAGTTC CCTTCTACTT CTATCTCTGC AGTTCTGTCT GACTTAGCTG	1560
55	ACTTGAGAAG CTGTGATGGC CAAGCTTTC CCTCCAGGA CCTGAGGTT GCTTTATCTC	1620
	TCAGTTGTGG CCATTCCAGA GGACTCTTTA GTCATATGCA GCAACATGAC ATTTTAGATA	1680
	CCCTGTGTAG GACCATTGAA TCTACAATCC ATGTCTGCAC AAGGGATATC TGGCAAAGGA	1740
60	AACCAAGCTG CTTCCTTGACA TTAGGTGTAG CATGTCTACT TTTAAGTCCC TCACCCCAA	1800

CCCCCATGCT GTTTGTATAA GTTTGTCTTA TTTGTTTTTG TGCTTCAGTT TGTCCAGTGC 1860
 5 TCTCTGCTTG AATGGCAAGA TAGATTTATA GGCTTAATTC TTGGTCAGGC AGAACTCCAG 1920
 ATGAAAAAAA CTTCATCTT CAGTATACTT CCTAAAGGGC AATCAGATAA TGGATATGTT 1980
 TTATGTAATT AAGAGTTCAC TTTAGTGGCT TTCATTTAAT ATGGCTGTCT GGGAAGAACA 2040
 10 GGGTTGCCA GCCCTGTACA ATGTAATTTA AACTTACAGC ATTTTACTG TGTATGATAT 2100
 GGTGTCCTCT GTGCCAGTTT TGTACCTTAT AGAGGCAGAT TGCCTCCGAT CGCTGTGGTT 2160
 CTTATTATCA AAATTAAGTT TACTTGTATA CGGAACAACC ACAAGAAATT TGATTCTGTA 2220
 15 AAGAATCCTC TTTAGCTGTG GCCTGGCAGT ATATAAATGG TGCTTTATTT AACAGAATAC 2280
 CTGTGGAGGA AATAAGCAC ACTTGATGTA AAAATAATTG TTTTATTTTT ATTGACATGA 2340
 20 CTGATTGATT GCTATTCTGT GCACTNAATT AACTGATTG TGATGACTTA AAAAAAAAAA 2400
 AAAAAAAAAA AAAAAAAAAA AAAA 2424

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(2) INFORMATION FOR SEQ ID NO: 226:

30 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1080 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 226:

ATATAGGACG GATAATCTGT TTACATTCTG TTCTTCTCGA TGCACTCACA AGCGGGTAAC 60
 TAGGTGACAA GAAAACAAAG ATCTTATTCA AAAGAGGTCT TACAGCAACC CAACGTCTCA 120
 40 TCTTCCCATG GTAAAGATGA CGGCGCCTTG AGGTAAGCTA CAGGCAACAC CACTTCCGCG 180
 TTCTCTTGC GCCCTGGTCC AAGATGGCGG ATGAAGCCAC GCGACGTGTT GTGTCTGAGA 240
 45 TCCCGGTGCT GAAGACTAAC GCCGGACCCC GAGATCGTGA GTTGTGGGTG CAGCGACTGA 300
 AGGAGGAATA TCAGTCCCTT ATCCGGTATG TGGAGAACAA CAAGAATGCT GACAACGATT 360
 GGTTCGGACT GGAGTCCAAC AAGGAAGGAA CTCGGTGGTT TGGAAAATGC TGGTATATCC 420
 50 ATGACCTCCT GAAATATGAG TTTGACATCG AGTTTGACAT TCCTATCACA TATCCTACTA 480
 CTGCCCCAGA AATGTCAGTT CCTGAGCTGG ATGGAAAGAC AGCAAAGATG TACAGGGGTG 540
 55 GCAAAATATG CCTGACGGAT CATTTCAAAC CTMTGTGGGC CAGGAATGTG CCCAAATTTG 600
 GACTAGCTCA TCTCATGGCT CTGGGGCTGG GTCCATGGCT GGCAGTGGAA ATCCCTGATC 660
 60 TGATTAGAA GGGCGTCATC CAACACAAAG AGAAATGCAA CCAATGAAGA ATCAAGCCAC 720

TGAGGCAGGG CAGAGGGACC TTGATAGGC TACGATACTA TTTTCTGTG CATCACACTT 780
 AACTCATCTA ACTGCTTCCC CGGACACCCT CCACCTCTAG TTGTTACTAA GTAGCTGCAG 840
 5 TAGGCATTGC TGGGGAAGAA ACAAACACAC ACCAAACAGT ACTGCTACTT AGTTTCTAAG 900
 GCTGCACAGG GAAGGGAAAG ACTGGGCTTT GGACAATCTA GAGGTAATTT ATATCCGCCC 960
 10 CCAGGTGGAG CAACATGCGA TTCTGGAGGC ACGGGGGTAA CTGAAAGTGA GTACATATAG 1020
 TCTTCTGGT TTCTGGAGAT AACCCATCAA TAAAAGCTGC TTCCTCTGGG TAAAAAAAAG 1080

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(2) INFORMATION FOR SEQ ID NO: 227:

(i) SEQUENCE CHARACTERISTICS:

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- (A) LENGTH: 1336 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 227:

25

TTGCATTAC AATTACTGGG AGGCAGGCAG GGCAGTTGC ATGCTGGGGG TGGCTGCATG 60
 GSCTGCCASC TCTCTGGGT TTGAAGGATG CGGTACASCT GCTTCAGCTG AGCAACGATG 120
 30 TTATCTTGA TGCTGGGGT TGAGATCTGC AGGCGGACAC TGCCACTATC AAAGGATCGT 180
 GTGAAATCAC CAGAAAACAT CTCGTAGATC ATCCGAGCCA CTA CTGGAAT GACCTGAACC 240
 AAGATGAGTT TCCTTTCCAA TGGTTTCCCA TCTGGCCATT CTTCCCCAAA GCATAAGTAG 300
 35 ATCTCAAACG GTGGCTGCTT CTCTATCTGT CCTTCTGGT GGGCAATGAG ATCGCTAAGG 360
 AATGTTTCCA GACAAAATAG CTTGACCTTC TTTTGTCTCT CAATCAGGTT GGGAGCAACA 420
 40 AGTGATGGGG CACATGGCCC AGACCAGTAC ACCTTGCACT GGCACAGYCT GATGGCATAA 480
 ATGGCATGAC CGCTGACCTC CAGGATCAGT CCTCTGTCCA TGACGTCCAG CAGCTTGCTA 540
 GTGAACAGCT TCTGCTTCTC ATTGTAATA TGCTCAGGAC CTGGGAATTT GACCTGCTCC 600
 45 AGNCTGACGG GACCAAAGAG CTCCTCTGG TCAGGCATGG GACCCAGGTC CCCATAGAAG 660
 AGTCGGCAGC CCTGAGGGTT GCTCAGGTC ATGGTCTGTC CCGTACTCCT TCCCACGGTA 720
 50 CTGAAACTTG ATGTCCAGGT CAGTCATTGG GAGAGAGCTG ATCCACAGTT CTGGAGAGCT 780
 ATAGAAGGRC TGTATAGGTG CTTGGGWAC TTCCATCTCC AGGGGTTTCTG TTTTGGGCCA 840
 CACTGCCTCC GGSCTGCAGT TGCCACACT GCAATTGCCC AACTTGGCTG GCGCCATGGG 900
 55 AGAACCATG ATGTTTCAGGA AGGGAAGGT GTCTGGATG GGAACATGGT GCTGCGACTG 960
 ATCCAGCTCA TCTTCTCAT CTCTTCATC CACATCATTA TCCTTCTCAT CCCAGGGAGC 1020
 60 AGACCCTGTG GATCCTGGGT TAATGATCGA SCCCTGGGGC TGAGGGATGT CACACACTTG 1080

ATATATCTTC ACTGGGTTCA TGGGCACCTC CCTTGGTGCC ATCCATACAT CCAGGTTGAA 1140
 TTCTCTGCTC TTATPGAGAG CACAGCGCAG CTGGGCCTTC CATTTAGCTG GGTGAGGGTC 1200
 5 ATCCACCCCT TCCTGGTACT TCCCTGTCTC TACAGCCCAG GCCTTAAAAA TGGTATTTTC 1260
 CTCTTCTTGT TGAGGGCTAT GCCGGGTGGC ATGTTTCCAG GGAATCTGGA AGCGTTTAGA 1320
 10 GTCCCTGTGT AGCCAG 1336

15 (2) INFORMATION FOR SEQ ID NO: 228:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2043 base pairs

(B) TYPE: nucleic acid

20 (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 228:

25 TCAGCTGGTC CCTTCCTTGT GTCCTGGGGG ACCTGCTGGC GGCTCTTCC TGGGAGCCAT 60
 GACCTCAGAC CCCACCCACA CTCCAGATCG AGACCCCTGC CTCCCCCCG CAAATGTCCT 120
 CCCGCTGCCT TGACGCTGC ACTTTGCACA TGCTCACCCC CAGCACAGTC CCACTGGCCC 180
 30 CTCAMCTCCC CTTCCTGAG CTCCTTCCCA AGGACTCCTG GTCAGTGCCT GCTGTGCAKT 240
 CAGAGGCCCA GGGTCCAGCA GCCCGSGGG AACGGGTGCT GCCTSTTCTT CCAGTTAGCT 300
 35 CCAGYTCAGG TCTGAGACCC GTGYTGAGTA AAGGTCTGAG CAMCGACCGT GCCCTCTGCC 360
 CAGGGCTGGG TCCTGAGCAG CTGGTTTTC TGCAGGAAGG TTGGAGCAAG CAAAGTCCTT 420
 CTCTGCCCTC AGGGTCAGCT GCCCAGACTG GGGCGGATGC AGAGAGGCAG GTGGGCTGTG 480
 40 GCTGGACTGG TCCGGAGCTG GCTTCCTTAC CAGAAAAGCC TCAGCCTTCC TCTGGAAGCA 540
 TCCCCGTTT TGGSCAAGGG GGAAGGGCTC CTTTAAGGGG TGTGCTTTC CAGTGGGGAG 600
 45 CAGTCTGGCC CTGCCCCCTA CTAAAGCCTC TGCTCTCAGC ACTTTCCCCC AAGTCCTTGT 660
 AACTTGCTTG AAGGTGGGTT CTGGCTGCCA GCCAGTCCCT GGACAAACTC TCCTGCCCCT 720
 TTTAAATTT ACTCATTTTG TATAAACCCA GCAGGCTGGT GTTTACTTAG CCCTGTAGCT 780
 50 TTTTTCATTT TTCTTTTCCG TCTTTCTTCT TGAGTTACAG GTTCAATATT GCCTCCTCGC 840
 CCTGGTGAGG GGAGGTGCTG CTTTCTTGCC CCACCTGCCG GCTGGTTCCA GCAGCGCTGG 900
 55 NGCCCAGCTG GGGGGCCGG ATGGGGCTT CTCTCTCTGG GAGGGGTGCA GGTGCCCTCC 960
 CCAGGCTGGG AGGGTTCTTT CCCTAGCTCC CCATCTGCCC CCGCTGGTGA GAGTTGGGCT 1020
 TCTTGGTCTT GGAAGTCCCT GCATPGGGA ACAGAGCATT TCCAGCATTT GTTGTGTTG 1080
 60

	TTTACTAC CTAACCCCTTA GAAAAATGAAT GTTAGAAGGT GCCTGCCGAG GCGGGACAGA	1140
	GTGTTTGCTC GCGCTGGAGA AGGCTCTGCT CAGCCCTGAG AGTCCCTTCC TGCCCCACCG	1200
5	ATACTGGCAC TTTAAAAAGG AAGCTGACCG CACAGTGTC AGACGAATTG GCCCCAGAA	1260
	GATGGGGAGT TCTGTCTGC CCTTCTGTGT CTGCGTGACC TCACCCAGCC TAGGAGGGAG	1320
10	GTGCATTCAG GGTAGATTG CCTCTCATT CAAAGTTCTGG GCCTTTGGGY GGAAAACAGC	1380
	CAGCTTTGGC GCTGTTGGGG AGACTCCTCC AGACCAGGAA CCCCAGAAG AGACAGAGCC	1440
	TGCCACATCC TCCCACGCCA GCCCCTGGGC CAGGGTGATT GGAAGTGAAG TTTGGCCACA	1500
15	ACCAAATTGA TGCTGGCTGG AACCAGAGGC CAGAAAGCCT GCCCTTGTC CCATGTGGGA	1560
	GCCCTGTCCT CAGCCCTCTT GTCCCTTGA GCTCAGTGAA TTCCACCCAG GTGCCACAG	1620
20	CTCTGGACT TCAAATTCTA TATATTGAGA GAGTTGGAGA GTATATCAGA GATATTTTGT	1680
	GAAAGGAGTT GGTCTATGCA ATGTCAGTTT GGAATCTTCT TGAAAGTTTA ATGTTTAT	1740
	TAGGAGATTT AAAGAAAATA AAGGTCTACA ATATCTTTAG GTTTTTTTT TTTCTGTTT	1800
25	ACCGCACAAA CTGACCACAT GGCATGTCTA TCAGGATGGA GGGTGTCAT GTTCTCTCT	1860
	GTCTTTAGGG AGGTGATAAG GAGATGGSCG RAGGGGTGTT TTTTCTTTG ACTCCCTCC	1920
30	TTTCTAACAG AATGTTGCCA CCACTGCTTG AGTGGGCTGT GTTGTTCCT CTGTCCAGC	1980
	TTCTGTGTGA GAAAATAACA TTGTTAGGGG AACTCAGGCT AGTGTGAGC TCTTGGTTT	2040
	GGG	2043

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(2) INFORMATION FOR SEQ ID NO: 229:

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- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 540 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 229:

	TAAAAAGAAG CCGGAGAATC TGGCGTCGC TCTAGAGATC GATGGGCTAG AGGAGAAGCT	60
50	GTCCCACTGT CGGAGAGACC TGGAGCCGT GAACTCCAGA CTCCACAGCC GGGAGCTGAG	120
	CCCAGAGGCC AGGAGGTCCC TGGAGAAGGA GAAAACAGC CTAATGAACA AAGCCTCAA	180
55	CTACGAGAAG GAACTGAAGT TTCTTCGGCA AGAGAACCGG AAGAACATGC TGCTCTCTGT	240
	GGCCATCTTT ATCTCTGA CGCTCGTCTA TGCTACTGG ACCATGTGAG CCTGGCACTT	300
	CCCCACAACC AGCAGAGCT TCCACTTGGC CCCTTGGTCA GGATCAAGCA GGCACCTCAA	360
60	GCCTCAATAG GACCAAGGTG CTGGGTGTT CCCCTCCCAA CCTAGTGTTC AAGCATGGCT	420

TCCTGGCGGC CCAGGCCTTG CCTCCCTGGC CTGCTGGGGG GTTCCGGGTC TCCAGAAGGA 480
CATGGTGCTG GTCCCTCCCT TAGCCCAAGG GAGAGGCAWT AAAGACACAA AGCTGGAAAT 540
5

10 (2) INFORMATION FOR SEQ ID NO: 230:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 448 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

15 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 230:

AATTGTGAAA TATTAGAATA TGTTACTAT TTGACCCAAC TCAAAATCTC CATGGGAAAA 60
20 TACCTGTGCA TACCACAGT ATTGTGAAA ATAATCAGAT GCAGTATCAC AGCTGTGTCA 120
GACTCTAGTA CCAGTTGGGC AATCAAGGCA CAGCTAAAAA TTGAAAACAA AGATCTGGAC 180
25 AACAAACAG CCAAAGGTGG GGGTCAAGAA GCTCTGACGT GTACCTAGCT GTAGAATGCT 240
ATGCACACGT GCCAGGTGTA GTGTGCATAT CCAGGAAAAA CTGCAGAGAG CCCCAGTCTT 300
CAMCTCTGGT TGACCATGAG CTCTGTGTAA GCAGGAAGTG AAGGCTAAGG CAGATTTAAG 360
30 CTCTGAAAGC ATTCCACAAC ATACACACAA ATCGTGCAAA GCATTAAGGA AATCTTGTTA 420
CTGCTAAGTG TTGCTGACCC AGGAACAA 448
35

(2) INFORMATION FOR SEQ ID NO: 231:

40 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 407 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

45 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 231:

GTATGCTGCC CCAAACCAAT ATGTGTGGCT GCCTTTWACC TGACTTCTCC AACATGTAGC 60
50 CCCAAGAGGA GGCCTCTAGA CTRAGGGAGG GGCTGGTGAC CCAGGTGTGG TGGGGCTGCA 120
TGARACTACC AGAGAGACAG ACATTCTGGA ACTCACCTTG GGGGATCCAG TGGATCTGCC 180
TATGGTCTGG TCCACCCAG ACCTGTGAGA TGTTCCTCAT GAGGATGCAC TTGTGCTTCT 240
55 GCAAGTATTG CTGCAGCTTC ATAGTGACTC CCACCAGCAC CAGCAATACA GYTAGCTACC 300
TGTGGCCTTG GATCTCAGCC AGCATGGCTG GGAGAGGGAG CARCTGGCA TGTACCCTAA 360
60 ATGCTGTTAC CAGGAAGGA CTCCAGAGT GAAGACAAGT AGGGACT 407

5 (2) INFORMATION FOR SEQ ID NO: 232:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 830 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 232:

15 GTATTGATT TCAGGCTGCT AAATGGGCTC ATTTAGCATT CATTCCTTGA TGTAGACATT 60
AAAAAAAA CTGAATAGCA TTCTTTCCAG GNTAACTAAT AAAGCAGACA TGCTAAGCCT 120
ATAAATACAT CAGCACTGCA GCACACGTTT AAGGTTGCCA CGGACAAGGA TCACACAATA 180
20 GAGAACACTG TAGTTCGGTC TGCTCACAAG ACCCAGAACA TTGATCAGTT TTTGTTGTTG 240
GTTTATTATT TTTCTGTTAA AAAATTGTGA AAAGTTTGTT TTAGCTAGAT GATATTTTAA 300
25 TAGCTGCGAG TGCTTTGGAA CTATAAAGAT GTCACTACTT AACACACATA CCTTATGTTT 360
TGTTTTGTTT TGTTTTACAC TCAGTATAAA TCAGGAGAAG TTAGCCAACC ATCTAGCATT 420
TAGAATCCTC TTTTTTATTG TCTTCTAAGG ATATGGATGT TCCCATACA GCAACAAAAC 480
30 AGCAACAAAA ACATTTTATA AATATCACTT GATAGACTGT AAGCACCTGC TTAACTTTGT 540
GTNCCAAATA TTTAGTGTGT ATATATATAT ATATATACAC ACACACACAC ATATATATTC 600
35 AACAAATAAA GCAAAATATA ACATGCATTT CACATTTTGT CTTTCCCTGT TACGATTTTA 660
ATAGCAGAAC TGTATGACAA GTTTAGGTGA TCCTAGCATA TGTTAAATTC AAATTAATGT 720
AAAACAGATT AACAACAACA AAGAACTGT CTATTTGAGT GAAGTCATGC TTTCTATTAT 780
40 AATAACTTGG CTTGGTTAT CCATCAAATG CACACTTATA CTGTTATCTG 830

45

(2) INFORMATION FOR SEQ ID NO: 233:

(i) SEQUENCE CHARACTERISTICS:

- 50 (A) LENGTH: 932 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 233:

55 CCAGAAGAAA GACCAATCTA GAATATGGAA CTCTAATCAC TTCTAGTATT TCAACTTCCT 60
AGCAGAAATG AACTTGCCCC TAGACCTAGG GGATAAGCAA TGTTCCTTAT GTAGCCAATG 120
60 CTACGGAAAC AAAAGAGGTG AAAGAGACCC TTTTTTTATA CTTAATGTAC ATATATTGAC 180

5 TTTTGTAGCA AGAATGCCAG AAATAGCCTT CATTTCTACC CTGCAAATA ATCCAGATCT 240
 GCTTTCTAAA ATGRANTCAG TTTCTAAAGT GAAACATGCA ATATTTATGC TCTGACTGAC 300
 TCCTGAATTG GARGAGGAAG RACTTCTGTT TACAGAAAAC YGTATTGTTA TATATGTCAG 360
 GCTGTGTATT GTGACTATCA GCATTCTGGT GCAAATGAAC TTTTCTCCAT CATCGACTGT 420
 10 GGAAAATTGA TACTTTTAAA GCATATTCTT CTATGAGCAC AGGTCCCTCT AGTGAAACTT 480
 AATTTGACAA AGGGTGTCTAT ATGCTTTCCT AACCTGAWT GTATTAACAT TCACAGAGCC 540
 TACATTTTCT CATTAGGGTT RTGATGCTCA GTATCTTTC AAGTGCCAGG CAGRGCTTNC 600
 15 CTTTCTGAT CAAACATACC ATTTTGTGA TTTCACACT ATAGACAGTC ACTTCTGCAG 660
 TCCCAATTGA AAAATGCAGA ACTGCTTAT CCAAGAATGC TGAAAAATAC TGTCTATCC 720
 20 AGGTTTCTTA AACTATAAAA GCAGATTTTG CTTTGTGTTG TTAATCATAG GCATGGCCGA 780
 GCATTGTGGA TTAGCCTGAG GCTTAAATC AGATGCATGT CTGGTAAGAT GACCACTGTC 840
 TCACTATCAA GAGCCTGCAG AGCCATTTC CAGACCTGTG ATGCCCAGA ACACATAGTC 900
 25 CCCACGTTTC TAATTGGAG CAAATCTAAA AG 932

30

(2) INFORMATION FOR SEQ ID NO: 234:

(i) SEQUENCE CHARACTERISTICS:

35

- (A) LENGTH: 2786 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 234:

40

TTAGCAGGGT GAGCTGTAA AACAGCACAC ATCTCTCATC CCCTCTTCCT TTATTCCCCC 60
 CTGGGTTTCA GAAAGGAAGG ATATATGGGG ACCACCTCCC CCTTCTTTGA TCCCAGCATC 120
 45 TCAGTCCCCC TCCCAACCCT CCATATGGCT CTCAATGGTG CTCACTTGCT TGGAAGCAGG 180
 CTCCAATAG GGAGGGGSCCT GCCCTCTACA GTCTCTTTGA CTGTAAGACA GGGCTCTGTA 240
 TCAGTGAGAC GATGAGAAAA GTCCAGGCT AATGGCAGAA APTTGCACTT TGAACATGTG 300
 50 TGTPTTTGTG TTGTGGAACC TGAGATTCCT TATTTATTAA CAGGAAGTCT GATTTTPTTT 360
 TTTTGGAGTC TTTGTTGCTA TATTTGTGG GGCTGGGAGA GAGAGATTAG ATTATTTTGA 420
 55 CATGGGATCC CTTCATAAC AGGTACTTTG AAGGCAAGAC ATAGGGTTGA AGAAGCACAA 480
 CCAGCCTCTG AAATCATAGC TCTCCAGTGG CTTTAAAGA AAGCTGGTCC TCAGCACTAA 540
 CAAATCACT ACAATAGCCT AGTGCTTTTT TGGAAGCCTT TTTAGGGAAG AATGTTAGGT 600

60

	TCATGGTAAC TAGTATGCTC TTTGAGATTT TTACAGTGT TAACTTAAG AATTTTGAGA	660
	GGGTGAGGAG GGTGTTCAG AATCTAAAT ACAGATAGAT GATTGTTTCT TGTGAATTTG	720
5	TTTCTTTTCC TTTTTTTTTG TCCCTACCAT TTCCTTACAT TTCCCTTGGG GCCCATCTCT	780
	GGCTCCTTGC TTTTGTTC TTGCTTTGCT TTATCAGTTC ATTCCAGCTC CCTGTTAGTG	840
10	AAGGACACTG CTGTTAGTGA AGGAACAAAG TCTATGAGTC CTAAAATTTT AAGTCAAAGA	900
	AAACTGCTCT GTTCCCTT TAGTAACACT TCTGAAGAGG AAAAATTCA ATAGCCAAAG	960
	TTAATAATCC TATATAATAA TTGCTTTGGC TTTCACCTAA AATCTGGGC ATCACAATTT	1020
15	CCTTGGGATA GAGTTTGTGT TGGGAATAG ATTGCTTATT GCTGTTCACT GGAGAGAAA	1080
	GGTAGTGT TGTACAAG TCATACCGCC AGAAGCCCA AATCTATTT TGGCTCATCT	1140
20	TCAGGTAAAG AGTAATTCCT ATCCTGTGTG CCTCAGAAGC TAGAATCGAA GGCTTACCCT	1200
	ATTCATGTT TATGTGAGA AATGCATGAT GGCTCTTGA AAGAATGACG TTTTGTGGA	1260
	AAAAAAAAA AGAACAGTT GTGTTTACA AACATGGCTT ATCAATTTT TCAAAGAATT	1320
25	CTTTTTTCCC AAAAAGAGGA GTAACAAAT GTCATTTCTG AAAGAGGCTT ACTTTATACC	1380
	AACTAGTGC AGCATTTGGG ATGCCAGGA ACAGAGAGTG AGACACCTAC AATCACCAGT	1440
30	CTCAAATGCG CTATGTTTC TTTTACAGT GTTGCAGATT TGCCATTTCT CCATAATATG	1500
	GGGATAGAAA ATGGAATAAA GATAGAAGG ATGTAGAATA TGCTTTCTG CCAACATGGT	1560
	TTGGAGTCGA CTTTGGTATA TTGACTAGAT TTGAAATAC AAGATTGATT AGATGAATCT	1620
35	ACAAAAAGT TGTCTCTC TCAGGTCCCT TTTACCTTT TTGACTAACT AGCATCTATA	1680
	TTCCACACTT AGCTTTTTTG TCACACTTAT CCTTTGTCTC CGTAAATTC ATTTGCAGTG	1740
40	GTTAGTCATC AGATATTTTA GCCACCTACA CAAAGCAAA CTGCATTTT AAAATCTTT	1800
	CTGAGATGGG AGAAAATGTA TTCTCCTTTC CTATACCGCT CTCCAACAA AAAACAACCT	1860
	AGTTAGTTCT ACTAATTAGA AACTTGCTGT ACTTTTCTT TTCTTTTAGG GGTCAAGGAC	1920
45	CCTCTTTATA GCTACCATTT GCCTACAATA AATTATTGCA GCAGTTTGCA ATACTAAAT	1980
	ATTTTTTATA GACTTTATAT TTTTCTTTT GATAAAGGA TGCTGCATAG TAGAGTTGGT	2040
50	GTAATTAAAC TATCTCAGCC GTTCCCTGC TTTCCCTTCT GCTCCATATG CCTCATGTC	2100
	CTCCAGGGA GCTCTTTTAA TCTTAAAGTT CTACATTTCA TGCTCTTAGT CAAATTTCTG	2160
	TACCTTTTTA ATAACCTCTC CCACTGCATA TTTCCATCTT GAATTGGTGG TTCTAAATTC	2220
55	TGAAACTGTA GTTGAGATAC AGCTATTTAA TATTTCTGGG AGATGTGCAT CCTCTTCTT	2280
	KGTTGTTGCC CAAGTTGTT TTGCGTAACT GAGACTCCTT GATATGCTTC AGAGAATTTA	2340
60	GGCAAACACT GGCCATGGCC GTGGGAGTAC TGGGAGTAAA ATAAAAATAT CGAGGTATAG	2400

ACTAGCATCC ACATAGAGCA CTGGAACCTC CTTGTACCT GTTGGGGAA AAAGTATAAT 2460
GAGTGTACTA CCAATCTAAC TAAGATTATT ATAGTCTGGT TGTGTGAAAT ACCATTTTTT 2520
5 TCTCCTTTTG TGTTTTCCC ACTTTCCAAT GTACTCAAGA AAATTGAACA AATGTAATGG 2580
ATCAATTTAA AATATTTTAT TTCTTAAAAG CCTTTTTTGC CTGTTGTAAT GTGCAGGACC 2640
CTTCTCCTTT CATGGGAGAG ACAGGTAGTT ACCTGAATAT AGGTTGAAAA GGTATGTAA 2700
10 AAAGAAATTA TAATAAAGG GATACTTTGC TTTTCAAATC TTTGTTTTCT CTTATTCTAG 2760
GTAAGGCATA TTAAAAATAA ATATGT 2786

15

(2) INFORMATION FOR SEQ ID NO: 235:

20

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 458 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 235:

GGGTGCAGGA ATTCGGCAG AGAGAATGTT TGATTTCCTT TCCTATTTTA AGGATCTTCT 60
30 CTCTTGTTGA TGTGAAAAC TTACCTTAGT GAAGATGTGT TTCAACATGC TGTGTCTCTT 120
TACCTGCATA ATCACAGCTA TGCATCTATT CAAAGTGATG ATCTGTGGGA TAGTTTTAAT 180
GAGGTCACAA ACCAAACACT AGATGTAAAG AGAATGATGA AAACCTGGAC CCTGCAGAAA 240
35 GGATTTCCTT TAGTGACTGT TCAAAAGAAA GGAAAGGAAC TTTTATACA ACAAGAGAGA 300
TTCTTTTTAA ATATGAAGCC TGAAATTCAG CCTTCAGATA CAAGGTACAT GCCCTCTTTC 360
40 TTTTCATGCC ATCTCTTTTG CACTCTCAGG TGGAAATATT TTAAAGTGT TTATAATCAT 420
AAGTTCCTGT GAAACCTAAC AAGATTATCC CTTCCTAA 458

45

(2) INFORMATION FOR SEQ ID NO: 236:

50

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 591 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 236:

AGGATGAAGA GGAAATTATC TCTTGATTG CTCTCCAGGA AATCCTTCTC TATACTTTAA 60
AAGCTCTTGT TCTTTCTAG GATCCAATG TGCTGATTGC TGCTAACAGT CAGGGTACAA 120
60

TTAAGGTGCT AGAATTGGTA TGAAGGGTTA ACTCAAGTCA AATTGTACTT GATCCTGCTG 180
 AAATACATCT GCAGCTGACA ATGAGAGARG AACAGAAAA TGTCATGTGA TGTCCTCTCCC 240
 5 CAAAGTCATC ATGGGTTTTG GATTTGTTTT GAATATTTTT TCTTTTTTTC TTKTCCCTCC 300
 TTTATGAGCC TTTGGGACAT TGGGAATACC CAGCCAACCTC TCCACCATCA ATGTAACCTCC 360
 10 ATGGACATTG CTGCTCTTGG TGGTGTATC TAAATTTTTGT GATAGGGAAA CAAATCTTTT 420
 TGAATAAAAA TAAATAACWA AACAATAAAA GTTTATTGAG CCACAGTTGA GCTTGGAAAG 480
 TTTTGTCAA ATGCNGCAAG AGATAACTCT TTTTANGAAG TAGCATATGT GAACTATAAT 540
 15 GTAACAGTGA ATAATTTGTA AAGTTCGTAT TTCCCAACCT CTTTGGGAAT T 591

20 (2) INFORMATION FOR SEQ ID NO: 237:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1286 base pairs

(B) TYPE: nucleic acid

25 (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 237:

30 TCTTTTTAAG GTACAGCAGG GAAGAACTGG AAATCAGAG AAAGAACTG CCCTTCCATC 60
 TACAAAAGCT GAGTTTACTT CTCTCCTTC TTTGTCAAG ACTGGGCTC CACCGAGCAG 120
 GAGATTACCT GGGCAATTG ATGTTATCGG TCAGACTATA ACTATCAGCC GAGTAGAAGG 180
 35 CAGGCGACGG GCAAATGAGA ACAGCAACAT ACAGGTCCTT TCTGAAAGAT CTGCTACTGA 240
 AGTAGACAAC AATTTTAGCA AACCACCTCC GTTTTTCCTT CCAGGAGCTC CTCCCACTCA 300
 40 CCTTCCACCT CCTCCATTTC TTCCACCTCC TCCGACTGTC AGCACTGCTC CACCTCTGAT 360
 TCCACCACCG GGTTTTCTC CTCCACCAGG CGCTCCACCT CCATCTCTTA TACCAACAAT 420
 AGAAAGTGGA CATTCCTCTG GTTATGATAG TSGTCTGCA CGTGCAATTC CATATGGCAA 480
 45 TCGATGAAG AACGATACAG ATACAGGGAA TATGCAGAAA GAGGTTATGA GCGTCACAGA 540
 GCAAGTCGAG AAAANGAAGA ACGACATAGA GAAAGACGAC ACAGGGAGAA AGAGGAAACC 600
 50 AGACATAAGT CTTCTCGAAG TAATAGTAGA CGTCGCCATG AAAGTGAAGA AGGAGATAGT 660
 CACAGGAGAC ACAAACACAA AAAATCTAAA AGAAGCAAAG AAGGAAAAGA AGCGGGCAGT 720
 GAGCCTGCCC CTGAACAGGA GAGCACCAGG GCTACACCTG CAGAATAGGC ATGGTTTTGG 780
 55 CCTTTTGTGT ATATTAGTAC CAGAAGTAGA TACTATAAAT CTTGTATT TTTCTGGATAA 840
 TGTTTAAGAA ATTTACCTTA AATCTGTGTC TGTTGTAG TATGAAAAGT TAACTTTTTT 900
 60 TCCAAAATAA AAGAGTGAAT TTTTCATGTT AAGTTAAAAA TCTTTGTCTT GTACTATTTT 960

5 AAAAATAAAA AGACAGCAAT GACTTTATAT CCAAGAAAG AATGTGAATG AGTCACTTAA 1020
 CAGGGAATCT AAAGAGCTGT GTTAGCTGTG TACATACACA GATTATCTGA GAAAAGGTCA 1080
 AGGGTTCCAC TTGGGCCACA GTTTTTTTGT TAATCAAACA CCACTCTCTT AAGRGGCTGC 1140
 ATCACAAARG GCAACCAARG GGCCCTCTT ARGGCTTTGA GGATTAAAC TAGTCTTTAT 1200
 10 CCATTACTGC TGTGGACACT CTGGCTTRG TATWTTTAGG GGGGNTCCTT ACCTTTTTTT 1260
 GGTTTTCCNC ACCTTTTTGG TTGGGC 1286

15

(2) INFORMATION FOR SEQ ID NO: 238:

20 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 734 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 238:

ATGGCAGCGC AGAAGGACCA GCAGAAAGAT GCCGAGGCGG AAGGGCTGAG CGGCACGACC 60
 30 CTGCTGCCGA AGCTGATTCC CTCCGGTGCA GGCCGGGAGT GGCTGGAGCG GCGCCGCGCG 120
 ACCATCCGGC CCTGGAGCAC CTTCGTGGAC CAGCAGCGCT TCTCACGGCC CCGCAACCTG 180
 GGAGAGCTGT GCCAGCGCCT CGTACGCAAC GTGGAGTACT ACCAGAGCAA CTATGTGTTC 240
 35 GTGTTCTTGG GCCTCATCCT GACTGTGTG GTGACGTCCC CTATGTTGCT GGTGGCTCTG 300
 GCTGTCTTTT TCGGCGCCTG TTAACATTCT CTATCTGCGC ACCTTGGAGT CCAAGCTTGT 360
 CCTCTTTGGC CGAAAGGTGA GCCCAGCGCA TCATATGCTC TGGCTGGAGG CATCTCCTTC 420
 40 CCCTTCTTCT GGCTGGCTGG TCGGGGCTCG GCCGTCTTCT GGGTGTCTGG AGCCACCCTG 480
 GTGGTCATCG GCTCCACGCG TGCCTTCCAC CAGATTGAGG CTGTGGACGG GGAGGAGCTG 540
 45 CAGATGGAAC CCGTGTGAGG TGTCTTCTGG GACCTGCCGG CCTCCCGGGC CAGCTGCCCC 600
 ACCCCTGCCC ATGCCTGTCC TGCACGGTCT GCTGCTCGGG CCCACAGCGC CGTCCCATCA 660
 50 CAAGCCCGGG GAGGGATCCC GCCTTTGAAA ATAAAGCTGT TATGGGTGTC ATTCAAAAAA 720
 AAAAAAAAAA AAAA 734

55

(2) INFORMATION FOR SEQ ID NO: 239:

60 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 809 base pairs
 (B) TYPE: nucleic acid

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 239:

5
CGGGGTCTTC AGGGTACCGG GCTGGTTACA GCAGCTCTAC CCCTCAGGAC GCARACATGG 60
CAGCGCAGAA GGACCAGCAG AAAGATGCCG AGGCGGAAGG GCTGAGCGGC ACGACCTTGC 120
10 TCGCGAAGCT GATTCCCTCC GGTGCAGGCC GGGAGTGGCT GGAGCGGCGC CGCGCGACCA 180
TCCGGCCCTG GAGCACTTC GTGGACCAGC AGCGCTTCTC ACGGCCCGC AACCTGGGAG 240
AGCTGTGCCA GCGCCTCGTA CGCAACGTGG AGTACTACCA GAGCAACTAT GTGTTCGTGT 300
15 TCCTGGGCCT CATCCTGTAC TGTGTGGTGA CGTCCCCTAT GTTGCTGGTG GCTCTGGCTG 360
TCTTTTTCGG CGCCTGTAC ATTCTCTATC TGCGCACCTT GGAGTCCAAG CTTGTGCTCT 420
20 TTGGCCGAGA GGTGAGCCCA GCGCATCAGT ATGCTCTGGC TGGAGGCATC TCCTTCCCCT 480
TCTTCTGGCT GGCTGGTGCG GGCTCGGCCG TCTTCTGGGT GCTGGGAGCC ACCCTGGTGG 540
TCATCGGCTC CCACGCTGCC TTCCACCAGA TTGAGGCTGT GGACGGGGAG GAGCTGCAGA 600
25 TGGAAACCGT GTGAGGTGTC TTCTGGGACC TGCCGGCCTC CCGGGCCAGC TGCCCCACCC 660
CTGCCCATGC CTGTCTGCA CGGCTCTGCT GCTCGGGCCC ACAGCGCCGT CCCATCACAA 720
30 GCCCGGGGAG GGATCCCGCC TTTGAAAATA AAGCTGTTAT GGGTGTCAAT CAGGAAAAAA 780
AAAAAAAAA AAAAAAAAAA AAAAAAAAAA 809

35

(2) INFORMATION FOR SEQ ID NO: 240:

(i) SEQUENCE CHARACTERISTICS:

40 (A) LENGTH: 2201 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 240:

TCGACCCACG CGTCCGCAA CATGGCGGCT GCCGTGGTGC AGCGCCCGGG CTGAGCGACA 60
GCAAGTGCAG CGGGCTCCTA CCCCGGGTGA GGGGTGGCCT CCGCGTGGGA TCGTGCCCTC 120
50 TTCAGCCCGC TCCTGTCCCC GACATCAGT GTAATCCGCA CGTCCCCTCC GCGCTGTGTG 180
TCTACTGAGA CGGGGAGGCG TGACAGGGCC CGGGTCCCTT CTCAGTGGTG CTCTGTGCTT 240
55 CAGGGCAAGC TCCCCGTCTC CGGGCGCACT TCCCTCGCCT GTGTTCGGTC CATCTCCTT 300
TCTCCAGCCT CCTCCCCTCG CAGGCGGATG AMCCGGACGA CGGGCCAGTG CCTGGCACCC 360
CGGGGTGGCC ARGGTCCAMG GGAACCCGA AGTCCGAGGA GCCCGARGTC CCGAACCAGG 420
60

	ARGGGCTGCA GCGCATCAMC GGCCCTGTCTC CCGGCCGPTC GGCTCTCATA GTGGCGGTGC	480
	TGTGCTACAT CAATCTCCTG AACTACATGG ACCGCTTCAC CGTGGCTGGC GTCCTTCOCG	540
5	ACATCGAGCA GTTCTTCAAC ATCGGGGACA GTAGCTCTGG GCTCATCCAG ACCGTGTTC	600
	TCTCCAGTTA CATGGTGTG GCACCTGTGT TTGGCTACCT GGGTGACAGG TACAATCGGA	660
10	AGTATCTCAT GTGCGGGGC ATTGCCCTCT GGTCCCTGGT GACACTGGG TCATCCTTCA	720
	TCCCCGAGA GCATTTCTGG CTGCTCCTCC TGACCCGGG CCTGGTGGG GTCGGGGAGG	780
	CCAGTTATTC CACCATCGG CCCACTCTCA TTGCCGACCT CTTTGTGGC GACCAGCGGA	840
15	CCGATGCTC AGCATCTTCT ACTTTGCCAT TCCGGTGGC AGTGGTCTGG GCTACATTGC	900
	AGGCTCCAA GTGAAGGATA TGGCTGGAGA CTGGCACTGG GCTCTGAGG TGACACCGG	960
20	TCTAGGAGTG GTGGCCGTC TGCTGCTGTT CCTGGTAGTG CGGGAGCCG CAAGGGGAGC	1020
	CGTGAGCGC CACTCAGATT TGCCACCCCT GAACCCACC TCGTGGTGG CAGATCTGAG	1080
	GGCTCTGSCA AGAAATCCTA GTTTCGTCTT GTCTTCCCTG GGTTCACATG CTGTGGCCTT	1140
25	TGTCACGGC TCCCTGGCTC TGTGGGCTCC GGCATTCTTG CTGCGTTCCC GCGTGGTCTT	1200
	TGGGAGACC CCACCTGCC TTCCCGAGA CTCTGCTCT TCCTCTGACA GTCTCATCTT	1260
30	TGGACTCATC ACCTGCCTGA CCGAGTCCT GGGTGTGGC CTGGGTGTG AGATCAGCCG	1320
	CCGGCTCCG CACTCCAACC CCCGGCTGA TCCCTGGTC TGTGCCATG GCCTCCTGG	1380
	CTCTGACCC TTCTCTTCC TGTCCCTGTC CTGCGCCGT GGTAGCATG TGGCCACTTA	1440
35	TATTTTATC TTCAATGGAG AGACCTCCT GTCCATGAAC TGGGCCATG TGGCCGACAT	1500
	TCTGCTGTAC GTGTGATCC CTACCCGACG CTCCACGCC GAGGCCTTCC AGATCGTGCT	1560
40	GTCCACCTG CTGGGTGATG CTGGGAGCCC CTACCTCATT GGCCTGATCT CTGACCCCT	1620
	GCGCCGAAC TGGCCCCCT CTTCTTGTG CGAGTTCCGG GCTCTGCAGT TCTCGCTCAT	1680
	GCTCTGCGG TTTGTGGGG CACTGGGCGG CGCACTTTC TGGGCACCG CATCTTCATT	1740
45	GAGGCCGACC GCCGCGGGC ACAGCTGCAC GTGCAGGGC TGCTGCACGA AGCAGGTCC	1800
	ACAGACGACC GGATGTGGT GCCCAGCGG GGCCGCTCCA CCCGCGTGC CGTGGCCAGT	1860
50	GTGCTCATCT GAGARGCTGC CGCTACCTA CTTGCACATC TGCCACAGCT GGCCCTGGC	1920
	CCACCCACG AAGGCGCTGG GCCTAACCCC TTGGCCTGGC CCAGCTTCCA GAGGGACCT	1980
	GGGCCGTGTG CCAGCTCCA GACACTACMT GGGTAGCTCA GGGGAGGAG TGGGGTCCA	2040
55	GGAGGGGAT CCTCTCCAC AGGGGAGCC CCAAGGGCTC GGTGCTATT GTAACGGAAT	2100
	AAAATTGTGA GCCAGACCC AGGTGCCTGC TCTGCTCTT CTCTGGGTGG CCTCTGATCT	2160
60	TGCACCCCGT CTTACCCCA GGGCTCCTGA AGACTGTGGG T	2201

(2) INFORMATION FOR SEQ ID NO: 241:

5

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1661 base pairs

(B) TYPE: nucleic acid

10

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 241:

15	GTCCTTCCCG ACATCGAGCA GTTCTTCAAC ATCGGGGACA GTAGCTCTGG GTCATCCAG	60
	ACCGTGTTCA TCTCCAGTTA CATGGTGTG GCACCTGTGT TTGGCTACCT GGGTGACAGG	120
	TACAATCGGA AGTATCTCAT GTGCGGGGGC ATTGCCTTCT GGTCCCTGGT GACACTGGGG	180
20	TCATSCITCA TCCCCGAGA GCATTCTGG CTGCTCCTCC TGACCCGGGG CCTGGTGGGG	240
	GTGCGGGAGG CCAGTTATTC CACCATCGCG CCCACTCTCA TTGCCGACCT CTTGTGTGGC	300
	GACCAGCGGA SCGGATGCTC AGCATCTTCT ACTTTGCCAT TCCGGTGGGC AGTGGTCTGG	360
25	GCTACATTGC AGGCTCCAAA GTGAAGGATA TGGCTGGAGA CTGGCACTGG GCTCTGAGGG	420
	TGACACCGGG TCTAGGAGTG GTGGCCGTC TGCTGCTGTT CCTGGTAGTG CGGGAGCCGC	480
30	CAAGGGGAGC CGTGGAGCGC CACTCAGATT TGCCACCCCT GAACCCACCC TCGTGGTGGG	540
	CAGATYTGAG GGCTCTGGCA AGAAATCCTA GTTTCGTCTT GTCTTCCCTG GGCTTCACTG	600
	CTGTGGCCTT TGTACCGGC TCCCTGGCTC TGTGGGCTCC GGCAATCCTG CTGCGTTCCC	660
35	GCGTGGTCTT TGGGGAGACC CCACCTGCC TTCCCGAGA CTCTGCTCT TCTCTGACA	720
	GTCTCATCTT TGGACTCATC ACCTGCCCTG CCGGAGTCCT GGGTGTGGGC CTGGGTGTGG	780
40	AGATCAGCCG CCGGYTCCGC CACTCCAACC CCCGGGCTGA TCCCCTGGTC TGTGCCACTG	840
	GCCTCCTGGG CTCTGCACCC TTCCTCTTCC TGTCCCTTGC CTGCGCCCGT GGTAGCATCG	900
	TGGCCACTTA TATTTTCATC TTCATTGGAG AGACCCTCCT GTCCATGAAC TGGGCCATCG	960
45	TGGCCGACAT TCTGCTGTAC GTGGTGATCC CTACCCGACG CTCCACCGCC GAGGCCTTCC	1020
	AGATCGTGCT GTCCACCTG CTGGGTGATG CTGGGAGCCC CTACCTCATT GGCCTGATCT	1080
50	CTGACCGCCT GCGCCGAAC TGGCCCCCCT CCTTCTTGTG CGAGTTCCGG GCTCTGCAGT	1140
	TCTCGCTCAT GCTCTGCGCG TTTGTTGGGG CACTGGGCGG CGCACTTTCC TGGGCACCGN	1200
	CATCTTCATT GAGGCCGACC GCCGGCGGGC ACAGCTGCAC GTGCAGGGCC TGCTGCACGA	1260
55	AGCAGGGTCC ACAGACGACC GGATTGTGGT GCCCCAGCGG GGCCGCTCCA CCCGCGTGCC	1320
	CGTGGCCAGT GTGCTCATCT GAGAGGCTGC CGCTCACCTA CCTGCACATC TGCCACAGCT	1380
60	KGCCCTGGGC CCACCCACG AAGGGCCTGG GCCTAACCCC TTGGCCTGGC CCAGCTTCCA	1440

GAGGGACCCCT GGGCCGTGTG CCAGCTCCCA GACACTACMT GGGTAGCTCA GGGGAGGAGG 1500
 TGGGGGTCCA GGAGGGGAT CCCTCTOCAC AGGGGNCACC CCAAGGGCTC GGTGCTATTT 1560
 5 GTAACGGAAT AAAATTGTGA GCCAGACCCC AGGTGCCTGC TCTCGTCTTT CTCTGGGTGG 1620
 CCTCTGATCT TGCACCCCGT CTTACCCCCA GGGCTCCTGA A 1661

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(2) INFORMATION FOR SEQ ID NO: 242:

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(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1146 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 242:

NGACAGAAAA GCAGAAGATG AGACTCTGTT CATTCACTTT TCCTAGGCCC ATCTGTGGT 60
 25 CATCTTTCCC CCTCCCATCA TACCTCCTCC TTCCTGGAGC CTCTGCCGGC TTGGCTGTAA 120
 TGGTGGCACT TACCTGGATA TTTCAGTGGG AGGATGAAAG GCGAGACTCA CCCTACGCGG 180
 TGGGACAGAT GGGGAGAGGA AAAAGGCAGA GATNGCCAGG AGAGGGGTGC AGGACAAACC 240
 30 AGAGAGGTG GGTGAGGGA AAAGTGTNGG GAGAAAGTGG GGTGCAGGCC CTGCAGGCCG 300
 GTTTAGCCAG CAGCTGCGGC CTCCCAGGC CCTTGGCATC CAACTTCGCA GACAGGGTAC 360
 35 CAGCTCCTG GTGTGTATCA TAGGATTTGT TCACATAGTG TTATGCATGA TCTTCGTAAG 420
 GTTAAGAAGC CGTGGTGGTG CACCATGACA TCCAACCCGT ATATATAAAG ATAAATATAT 480
 ATATATATGT ATGTAAATTA TAGCACTGAG GGCCCTGCTG CCCTGCTGGA CCAAGCAAAA 540
 40 CTAAGCCTTT TGGTTTGGGT ATTATGTTTC GTTTTGTAT TTGTTTGTTC TTGTGGCTTG 600
 TCTTATGTCG TGATAGCACA AGTGCCAGTC GGATTGCTCT GTATTACAGA ATAGTGTTC 660
 45 TAATTCATCA ATGTTCTAGT TAATGCTAC CTCAGCACCT CCTCTTAGCC TAATTTTAGG 720
 AGGTGCCCCA ATTTTGTTC TTCAATTTTA CTGGTTACTT TTTGTACAA ATCAATCTCT 780
 TTCTCTCTTT CTCTCCTCCC CACCTCTCAC CCTTGCCCTC TCCATCTCCC TCTCCGCCC 840
 50 TCCCCCTCTC CCTCTGGCTC CCCGTCTCAT TTCTGTCCAC TCCATTCTCT CTCCCTCTCT 900
 CCTGCCTCTT GCTGCCCCCT CCCAGCCCA CTTSCCGAG TTGTGCTTGC CGCTCCTTAT 960
 55 CTGTTCTAGT TCCGAAGCAG TTCACTCGA AGTTGTGCAG TCCTGGTTGC AGCTTTCCGC 1020
 ATCTGCCTTC GTTTCGTGTA GATTGACGCG TTTCTTTGTA ATTTCACTGT TTCTGACAAG 1080
 ATTTAAAAAA AAAAAAGGA AAAAAAAA AAAAAAAC TCGAGGGGGG GCCCGGTACC 1140
 60

CAATTG

1146

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(2) INFORMATION FOR SEQ ID NO: 243:

(i) SEQUENCE CHARACTERISTICS:

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(A) LENGTH: 1350 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 243:

15	AACCCACGGC TGCTGCGGCA GGGCGTGGAG GGCAGAGGGC CGCGGAGGCG CAGTTGCAAA	60
	CATGGCTCAG AGCAGAGACG GCGGAAACCC GTTCGCCGAG CCCAGCGAGC TTGACAACCC	120
20	CTTTCAGCCA CCACCAGCCT ATGAGCCTCC AGCCCCTGCC CCATTGCCTC CACCCTCAGC	180
	TCCCTCCTTG CAGCCCTCGA GAAAGCTCAG CCCCACAGAA CCTAAGAACT ATGGCTCATA	240
	CAGCACTCAG GCCTCAGCTG CAGCAGCCAC AGCTGAGCTG CTGAAGAAAC AGGAGGAGCT	300
25	CAACCGGAAG GCAGAGGAGT TGGACCGAAG GAGNCGAGAG CTGCAGCATG CTGCCCTGGG	360
	RGGCACAGCT ACTCGACAGA ACAATTGGCC CCCTCTACCT TCTTTTGTGTC CAGTTCAGCC	420
30	CTGCTTTTTC CAGGACATCT CCAITGGAGAT CCCCCAAGAA TTTCAGAAGA CTGTATCCAC	480
	CATGTACTAC CTCTGGATGT GCAGCAGST GGCTCTTCTC CTGAACCTCC TCGCCTGCCT	540
	GGCCAGCTTC TGTGTGGAAC CCAACAATGG CGCAGGCTTT GGGCTTTCTA TCCCTCTGGT	600
35	CCTCCTTTTC ACTCCCTGCT CTTTGTCTG CTGGTACCGC CCCATGTATA AGGCTTTCCG	660
	GAGTGACAGT TCATTCAATT TCTTCGTTTT CTCTTTCATT TTCTTCGTCC AGGATGTGCT	720
40	CTTTGTCTC CAGGCCATTG GTATCCCAGG TTGGGGATTG AGTGGCTGGA TCTCTGCTCT	780
	GGTGGTGCCG AAGGCAACAC AGCAGTATCC GTGCTCATGC TGCTGGTCGC CCTGCTCTTC	840
	ACTGGCATTG CTGTGCTAGG AATTGTTCATG CTGAAACGGA TCCACTCCTT ATACCGCCGC	900
45	ACAGGTGCCA GCTTTCAGAA GGCCAGCAA GAATTGTCTG CTGGTGTCTT CTCCAACCCT	960
	GCGGTGCGAA CCGCARCTTG CCAATGCAGC CGCTGGGGCT GCTGAAAATG CCTTCCGGGC	1020
50	CCCGTGACCC CTGACTGGGA TGCCCTGGCC CTGCTACTTG AGGGAGCTGA CTTAGCTCCC	1080
	GTCCCTAAGG TCTCTGGGAC TTGGAGAGAC ATCACTAACT GATGGCTCCT CCGTAGTGCT	1140
	CCCAATCCTA TGGCCATGAC TGCTGAACCT GACAGGCGTG TGGGGAGTTC ACTGTGACCT	1200
55	AGTCCCCCA TCAGGCACA CTGCTGCCAC CTCTCACACG CCCCACCCA GCTTCCCTCT	1260
	GCTGTGCCAC GGCTGTGCT TCGGTATTT AAATAAAAAG AAAGTGAAC TGGAAAAAA	1320
60	AAAAAAAAA AAAAAAAG GGGGNCNC	1350

5 (2) INFORMATION FOR SEQ ID NO: 244:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1529 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 244:

15 TCCCAGAGGC CGGGGGGTC CAGCTCTGCC TGTAGCAGAG CCCTGAGGAG GAGGAGGAAG 60
 AGGATGTGCT GAAATACGTC CGGAGATCT TTTTCAGCTA GGGCATAAAC TGTGCACTGA 120
 ACTGTCTGCC GAGAGCAGCT GGAGGACAGC TGAGCTTCCA CTGGTGCTGC TGGGCCGMCC 180
 20 GCGTGTGGGA ATGGGGCTCT CTGTGCTCCT ACCTTTGTGC CTTCTTGGGC CTGGCAGATT 240
 CACCTCAGGC CAGAAGCCCC TGGACACTCC GGGCCTTGGG GTGCCGTTCT GAGTGTGCGG 300
 25 AAGGCAGGAC TCAAAATGAG ATCCCATTTG ACTCCCTCTG TATGTACTGT GCCCTCTCCT 360
 GGCTCTTGAG GCTCTGGAGT CCCAATTGTC TGTGTTAGTC AGTGACCAGG TTCCAGGGAA 420
 AATRATGTCA TGTGGTGGTC CAACTTACTG GAACCAAGA GACAGTACTT TGCAAAGAAA 480
 30 AGGATCACTG CCAGGTGCAC TGAATTGCT ACAGTTTAGT CCGCATGATC TCTCCTGAAG 540
 GAGGAAGCCT GTTTCAAAAA TAGTTTCCAT CATGAGTCTA TCAATGAGCT CCCACCTCTC 600
 35 CAGCCAGCCT AGAAAGCAAA CGAGCTGCCC ACAGTTCTCT GCCCTGTCTG GGAGGTTGAG 660
 GCCACAGTGT ATAGACTGGT AAGCCAGACA GGCCTCCTCC CGCAAGCTGC TACCTTGCTT 720
 TCACCTGTAC CTTGGTCCCC GGGCAGCTAG CTATAAAGCA AGAGGGACAG GAGCCCAGAA 780
 40 GAGACACTGA GGACAAGAGA TCACACCAGA GTACATGTCT CTGCTCTGT TTTCACTGTG 840
 GCTTTGGACA GGAATATATG AATAAATCAC TGCCATACAG GTTTTCCAAT ACACAAGTGC 900
 45 TAGAAAATAC ACACAATTCC CCAATGCGTA AGTTGTGCTA ATGTCTTTCC AAGTTCTGGG 960
 TTGGGAAGTG GAGGGTGGCA GCGTTTGTTT GTGCGCAACC GTCCAGTCCT GTTCACAGCG 1020
 50 AGGATTGGA GTCTCCAGG GTCTCATCAT GGGAGTGATT TGTGAGCGGA CGCCTCTGCC 1080
 CTGTCTGGCT TCAGGTCCAG GGAAGCTTTG AAGCAGTCAA GCCTTGCTTT TGTACCCCAT 1140
 GTGTCTGTG TTTGTTGAGT CACTCAGAGA TCACTCCTGG ACCTCTGGGG TTGGAGTTCC 1200
 55 AGTGATGGCT TATGGCGGCC CACTCACTAT GGTGGGCTGA GTGGAAGCTC CTTAACCATG 1260
 TCCCAGAGA CACTGAGGTG CTCGCTCTTT TAATGTCTC GTTTGTTGCC GTAAGTTCTT 1320
 60 TGCTAGGTTT CATTTTGCCA TTGGGCAAAT CAGCCTGGAA GTCTGGCCCC ATGACAGCAA 1380

	TCACTCCCTC CCCACCTCC TGAAGCTAGA GGAAGATTG CTCAGATCCA TTAATTAAAG	1440
	CAGGAATTGG TGTGACAATG AGCTGCATGG TTTAGGGAGT CTTTGGGAGC CTTGGAAGTC	1500
5	CTGAAGGACA AACAATCTTG TACTAAGAA	1529
10	(2) INFORMATION FOR SEQ ID NO: 245:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 1537 base pairs	
	(B) TYPE: nucleic acid	
15	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 245:	
20	GTGCGAGGTC CCCGCCAGCC CCCAGCGGCC TTCCCGGCC GGGGCGCTCC CAGAGCAAAC	60
	GAGGCCCTG AGAGCTCCAC CTAGTTCACA GGATAAAATC CCACAGCAGA ACTCGGAGTC	120
	AGCAATGGCT AAGCCCCAGG TGGTTGTAGC TCCTGTATTA ATGTCTAAGC TGTCGTGAA	180
25	TGCCCCTGAA TTTTACCCTT CAGGTTATTC TTCCAGTTAC ACAGAATCCT ATGAGGATGG	240
	TTGTGAGGAT TATCCTACTC TATCAGAATA TGTTTCAGGAT TTTTGAATC ATCTTACAGA	300
30	GCAGCTGGC AGTTTGTAAA CTGAAATTGA ACAGTTTGCA GAGACCTGA ATGGTTGTGT	360
	TACAACAGAT GATGCTTTGC AAGAACTTGT GGAATCATC TATCAACAGG CCACATCTAT	420
	CCCAAATTTT TCTTATATGG GAGCTCGCCT GTGTAATTAC CTGTCCCATC ATCTGACAAT	480
35	TAGCCACAG AGTGCAACT TCCGCCAAT GCTACTTCAA AGATGTCGGA CTGAATATGA	540
	AGTTAAAGAT CAAGCTGCAA AAGGGGATGA AGTTACTCGA AAACGATTTT ATGCATTTGT	600
40	ACTCTTTCTG GGAGAACTTT ATCTTAACCT GGAGATCAAG GGAACAAATG GACAGGTTAC	660
	AAGAGCAGAT ATTCTTCAGG TTGGTCTTCG AGAATTGCTG AATGCCCTGT TTTCTAATCC	720
	TATGGATGAC AATTTAATTT GTGCAGTAAA ATGTTTAAAG TTGACAGGAT CAGTTTGGGA	780
45	AGATGCTTGG AAGGAAAAAG GAAAGATGGA TATGGAAGAA ATTATTCAGA GAATTGAAAA	840
	CGTTGTCCTA GATGCAAACT GCAGTAGAGA TGTAACACAG ATGCTCTTGA AGCTTGTAGA	900
50	ACTCCGCTCA AGTAACTGGG GCAGAGTCCA TGCAACTTCA ACATATAGAG AAGCAACACC	960
	AGAAAATGAT CTTAACTACT TTATGAATGA ACCAACATTT TATACATCTG ATGGTGTTC	1020
	TTTCACTGCA GCTGATCCAG ATTACCAAGA GAAATACCAA GAATTACTTG AAAGAGAGGA	1080
55	CTTTTTCCTA GATTATGAAG AAAATGGAAC AGATTTATCC GGGGCTGGTG ATCCATACTT	1140
	GGATGATATT GATGATGAGA TGGACCCAGA GATAGAAGAA GCTTATGAAA AGTTTGTGTT	1200
60	GGAATCAGAG CGTAAGCGAA AACAGTAAAG TTAAATTTCA GCATATCAGT TTTATAAAGC	1260

AGTTTAGGTA TGGTGATTTA GCAGAACACA AGAGAGCAAG AAAATGTGTC ACATCTATAC 1320
CAAATTRAGG ATGTTGAGTT ATGTTACTAA TGTATGCAAC TTAAATTTTG TTAAACACTA 1380
5 TCTGCCAAAA TAAACTTTAT TCCCTATAAC TTAAAATGTG TATATATATA TAATAGTTTA 1440
TTATGTACAG TTAATCTAC TGTMTTGGCT GCAATAAAAT CGATTTTGAA ATAAAWRAAA 1500
10 AAAAAAAAAA AAGGGNGGCC GCTCTAGAGG ANCCAAG 1537

15 (2) INFORMATION FOR SEQ ID NO: 246:

(i) SEQUENCE CHARACTERISTICS:

- 20 (A) LENGTH: 506 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 246:

25 TGCAGGATTT GGCCAGGACC CSCCGCGGTG GCGGTGCTA TCGCTTCGCA GAACCTACTC 60
AGGCAGCCAG CTGAGAAGAG TTGAGGGAAA GTGCTGCTGC TGGGTCTGCA GACGCGATGG 120
ATAACGTGCA GCCGAAAATA AAACATCGCC CCTTCTGCTT CAGTGTGAAA GGCCACGTGA 180
30 AGATGCTGCG GCTGGATATT ATCAACTCAC TGGTAACAAC AGTATTCATG CTCATCGTAT 240
CTGTGTTGGC ACTGATACCA GAAACCACAA CATTGACAGT TGGTGGAGGG GTGTTTGCAC 300
35 TTGTGACAGC AGTATGCTGT CTGCGGACG GGGCCCTTAT TTACCGGAAG CTTCGTGTCA 360
ATCCCAGCGG TCCTTACCAG AAAAAGCCTG TGCATGAAAA AAAAGAAGTT TTGTAATTTT 420
ATATTACTTT TTAGTTTGAT ACTAAGTATT AAACATATTT CTGKATTATT CCAAAAAAAAA 480
40 AAAAAAAAAA AAAAAAATT TGGTGG 506

45

(2) INFORMATION FOR SEQ ID NO: 247:

(i) SEQUENCE CHARACTERISTICS:

- 50 (A) LENGTH: 1348 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 247:

55 GTCTTCTTTT TNCTGTTTTG AGTGGTGAG TGAGTGAATA GGTAACATG GGCCTTCAGG 60
ATGACCCCTT GGAAGTGTGC CGAGTTCCTT AAATCTCAGC TGGGATCCTG GACCTGGGAG 120
60 GCCCCTGTGA GGGCCAGCTC TGGAAAAACC TGGGAGTTGA TGCCGGAGGY TGGGAAGAAC 180

	TCTGCTCGAG GGCAGGGTGC CCTGGAACAC TGGTAGTTCT GGGGCTGGGA GGGAGAGGGG	240
5	CTCCGGCTTT CTCTGAAATG AACACTGCTC TTCAGCAGTT CAAGTACTTG TTCTCAAAAC	300
	ATTTTCTAAT TGATTGGTAG GTTTTCATAA GCATTGTTTC TTTAAGGCAT GGAAAGGGAA	360
	GAATGCTCAA GCAAGTCATG TTTGTTTTCA GTGGGATGGG CCCGCGTTCT CACTGCTGGG	420
10	GGCTTCCCCT TGCATGTGGC ACCTTTGTGC AGGGCCACCA GGCAGACTCT TCCCACCTTC	480
	TCCCCTGAA GCACCAAGGG GCTTGAACCG TAATTGGCT AATCAGAGGC ATTTTTTTTG	540
15	TCCTAGTATC TTTCACACTT GTCCAACCGT CTTATTTTTT TAAAAGTTCT GTTGCTTGTA	600
	TTAACACGAA ACTAGAGAGA AATAGTTTCT GAAGCCAGTT TATTGTGAAG ATCCCCAAGG	660
	GGAGGTTCCG TAGAGAAAAA TAGTAAGCTG GTTTAGAAAC TGACGAGGGC AAACAGCCAG	720
20	GACGCATTGG AGAGGAATTT GCCAAAGATC TACCCTGAGA TAACGCCTGT CCAGTGCTCT	780
	CACCACGTGA ATAACCAGCG CTCCAAAGTG TTTTCTGCT TTGAAAAAA AAATTCCACA	840
25	AGCTTTTAAA GGTGCATTTA AGAATCCATG TGACTTTAGA ATGGAAGTGC CGGCCCTGGC	900
	AACTGTCACG TGTGCTAGAA GGTTCGATGC CTCTGGAATG CATGTGATAC TCATCTCCAT	960
	TTTGTTCCT TGATTGCATT TTTGTTCPTT TAGCAGATCT GTCCCTGTGG GTGGTGTCTA	1020
30	AGAAGTCGGA CACCTTGGTT TTTGTGTTAG ATTGAGCTGG GCAGCTGCAA TCAGCTTCTT	1080
	TATATGCAA TTAGGCACGA CCCATCTGTG GTTCCCTGGT TGGTGGCTAA TGAAGTGAGG	1140
35	GGAGGGAGGG ATGTCACCCC AAAAGTAGGC CCTCCATTG GCTTTGGCCA GGCCAGACAC	1200
	TTACATCGT TTACATGGTT CTGTGTAATT TTAAAGTTTA TGTGTATAAA GCGAAGCTGT	1260
	TTCTGTGAAA CTGTATATTT TGTAAATAAA TATATTGCTA CTTTGAGAWR AAAAAAAAAA	1320
40	AAAAACTCGA GGGGGGCCCC GTACCCAA	1348

45 (2) INFORMATION FOR SEQ ID NO: 248:

(i) SEQUENCE CHARACTERISTICS:

- 50 (A) LENGTH: 1766 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 248:

55	GTCCCGAATC GGCAGAGCGG CACGAGCGGC CACGAGAGCA GGCGGAGTAA AGGGACTTGA	60
	GCGAGCCAGT TGCCGGATTA TTCTATTTCC CCTCCCTCTC TCCCGCCCCG TATCTCTTTT	120
60	CACCCTTCTC CCACCCCTGC TCGCGTASCA TGGCGGAGCG TCGCGGCCA CTCAGTCCCA	180

	TTCCATCTCC TCGTCGTCTT TGGAGCCGA GCCGTCCGCG CCCGGCGGCG GCGGGAGCCC	240
	AGGAGCCTGC CCCGCCCTGG GGACGAAGAG CTGCAGCTCC TCCTGTGCGG TGCACGATCT	300
5	GATTTTCTGG AGAGATGTGA AGAAGACTGG GTTGTCTTTT GGCACCACGC TGATCATGCT	360
	GCTTTCCTTG GCAGCTTTCA GTGTCATCAG TGTGGTTTCT TACCTCATCC TGGCTCTTCT	420
10	CTCTGTCACC ATCAGCTTCA GGATCTACAA GTCCGTCATC CAAGCTGTAC AGAAGTCAGA	480
	AGAAGGCCAT CCATTCAAAG CCTACCTGGA CGTAGACATT ACTCTGTCCT CAGAAGCTTT	540
	CCATAATTAC ATGAATGCTG CCATGGTGCA CATCAACAGG GCCCTGAAAC TCATTATTCTG	600
15	TCTCTTTCTG GTAGAAGATC TGGTTGACTC CTTGAAGCTG GCTGTCTTCA TGTGGCTGAT	660
	GACCTATGTT GGTGCTGTTT TTAACGGAAT CACCCTTCTA ATTCTTGCTG AACTGCTCAT	720
20	TTTCAGTGTC CCGATTGTCT ATGAGAAGTA CAAGACCCAG ATTGATCACT ATGTTGGCAT	780
	CGCCCCGAGAT CAGACCAAGT CAATTGTTGA AAAGATCCAA GCAAAACTCC CTGGAATCGC	840
	CAAAAAAAG GCAGAATAAG TACATGGAAA CCAGAAATGC AACAGTTACT AAAACACCAT	900
25	TTAATAGTTA TAACGTCGTT ACTTGTAATA TGAAGGAAAA TACTCAGTGT CAGCTTGAGC	960
	CTGCATTCCA AGCTTTTTTT TTAATTGGT GTTTTCTCCC ATCCTTTCCC TTTAACCCCTC	1020
30	AGTATCAAGC ACAAAAATTG ATGGACTGAT AAAAGAATA TCTTAGAACT CAGAAGAAGA	1080
	AAGAATCAAA TTCATAGGAT AAGTCAATAC CTTAATGGTG GTAGAGCCTT TACCTGTAGC	1140
	TTGAAAGGGG AAAGATTGGA GGTAAGAGAG AAAATGAAAG AACACCTCTG GGTCTTCTG	1200
35	TCCAGTTTTC AGCACTAGTC TTAATCAGCT ATCCATTATA GTTTTGCCCT TAAGAAGTCA	1260
	TGATTAACTT ATGAAAAAAT TATTTGGGGA CAGGAGTGTG ATACCTTCCT TGGTTTTTTT	1320
40	TTGCAGCCCT CAAATCCTAT CTCCTGCCC CACAATGTGA GCAGCTACCC CTGATACTCC	1380
	TTTTCTTTAA TGATTAACT ATCAACTTGA TAAATACTT ATAGGTGATA GTGATAATTC	1440
	CTGATTCCAA GAATGCCATC TGATAAAAAA GAATAGAAAT GGAAAGTGGG ACTGAGAGGG	1500
45	AGTCAGCAGG CATGCTGCGG TGGCGGTCAC TCCTCTGCC ACTATCCCCA GGAAGGAAA	1560
	RGCTCCGCCA TTTGGGAAAG TGGTTTCTAC GTCAGTGGAC ACCGGTTCTG AGCATTAGTT	1620
50	TGAGAACTCG TTCCCGAATG TGCTTTCCTC CCTCTCCCTT GCCCACCCTA AGTTTAATAA	1680
	ATAAGGTGT ACTTTTCTTA CTATAAAATA AAAAAAAAAA AACTCGAGGG GGGCCCGGTA	1740
	CCCAAATCGC CGGATATGAT CGTAAA	1766

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(2) INFORMATION FOR SEQ ID NO: 249:

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(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2664 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 249:

	AGTGTCTCTCG GAGCAGGCGG AGTAAAGGGA CTGAGCGAG CCAGTTGCCG GATTATTCTA	60
10	TTTCCCTCC CTCTCTCCG CCCCGTATCT CTTTTCACCC TTCTCCACC CTCGCTCGCG	120
	TASCATGGCG GAGCGTCGGC GGCCACTCAG TCCCATTCCTA TCTCCTCGTC GTCCTTCGGA	180
15	GCCGAGCCGT CCGCGCCCGG CGGCGGCGGG AGCCCAGGAG CCTGCCCCGC CCTGGGGACG	240
	AAGAGCTGCA GCTCTCTCTG TCGGTGCAC GATCTGATTT TCTGGAGAGA TGTGAAGAAG	300
	ACTGGGTTTG TCTTTGGCAC CACGCTGATC ATGCTGCTTT CCCTGGCAGC TTTCACTGTC	360
20	ATCAGTGTGG TTTCTTACCT CATCTGGCT CTCTCTCTG TCACCATCAG CTTCAGGATC	420
	TACAAGTCCG TCATCCAAGC TGTACAGAAG TCAGAAGAAG GCCATCCATT CAAAGCCTAC	480
25	CTGGACGTAG ACATTACTCT GTCCTCAGAA GCTTTCCATA ATTACATGAA TGCTGCCATG	540
	GTGCACATCA ACAGGGCCCT GAAACTCATT ATTCGTCTCT TTCTGGTAGA AGATCTGGTT	600
	GACTCCTTGA AGCTGGCTGT CTTTATGTGG CTGATGACCT ATGTTGGTGC TGTTTTAAAC	660
30	GGAATCACCC TTCTAATTCT TGCTGAACTG CTCATTTTCA GTGTCCCGAT TGTCTATGAG	720
	AAGTACAAGA CCCAGATTGA TCACTATGTT GGCATCGCCC GAGATCAGAC CAAGTCAATT	780
35	GTTGAAAAGA TCCAAGCAAA ACTCCCTGGA ATCGCCAAA AAAAGGCAGA ATAAGTACAT	840
	GGAAACCAGA AATGCAACAG TTAATAAAAC ACCATTTAAT AGTTATAACG TCGTTACTTG	900
	TACTATGAAG GAAATACTC AGTGTGAGCT TGAGCCTGCA TTCCAAGCTT TTTTTTTAAT	960
40	TTGGTGTTTT CTCCCATCCT TTCCCTTTAA CCCTCAGTAT CAAGCACAAA AATTGATGGA	1020
	CTGATAAAAG AACTATCTTA GAACTCAGAA GAAGAAAGAA TCAAATTCAT AGGATAAGTC	1080
45	AATACCTTAA TGGTGGTAGA GCCTTTACCT GTAGCTTGAA AGGGGAAAGA TTGGAGGTAA	1140
	GAGAGAAAAT GAAAGAACAC CTCTGGGTCC TTCTGTCCAG TTTCAGCAC TAGTCTTACT	1200
	CAGCTATCCA TTATAGTTTT GCCCTAAGA AGTCATGATT AACTTATGAA AAAATTATTT	1260
50	GGGACAGGA GTGTGATACC TTCCTTGGTT TTTTMTTGCA GCCCTCAAAT CCTATCTTCC	1320
	TGCCCCACAA TGTGAGCAGC TACCCCTGAT ACTCCTTTTC TTTAATGATT TAACTATCAA	1380
55	CTTGATAAAT AACTTATAGG TGATAGTGAT AATTCCTGAT TCCAAGAATG CCATCTGATA	1440
	AAAAAGAATA GAAATGGAAA GTGGGACTGA GAGGGAGTCA GCAGGCATGC TCGGGTGGCG	1500
	GTCACCTCCT CTGCCACTAT CCCCAGGGAA GGAAARGCTC CGCCATTTGG GAAAGTGGTT	1560
60	TCTACGTAC TGGACACCGG TTCTGAGCAT TAGTTTGAGA ACTCGTTCCC GAATGTGCTT	1620

	TCCTCCCTCT CCCCTGCCCA CCTCAAGTTT AATAAATAAG GTTGTACTTT TCTTACTATA	1680
5	AAATAAATGT CTGTAAGTGC TGTGCACTGC TGTAAACTTG TTAGAGAAAA AAATAACCTG	1740
	CATGTGGGCT CCTCAGTTAT TGAGTPTTTG TGATCCTATC TCAGTCTGGG GGGGAACATT	1800
	CTCAAGAGGT GAAATACAGA AAGCCTTTTT TTCTTGATCT TTTCCCGAGA TTCAAATCTC	1860
10	CGATTCCCAT TTGGGGGCAA GTTTTMTTCT TCACCTTCAA TATGAGAATT CAGCGAACTT	1920
	GAAAGAAAA TCATCTGTGA GTTCCTTCAG GTTCTCACTC ATAGTCATGA TCCTTCAGAG	1980
15	GGAATATGCA CTGGCGAGTT TAAAGTAAGG GCTATGATAT TTGATGGTCC CAAAGTACGG	2040
	CAGCTGCAAA AAGTAGTGGA AGGAAATTGT CTACGTGTCT TGGAAAAATT AGTTAGGAAT	2100
	TTGGATGGGT AAAAGGTACC CTTCCTTAC TCCATCTTAT TTTCTTAGCC CCCTTTGAGT	2160
20	GTTTTAACTG GTTTCATGTC CTAGTAGGAA GTGCATCTC CATCCTCATC CTCTGCCCTC	2220
	CCAGGAAGTC AGTGATTGTC TTTTGGGCT TCCCTCCAA AGGACCTTCT GCAGTGAAG	2280
25	TGCCACATCC AGTTCCTTTC TTTTGTGTCT GCTGTGTTA GATAATTGAA GAGATCTTTG	2340
	TGCCACACAG GATTTTTTTT TTTTFTAAGA AAAACCTATA GATGAAAAAT TACTAATGAA	2400
	ACTGTGTGTA CGTGTCTGTG CGTGCAACAT AAAAATACAG TAGCACCTAA GGAGCTTGAA	2460
30	TCTTGGTTC TGTAATAATT CAAATTGATG TGGTATTAAAT AAAAAAAAA AAAACAMAAA	2520
	AAAAAAAAA AAAAGGGCGG CCGCTCTAGA GGATCCAAGC TTACGTACGC GTGCATGCCA	2580
35	CGTCCATAGC TCTTCTTATA GGGGTCCCC AAATTCCATT CACGGGGCG TCGGTTTAN	2640
	AAAGGTCGTG ANTGGGGGAA ANCC	2664

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(2) INFORMATION FOR SEQ ID NO: 250:

(i) SEQUENCE CHARACTERISTICS:

- 45 (A) LENGTH: 865 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 250:

50

	CGTGGGAGTG AGGTACCAGA TTCAGCCCAT TTGGCCCCGA CGCCTCTTCT CTCGGAATCC	60
	GGGTGCTGCG GATTGAGGTC CCGGTTCCTA ACGGTGGGAT CGGTGCTCTC GGGATGAGAT	120
55	TTGGCGTTTC CTCGGGGCTT TGGTGGGATC GGTGTCTCA GGATGAGATT TAGGGTTTCC	180
	TCGGGGCTTT CGGGATCTTC ACCTAATATC CGGACTGCAA GATGGAGGAA GCGGGGAACC	240
60	TAGGAGGCCT GATTAAATG GTCCATCTAC TGGTCTGTG AGGTGCCTGG GGCATGCAAA	300

	TGTGGGTGAC CTTCGTCTCA GGCTTCCTGC TTTTCGGAAG CCTTCCCCGA CATACCTTCG	360
	GACTAGTGCA GAGCAAATC TTCCCCTTCT ACTTCCACAT CTCCATGGGC TGTGCCTTCA	420
5	TCAACCTCTG CATCTTGGCT TCACAGCATG CTTGGGCTCA GCTCACATTC TGGGAGGCCA	480
	GCCAGCTTTA CCTGCTGTTC CTGAGCCTTA CGCTGGCCAC TGTCAACGCC CGCTGGCTGG	540
10	AACCCCGCAC CACAGCTGCC ATGTGGGCCC TGCAAACCGT GGAGAAGGAG CGAGGCCTGG	600
	GTGGGGAGGT ACCAGGCAGC CACCAGGGTC CCGATCCCTA CCGCCAGCTG CGAGAGAAGG	660
	ACCCCAAGTA CAGTGTCTTC CGCCAGAATT TCTCCGCTA CCATGGGCTG TCCTCTCTTT	720
15	GCAATCTGGG CTGCGTCCTG AGCAATGGGC TCTGTCTCGC TGGCCTTGCC CTGGAATAA	780
	GGAGCCTCTA GCATGGGCCC TGCATGCTAA TAAATGCTTC TTCAGAAAAA AAAAAAAAAA	840
20	AAACTCGAGG GGGGCCCGGT ACCCA	865

25 (2) INFORMATION FOR SEQ ID NO: 251:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 2082 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 30 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 251:

35	TGGGGGGGGN AATGGGTGTC TGGCTCANGG ATTGCCNAAT CTGGAAATTC TCCATAACTT	60
	GCTAGCTTGT TTTTITTTTT TTTTITTTACA CCCCCCGCC CCACCCCGG ACTTGCACAA	120
	TGTTCAATGA TCTCAGCAGA GTTCTTCATG TGAAACGTTG ATCACCTTTG AAGCCTGCAT	180
40	CATTACATA TTTTITCTTC TTCTTCCCTC TCAGTTCATG AACTGGTGT CATTTTCTGT	240
	GTTGTGTGT GTTTATTTTT GTTTGGATTT TTTTITTTAA TTTTACTTTT AGAGCTTGCT	300
45	GTGTTGCCCA CCTTTTTTCC AACCTCCACC CTCACTCCTT CTCAACCCAT CTCTTCCGAG	360
	ATGAAAGAAA AAAAAAAGCA AAGTTTTTTT TTCTTCTCCT GAGTTCTTCA TGTGAGATTG	420
	AGCTTGCAAA GGAAAAAAA ATGTGAAATG TTATAGACTT GCAGCGTGCC GAGTTCCATC	480
50	GGGTTTTTTT TTTAGCATG TTATGCTAAA ATAGAGAAAA AAATGCTCAT GAACCTTCCA	540
	CAATCAAGCC TGCATCAACC TTCTGGGTGT GACTTGTGAG TTTTGGCCTT GTGATGCCAA	600
55	ATCTGAGAGT TTAGTCTGCC ATTAAAAAAA CTCATTCTCA TCTCATGCAT TATTATGCTT	660
	GCTACTTTGT CTTAGCAACA ATGAACTATA ACTGTTTCAA AGACTTTATG GAAAAGAGAC	720
	ATTATATTAA TAAAAAAA AAGCCTGCAT GCTGGACATG TATGGTATAA TTATTTTTTC	780
60	CTTTTTTTTT CCTTTTGGCT TGGAAATGGA CGTTCGAAGA CTTATAGCAT GGCATTCTA	840

CTTTTGT TTTT ATGCTCAT GACTTTTTTG AGTTTAGAAC AAAACAGTGC AACCGTAGAG 900
5 CCTTCTTCCC ATGAAATTTT GCATCTGCTC CAAACTGCT TTGAGTTACT CAGAACTTCA 960
ACCTCCCAAT GCACTGAAGG CATTCTTGT GCAAAGATAC CAGAATGGGT TACACATTTA 1020
ACCTGGCAAA CATGAAGAA CTCCTTATGT TTTCTTTTA ATAAGAATGA CGCCCCACTT 1080
10 TGGGGACTAA AATTGTGCTA TTGCCGAGAA GCAGTCTAAA ATTTATTTTT TAAAAAGAGA 1140
AACTGCCCCA TTATTTTGG TTGTTTTAT TTTTATTTA TATTTTTGG CTTTGGTCA 1200
TTGTCAAATG TGAATGCTC TGGGTTCTA GTATATAATT TAATCTAGT TTTTATAATC 1260
15 TGTAGCCCA GTTAAATGT ATGCTACAGA TAAAGGAATG TTATAGATAA ATTTGAAAGA 1320
GTTAGGCTG TTAGCTGTA GATTTTTAA ACGATTGATG CACTAAATG TTTACTATTG 1380
20 TGATGTTAAG GGGGGTAGAG TTTGCAAGG GACTGTITAA AAAAAGTAGC TTATACAGCA 1440
TGTGCTTGCA ACTTAAATAT AAGTGGGTA TGTGTAGTCT TTGCTATACC ACTGACTGTA 1500
TTGAAAACCA AAGTATTAAG AGGGGAAACG CCCCTGTTA TATCTGTAGG GGTATTTTAC 1560
25 ATTCAAAAAT GTATGTTTT TTTCTTTTC AAAATTAAAG TATTTGGGAC TGAATTGCAC 1620
TAAGATATAA CCTGCAAGCA TATAATACAA AAAAAATTG CAAACTGTT TAGAACGCTA 1680
30 ATAAATTTA TGCAGTTATA AAAATGGCAT TACTGCACAG TTTTAAGATG ATGCAGATTT 1740
TTTTACAGTT GTATTGTGGT GCAGAACTGG ATTTCTGTA ACTTAAAAA AAATCCACAG 1800
TTTTAAAGC AATAATCAGT AAATGTTATT TTCAGGACT GACATCCTGT CTTTAAAAAG 1860
35 AAATGAAAAG TAAATCTTAC CACAATAAAT ATAAAAAAT CTGTGTCAGT ACTTTTCTTT 1920
TACATATTTT GCTGTGCAAA ATTGTTTTAT ATCTTGAGTT ACTAACTAAC CACGCGTGT 1980
40 GTTCCTATGT GCTTTTCTTT CATTTTCAAT TCTGGTTATA TCAAGAAAAG AATAATCTAC 2040
AATAATAAAC GGCATTTTTT TTTGAAAAA AAAAAAAAAA AA 2082

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(2) INFORMATION FOR SEQ ID NO: 252:

50 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1482 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 252:

CAGGCAGGCT GGCCCCGGG ACTTCTCTCT GGCCCTGCTC CCTCCGAGCG CTCCGCCGTT 60
60 GCCCGCCTGG CCCCTACGGA GTCCTTAGCC AGGATGGAGG CTGTTGTGAA CTTGTACCAA 120

	GAGGTGATGA AGCACGCAGA TCCCCGATC CAGGGCTACC CTCTGATGGG GTCCCCCTTG	180
	CTAATGACCT CCATTCTCCT GACCTACGTG TACTTCGTTT TCTCACTTGG GCCTCGCATC	240
5	ATGGCTAATC GGAAGCCCTT CCAGCTCCGT GGCTTCATGA TTGTCTACAA CTTCTCACTG	300
	GTGGCACTCT CCTCTACAT TGTCTATGAG TTCTTGATGT CGGGCTGGCT GAGCACCTAT	360
10	ACCTGGCGCT GTGACCCTGT GGACTATTCC AACAGCCCTG AGGCACTTAG GATGGTTCCG	420
	GTGGCCTGGC TCTTCTCTT CTCCAAGTTC ATTGAGCTGA TGGACACAGT GATCTTTATT	480
	CTCCGAAAGA AAGACGGGCA GGTGACCTTC CTACATGTCT TCCATCACTC TGTGCTTCCC	540
15	TGGAGCTGGT GGTGGGGGGT AAAGATTGCC CCGGGAGGAA TGGGCTCTTT CCATGCCATG	600
	ATAAACTCTT CCGTGCATGT CATAATGTAC CTGTACTACG GATTATCTGC CTTTGGCCCT	660
20	GTGGCACAAC CCTACCTTTG GTGGAAAAAG CACATGACAG CCATTTCAGT GATCCAGTTT	720
	GTCTGGTCT CACTGCACAT CTCCCAGTAC TACTTTATGT CCAGCTGTAA CTACCAGTAC	780
	CCAGTCATTA TTCACCTCAT CTGGATGTAT GGCACCATCT TCTTCATGCT GTTCTCCAAC	840
25	TTCTGGTATC ACTCTTATAC CAAGGGCAAG CGGCTGCCCC GTGCACTTCA GCAAAATGGA	900
	GCTCCAGGTA TTGCCAAGGT CAAGGCCAAC TGAGAAGCAT GGCCTAGATA GCGCCCCACC	960
30	TAAGTGCTC AGGACTGCAC CTTAGGGCAG TGTCCGTCAG TGCCCTCTCC ACCTACACCT	1020
	GTGACCAAGG CTTATGTGGT CAGGACTGAG CAGGGGACTG GCCCTCCCT CCCACAGCT	1080
	GCTCTACAGG GACCACGGCT TTGGTTCTC ACCCACTTCC CCGGGCAGC TCCAGGGATG	1140
35	TGGCCTCATT GCTGTCTGCC ACTCCAGAGC TGGGGGCTAA AAGGGCTGTA CAGTTATTTT	1200
	CCCCCTCCCTG CCTTAAACT TGGGAGAGGA GCACTCAGG CTGGCCCCAC AAAGGGTCTC	1260
40	GTGGCCTTTT TCCTCACACA GAAGAGGTCA GCAATAATGT CACTGTGGAC CCAGTCTCAC	1320
	TCCTCCACCC CACACACTGA AGCAGTAGCT TCTGGGCCAA AGGTCAGGT GGGCGGGGC	1380
	CTGGGAATAC AGCCTGTGGA GGCTGCTTAC TCAACTTGTG TCTTAATTAA AAGTGACAGA	1440
45	GGAAACCAAA AAAAAAAAAA AAAAAGTCTGA GGGGGGCCG TA	1482

50 (2) INFORMATION FOR SEQ ID NO: 253:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 834 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 253:

60 GGCACGAGCG CCGTTGCCCG CCTGGCCCTT ACGGAGTCTT TAGCCAGGAT GGAGGCTGTT 60

	GTGAACTTGT ACCAAGAGGT GATGAAGCAC GCAGATCCCC GGATCCAGGG CTACCCCTCTG	120
5	ATGGGGTCCC CCTTGCTAAT GACCTCCATT CTCTGACCT ACGTGTACTT CGTTCTCTCA	180
	CTTGGGCCTC GCATCATGGC TAATCGGAAG CCCTTCCAGC TCCGTGGCTT CATGATTGTC	240
	TACAACTTCT CACTGGTGGC ACTCTCCCTC TACATTGTCT ATGAGTTCCT GATGTCGGGC	300
10	TGGCTGAGCA CCTATACCTG GCGCTGTGAC OCTCAGGACT GCACCTTAGG GCAGTGTCCG	360
	TCAGTGCCTT CTCCAMCTAC ACCTGTGACC AAGGCTTATG TGGTCAGGAC TGAGCAGGGG	420
15	ACTGGCCCTC CCCTCCCCAC AGCTGCTCTA CAGGGACCAC GGCTTTGGTT CCTCACCAC	480
	TTCCCCCGGG CAGCTCCAGG GATGTGGCCT CATGTCTGTC TGCCACTCCA GAGCTGGGGG	540
	CTAAAAGGGC TGTACAGTTA TTTCCCCCTC CCTGCCITAA AACTTGGGAG AGGAGCACTC	600
20	AGGGCTGGCC CCACAAAGGG TCTCGTGCC TTTTTCCTCA CACAGAAGAG GTCAGCAATA	660
	ATGTCACTGT GGACCCAGTC TCACTCCTCC ACCCCACACA CTGAAGCAGT AGCTTCTGGG	720
25	CCAAAGGTCA GGGTGGGCGG GGGCCTGGGA ATACAGCCTG TGGAGGCTGC TTACTIONACT	780
	TGTGTCTTAA TTAAAAGTGA CAGAGGAAAC CACGAAAAA AAAAAAAAAA AAAA	834

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(2) INFORMATION FOR SEQ ID NO: 254:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1508 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 254:

40

	TTGAACTTTT AAAATTTTAG ATCAGCAAAC TCTAAGATCC TAGAATGGAA GCTGTTCTCTC	60
	ATTTCTCCAT GCTCACCTC CCAGGTCAGC GAGATGGTGA AGAAGCTGCA CGCGGCAACA	120
45	CCACCAACGT TCGGAGTGA CCTCATCAAT GAGCTTGTTG AGAACTTTGG CAGATGTCCC	180
	AAGTGGTCTG GTCGGCAAGC CTTTGTCTTT GTCTGCCAGA CTGTCAATTGA GGATGACTGC	240
50	CTTCCCATGG ACCAGTTTGC TGTGCATCTC ATGCCGCATC TGCTAACCTT AGCAAATGAC	300
	AGGGTTCCCTA ACGTGCAGT GCTGCTTGCA AAGACATTAA GACAAACTCT ACTAGAAAAA	360
	GACTATTCTT TGGCCTCTGC CAGCTGCCAC CAGGAGGCTG TGGAGCAGAC CATCATGGCT	420
55	CTTCAGATGG ACCGTGACAG CGATGTCAAG TATTTTGCAA GCATCCACCC TGCCAGTACC	480
	AAAATCTCCG AAGATGCCAT GAGCACAGCG TCCTCAACCT ACTAGAAGGC TTGAATCTCG	540
60	GTGTCTTTCC TGCTTCCATG AGAGCCGAGG TTCAGTGGGC ATTCGCCACG CATGTGACCT	600

	GGGATAGCTT TCGGGGAGG AGAGACCTTC CTCTCCTGCG GACTTCATTG CAGGTGCAAG	660
	TTGCCTACAC CCAATACCAG GGATTTCAG AGTCAAGAGA AAGTACAGTA AACACTATTA	720
5	TCTTATCTTG ACTTTAAGGG GAAATAATTT CTCAGAGGAT TATAATTGTC ACCGAAGCCT	780
	TAAATCCTTC TGTCTTCCTG ACTGAATGAA ACTTGAATTG GCAGAGCATT TTCCTTATGG	840
10	AAGGGATGAG ATTCCCAGAG ACCTGCATTG CTTTCTCCTG GTTTTATTTA ACAATCGACA	900
	AATGAAATTC TTACAGCCTG AAGGCAGACG TGTGCCCAGA TGTGAAAGAG ACCTTCAGTA	960
	TCAGCCCTAA CTCTTCTCTC CCAGGAAGGA CTGTCTGGGC TCTGTGGCCA GCTGTCCAGC	1020
15	CCAGCCCTGT GTGTGAATCG TTTGTGACGT GTGCAAATGG GAAAGGAGGG GTTTTACAT	1080
	CTCTAAAGG ACCTGATGCC AACACAAGTA GGATTGACTT AAACCTTAA GCGCAGCATA	1140
20	TTGCTGTACA CATTTACAGA ATGGTTGCTG AGTGTCTGTG TCTGATTTTT TCATGCTGGT	1200
	CATGACCTGA AGGAAATTTA TTAGACGTAT AATGTATGTC TGGTGTTTTT AACTTGATCA	1260
	TGATCAGCTC TGAGGTGCAA CTTCTTCACA TACTGTACAT ACCTGTGACC ACTCTGGGA	1320
25	GTGCTGCAGT CTTTAATCAT GCTGTTTAAA CTGTTGTGGC ACAAGTCTC TTGTCCAAAT	1380
	AAAATTTATT AATAAGATCT ATAGAGAGAG ATATATACAC TTTTGATTGT TTTCTAGATG	1440
30	TCTACCAATA AATGCAATTT GTGACCTGTA TTAACAAAAA NTAAAAAAC TCGAGGGGGG	1500
	CCCGGTAC	1508

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(2) INFORMATION FOR SEQ ID NO: 255:

(i) SEQUENCE CHARACTERISTICS:

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- (A) LENGTH: 2514 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 255:

45

	GAGAGACTCA CACTTCTTTT CCATTATCAC TGACGATGTA GTGGACATAG CAGGGGAAGA	60
	GCACCTACCT GTGTTGGTGA GGTGTGTGA TGAATCTCAT AACCTAAGAG AGGAATTTAT	120
50	AGGCTTCCTG CCTTATGAAG CCGATGCAGA AATTTTGGCT GTGAAATTTT AACTATGAT	180
	AACTGAGAAG TGGGGATTAA ATATGGAGTA TTGTCTGGC CAGGCTTACA TTGWCTCTAG	240
55	TGGATTTTCT TCCAAAATGA AAGTTGTGTC TTCTAGACTT TTAGAGAAAT ATCCCCAAGC	300
	TATCTACACA CTCTGCTCTT CCTGTGCCTT AAATATGTGG TTGGCAAAAT CAGTACCTGT	360
	TATGGGAGTA TCTGTGTCAT TAGGAACAAT TGAGGAAGTT TGTTCTTTTT TCCATCGATC	420
60	ACCACAACCTG CTTTTAGAAC TTGACAACGT AATTTCTGTT CTTTTTCAGA ACAGTAAAGA	480

	AAGGGGTAAA GAACTGAAGG AAATCTGCCA TTCTCAGTGG ACAGGCAGGC ATGATGCTTT	540
5	TGAAATTTTA GTGGAACCTC TGCAAGCACT TGTTTTATGT TTAGATGGTA TAAATAGTGA	600
	CACAAATATT AGATGGAATA ACTATATAGC TGGCCGAGCA TTTGTACTCT GCAGTGCAGT	660
	GTCAGATTTT GATTTTCATTG TTAATATGT TGTTCCTAAA AATGTCCTAT CTTTACAAAG	720
10	AGCCTTTGGG AAAAACCTCC AGGGGCAAAC CTCTGATGTC TTCTTTGCGG CCGGTAGCTT	780
	GACTGCAGTA CTGCATTCAC TCAACGAAGT GATTGGAAAA TATTGAAGTT TATCATGAAT	840
15	TTTGGTTTGA GGAAGCCACA AATTTGGCAA CCAAACTTGA TATTCAAATG AAACCTCCCTG	900
	GGAAATTCCTG CAGAGCTCAC CAGGGTAACT TGAATCTCA GCTAACCTCT GAGAGTTACT	960
	ATAAGAAAC CCTAAGTGT CCAACAGTGG AGCACATTAT TCAGGAACTT AAAGATATAT	1020
20	TCTCAGAACA GCACCTCAAA GCTCTTAAAT GCTTATCTCT GGTACCCTCA GTCATGGGAC	1080
	AACTCAAATT CAATACGTCG GAGGAACACC ATGCTGACAT GTATAGAAGT GACTTACCCA	1140
25	ATCCTGACAC GCTGTCAGCT GAGCTTCATT GTTGGAGAAT CAAATGGAAA CACAGGGGGA	1200
	AAGATATAGA GCTTCCGTCC ACCATCTATG AAGCCCTCCA CCTGCCTGAC ATCAAGTTT	1260
	TTCTAATGT GTATGCATTG CTGAAGGTCC TGTGTATTCT TCCTGTGATG AAGGTTGAGA	1320
30	ATGAGCGGTA TGAAATGGA CGAAAGCGTC TTAAAGCATA TTTGAGGAAC ACTTTGACAG	1380
	ACCAAAGTTC AAGTAACTTG GCTTTGCTTA ACATAAATT TGATATAAAA CACGACCTGG	1440
35	ATTTAATGGT GGACACATAT ATTAACTCT ATACAAGTAA GTCAGAGCTT CCTACAGATA	1500
	ATTCGGAAAC TGTGGAAAAT ACCTAAGAGA CTTTAAAAA TAGGCTTTCT TATATTTGAT	1560
	ATTTGGAAGA AAAAGCCGTA AGTGTATGTA GACCACTTAA TCACTAAATA TCTTGCCTA	1620
40	TAGGACTCCA TTGAATACAT TAGCCATTGA TAATCTACCT GTTTAAATGG CCCCTGTTTG	1680
	AACTCTCAAG CTTTGAAGAC CTACCTGTTT TCCAGAAGA GAACGTTGAA AGTGCCATGT	1740
45	TTCTTTTTC GTGATCTCTG TTGATGGCAC TCTGGAATTG TTTCACTTAA GTCATTTTAG	1800
	ACATAGCATT TATTATCACT GTGGATCTCT ACTTGTGGG TGTATGAAT TCTTTGAAGA	1860
	AATATATTTT GAAGAGGTGT GGGAGGAAGG AATACATTTT ATAAAATGTT GTAGTGAAGC	1920
50	CCACAATTGA CCTTTGACTA ATAGGAGTTT TAAGTATGTT AAAAATCTAT ACTGGACAGT	1980
	TACAAGAAAT TACCGAGAA AAGCTTGTGA GCTCACCAA CAAGGATTTT AGTGTAGATT	2040
55	TTGTCTTTCT TGAACCTAAA GAAACAAATG ACAAAGTTTG AATGGAAAAG CCTGCTGTTG	2100
	TTCCACATCT CGTTGCTGTT TACATTCCTT TGTGGAGCCT ACATCTTCCT AAGCTTTTTA	2160
	GCAGGTATAT GTTGAACACT TCTGTTTCAT GGTGAGACA GAATCAGAGG CCATGGATAC	2220
60	TGACAACTGA TTTGTCTGTT TTTTCTCTCT GTCTTTTCC ATGACTCTTA TATACTGCCT	2280

CATCTTGATT TATAAGCAAA ACCTGGAAAA CCTACAAAAT AAGTGTGTG GTTTATCTAG 2340
 5 AAAAATATGG AAAATATTGC TGTATTTTT GGTGAAGAAA ATCAATTTTG TATAGTTTAT 2400
 TTCAATCTAA ATAAATGTG AATTTGTGTT AAAGCTTAGG CACATTATTT TTTGTGGGGT 2460
 CAAAACATTC TTGTGTAAAT TCTCTTAAAC ATTTGATAAA CAGCTTCACA ATTC 2514
 10

(2) INFORMATION FOR SEQ ID NO: 256:

15 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 2357 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 20 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 256:

CTGCCCTATG AAGCCGATGC AGAAATTTTG GCTGTGAAAT TTCACACTAT GATAACTGAG 60
 25 AAGTGGGGAT TAAATATGGA GTATTGTCGT GGCCAGGCTT ACATTGTCTC TAGTGGATTT 120
 TCTTCCAAAA TGAAAGTTGT TGCTTCTAGA CTMTTAGAGA AATATCCCCA AGCTATCTAC 180
 ACACTCTGCT CTTCCTGTGC CTTAAATATG TGGTTGGCAA AATCAGTACC TGTATATGGA 240
 30 GTATCTGTTG CATTAGGAAC AATTGAGGAA GTTTGTCTTT TTTCCATCG ATCACCACAA 300
 CTGCTTTTAG AACTTGACAA CGTAATTYCT GTTCTTTTTC AGAACAGTAA AGAAAGGGGT 360
 35 AAAGAACTGA AGGAAATCTG CCATTCTCAG TGGACAGGCA GGCATGATGC TTTTGAAATT 420
 TTAGTGGAAC TCCTGCAAGC ACTTGTTTTA TGTTTAGATG GTATAAATAG TGACACAAAT 480
 ATTAGATGGA ATAACTATAT AGCTGGCCGA GCATTTGTAC TCTGCAGTGC AGTGTGAGAT 540
 40 TTTGATTTCA TTGTTACTAT TGTGTCTCTT AAAAATGTCC TATCTTTTAC AAGAGCCTTT 600
 GGGAAAAACC TCCAGGGGCA AACCTCTGAT GTCTTCTTTG CGGCCGGTAG CTTGACTGCA 660
 45 GTACTGCATT CACTCAACGA AGTGANTGGA AAATATTGAA GTTTATCATG AATTTTGGTT 720
 TGAGGAAGCC ACAAATTTGG CAACCAAACT TGATATTCAA ATGAAACTCC CTGGGAAATT 780
 CCGCAGAGCT CACCAGGGTA ACTTGAATC TCAGCTAACC TCTGAGAGTT ACTATAAAGA 840
 50 AACCCTAAGT GTCCCAACAG TGGAGCACAT TATTCAGGAA CTTAAAGATA TATTCTCAGA 900
 ACAGCACCTC AAAGCTCTTA AATGCTTATC TCTGGTACCC TCAGTCATGG GACAACTCAA 960
 55 ATTCAATACG TCGGAGGAAC ACCATGCTGA CATGTATAGA AGTGACTTAC CCAATCCTGA 1020
 CACGCTGTCA GCTGAGCTTC ATTTGTGGAG AATCAAATGG AAACACAGGG GGAAAGATAT 1080
 AGAGCTTCCG TCCACCATCT ATGAAGCCCT CCACCTGCCT GACATCAAGT TTTTCTCTAA 1140
 60

	TGTTGATGCA TTGCTGAAGG TCCTGTGTAT TCTTCCTGTG ATGAAGGTG AGAATGAGCG	1200
	GTATGAAAT GGACGAAAGC GTCTTAAAGC ATATTGAGG AACACTTTGA CAGACCAAAG	1260
5	GTCAAGTAAC TTGGCTTTGC TTAACATAAA TTTTGATATA AAACACGACC TGGATTTAAT	1320
	GGTGGACACA TATATTAAAC TCTATACAAG TAAGTCAGAG CTTCTACAG ATAATTCCGA	1380
10	AACTGTGGAA AATACCTAAG AGACTTTTAA AAATAGGCTT TCTTATATTT GATATTTGGA	1440
	AGAAAAAGCC GTAAGTGTAT GTAGACCACT TAATCACTAA ATATCTTTGC CTATAGGACT	1500
	CCATTGAATA CATTAGCCAT TGATAATCTA CCTGTTTAAA TGGCCCTGT TTGAACCTC	1560
15	AAGCTTTGAA GACCTACCTG TTCTTCCAGA AGAGAACGTT GAAAGTGCCA TGTTCCTTT	1620
	TGCGTGATCT CTGTTGATGG CACTCTGGAA TTGTTTCAGT TAAGTCATTT TAGACATAGC	1680
20	ATTTATTATC ACTGTGGATC TCTACTTGTT GGGTGTATG AATTCCTTGA AGAAATATAT	1740
	TTTGAAGAGG TGTGGGAGGA AGGAATACAT TTTATAAAAT GTTGTAGTGA AGCCACAAT	1800
	TGACCTTTGA CTAATAGGAG TTITAAGTAT GTTAAAAATC TATACTGGAC AGTTACAAGA	1860
25	AATTACCGGA GAAAAGCTTG TGAGCTCACC AAACAAGGAT TTCAGTGTAG ATTTTGCTTT	1920
	TCTTGAACCT AAAGAAACAA ATGACAAAGT TTGAATGGAA AAGCCTGCTG TTGTTCCACA	1980
30	TCTCGTTGCT GTTTACATTC CTTGTGGAG CCTACATCTT CCTAAGCTTT TTAGCAGGTA	2040
	TATGTTGAAC ACTTCTGTTT CATGGTTGAG ACAGAATCAG AGGCCATGGA TACTGACAAC	2100
	TGATTTGTCT GTTTTTTTTC TCTGCTTTT TCCATGACTC TTATATACTG CCTCATCTTG	2160
35	ATTTATAAGC AAAACCTGGA AAACCTACAA AATAAGTGTG GTGGTTTATC TAGAAAAATA	2220
	TGGAAAAATAT TGCTGTTATT TTGGTGAAG AAAATCAATT TTGTATAGTT TATTTCAATC	2280
40	TAAATAAAAT GTGAATTTTG TTTAAAGCTT AGGCACATTA TTTTGTGTGG GGTCAAAACA	2340
	TTCTTGTTGA AATCTC	2357

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(2) INFORMATION FOR SEQ ID NO: 257:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 689 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 257:

ACTTTCCTGGT GCAAAAAGAT GTTCAAGCCT TATTTTATAC TTGCCTGCCC CTTTCTCTTT	60
CATTTATGAG AGTGAGCTGC AGCTCTAAGA AGACCTGTTT TTTTGAATGG AGAGTAGCAT	120
CAGGAACCAG GATGTGGGTG CGAGGCGTGC TCCTGGCTGT TGCAGATTGC TGCACCCGGG	180

AGCTCTTAGT GGACAGAGCT AGAGGATATG TGCACGTACT TCCATCTCTC TCTCTGTCTC 240
 5 CGATTTTAGC CCAGCACCAC AGGGTACGTT CCAGTTTTTC TCTCTTTCCA TAGCTGTAAG 300
 GCCCTTTCTG GGAATGGTTC TCATTCTCCT TAATCTATTA TTGGGTCACT TTTCTGTCAT 360
 GTCCCCAGCC TCCCATCACT GCCACCCACT CCCACAGAG ATGCCCTGCT CATCCGACTG 420
 10 GGGCTTTGAC TCCCACACTG TGTACCCCTC TTGTGTGGAC GCCCTGCTGC CAAAACCTTC 480
 AGCAACAGC TTTCCAAATG GAAGTTGTCA CTGTCAAGGS CTTTACAATC AGCAACAGCA 540
 AAATCTACAT GCTGCTGAGG GTCTGCCTC ATTAAGATGC AATAAATATG TAAGTACATA 600
 15 AAAACAGCAA TAGAAGAAAC GTAATGCTTT ATTCTCAAAT ATGNATGTCT ACATAGAAAA 660
 GCCAAAATTA TTAAGAATAG TAAGGAATT 689

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(2) INFORMATION FOR SEQ ID NO: 258:

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- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 2377 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 258:

TCGACCCACG CGTCCGCCGA TGTGATGATT CCTGCGTATT CCAAGAACCG GGCCTATGCC 60
 35 ATCTTCTTCA TAGTCTTCAC TGTGATAGGG GACGCCCCCG GCGCTGTGCT ATCCTGTGCC 120
 GGCCACCCTT GCGTTGGTTT TGCTGCTGTA CTGGTGGCGC CCCTGACCGT GGCTGTCTCC 180
 TCTTGAAGGA AGCCTGTTTC TGATGAACCT GCTGACAGCC ATCATCTACA GTCAGTTCCG 240
 40 GGGTACCTG ATGAAATCTC TCCAGACCTC GCTGTTTCGG AGGCGGGTGG GAACCCGGCT 300
 GCCTTTGAAG TCCTATCCTC CATGGTGGGG GAGGGAGGAG CCTTCCCTCA GGCAGTTGGG 360
 45 GTGAAGCCCC AGAACTTGCT GCAGGTGCTT CAGAAGGTCC AGCTGGACAG CTCCCACAGA 420
 CAGGCCATGA TGGAGAAGGT GCGTTCCTAT GGCAGTGTTC TGCTCTCAGC TGAGGAGTTT 480
 CAGAAGCTCT TCAACGAGCT TGACAGAAGT GTGGTTAAAG AGCACCCGCC GAGGCCCGAG 540
 50 TACCAGTCTC CGTTTCTGCA GAGCGNCCCA GTTCCTCTTC GGCCACTNAC TACTTTGACT 600
 ACCTGGGGAA CCTCATCGCC CTGGCAAACC TGGTGTCCAT TTGCGTGTTC CTGGTGTG 660
 55 ATGCAGATGT TGCTGCCTGC TGAGCGTGAT GACTTCATCC TGGGGGGTCT CAACTGCGTC 720
 TTCAITGTGT ACTACCTGTT GGAGATGCTG GCTCAAGGTC TTTTGCCCTG GGGCCTGCGA 780
 60 RGGTACYKKT CCTAACCCCA RCAAMGTGTT TTGAACGGGC TCCTCAMCGT TTGTCTGGC 840

	TGGWKKGSM GATCTCAACT CTGGCTGTGT ACCGATTGCC ACACCCAGGC TGGAGGCCGG	900
	ANATGGTGGG CCTGCTGTCTG CTGTGGGACA TGACCCGCAT ACTGAACATG CTCATCGTGT	960
5	TCCGCTTCCT GCGTATCATC CCCAGCATGA AGCCGATGGC CGTGGTGGCC AGTACCGTCC	1020
	TGGGCCCTGGT GCAAAACATG CGTGCCTTTG GCGGGATCCT GGTGGTGGTC TACTACGTAT	1080
10	TTGCCATCAT TGGGATCAAC TTGTTTAGAG GCGTCATGT GGCTCTTCCT GGAAACAGCA	1140
	GCCTGGCCCC TGCCAATAGG TCGGCGCCCT GTGGGAGCTT CGAGCAGCTG GAGTACTGGG	1200
	CCAACAACCT CGATGACTTT GCGGCTGCCC TGGTCACTCT GTGGAACCTG ATGGTGGTGA	1260
15	ACAACTGGCA GGTGTTTCTG GATGCATATC GCGCTACTA AGGCCCGTGG TCCAAGATCT	1320
	ATTTTGTAT TGGGTGGCTG GTGTCGTCTG TCATCTGGGT CAACCTGTTT CTGGCCCTGA	1380
20	TTCTGGAGAA CTTCCTTCAC AAGTGGGACC CCCGCAGCCA CTTGCAGCCC CTTGCTGGGA	1440
	CCCCAGAGGC CACCTACCAG ATGACTGTGG AGCTCCTGTT CAGGGATATT CTGGAGGAGC	1500
	CCGGGGAGGA TGAGCTCACA GAGAGGCTGA GCCAGCACCC GCACCTGTGG CTGTGCAGGT	1560
25	GACGTCCGGG TCTGCCATCC CAGCAGGGGC GGCAGGAGAG AGAGGCTGGC ATAACACAGG	1620
	TGCCCATCAT GGAAGAGGCG GCCATGCTGT GGCCAGCCAG GCAGGAAGAG ACCTTTCCTC	1680
30	TGACGGACCA CTAAGCTGGG GACAGGAACC AAGTCCTTTG CGTGTGGCCC AACAACCAT	1740
	TACAGAACAG CTGCTGGTGC TTCAGGGAGG CGCCGTGCCC TCCGCTTTCT TTTATAGCTG	1800
	CTTCAGTGAG AATTCCCTTG TCGACTCCAC AGGGACCTTT CAGACAAAAA TGCAAGAAGC	1860
35	AGCGGCCTCC CCGTCCCTT GCAGCTCCG TGGTGCCTTT GCTGCCGCA GCCCTTGGGG	1920
	ACCACAGGCC TGACCAGGGC CTGCACAGGT TAACCGTCAG ACTTCCGGGG CATTTCAGCTG	1980
40	GGAATGATAC TAATACCTCC GATTTTAGCC CAGCACCACA GGTACGTTT CAGTTTATAT	2040
	TTCTTTCCAT AGCTGTAAGG CCCTTTCTGG GAATGGTTAT CATTCCTCTT AATCTATTAT	2100
	TGGGTCACTT TTCTGTCATG TCCCAGCCT CCCATCACTG CCACCCACTC CCCACAGAGA	2160
45	TGCCCTGCTC ATCCGACTGG GCCTTTGACT CCCACACTGT GTACCCCTCT TGTGTGGACG	2220
	CCCTGCTGCC AAAACCTTCA GCAAACAGCT TTCCAAATGG AAGTTGTCAC TGTACAGGGC	2280
50	TTTACAATCA GCAACAGCAA AATCTACATG CTGCTGAGGG TCCTGCCTCA TTAAGATGCA	2340
	ATAAATATGT AAGTACATAA AAAAAAAAAA AAAAAA	2377

55

(2) INFORMATION FOR SEQ ID NO: 259:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1193 base pairs

(B) TYPE: nucleic acid

60

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 259:

5
TCTGNTCGCC GTCGCCCCGC CCCTGGCCTT TGCCCCGGTCG GCGGGGACTT CCTGTGTGCT 60
ATTTCCAAGG ACTCCAAAGC GAGGCCGGGG ACTGAAGGTG TGGGTGTGCA GCCCTCTGGC 120
10 AGAGGGTTAA CCTGGGTCAA ATGCACGGAT TCTCACCTCG TACAGTTACG CTCTCCCGCG 180
GCACGTCCGC GAGGMYTTGA AGTCCTGAGC GCTCAAGTTT GTCCGTAGTC GAGAGAAGGC 240
CATGGAGGTG CCGCCACCGG CACCGCGGAG CTTTCTCTGT AGAGCATTGT GCCTATTTCC 300
15 CCGAGTCTTT GCTGCCGAAG CTGTGACTGC CGATTTCGAA GTCCTTGAGG AGCGTCAGAA 360
GCGGCTTCCC TACGTCCCAG AGCCCTATTA CCCGGAATCT GGATGGGACC GCCTCCGGGA 420
20 GCTGTTTGGC AAAGACACAG TGAACACTAG TCTGAATGTA TACCGAAATA AAGATGCCTT 480
AAGCCATTTT GTAATTGCAG GAGCTGTAC GGAAGTCTT TTTAGGATAA ACGTAGGCCT 540
GCGTGGCTGG TGGCTGGTGG CATAATGGA GCCTTGCTGG GCACTCCTGT AGGAGGCCTG 600
25 CTGATGGCAT TTCAGAAGTA CTCTGGTGAG ACTGTTTCAAG AAAGAAAACA GAAGGATCGA 660
AAGGCACTCC ATGAGCTAAA ACTGGAAGAG TGGAAAGGCA GACTACAAGT TACTGAGCAC 720
30 CTCCCTGAGA AAATTGAAAG TAGTTTACAG GAAGATGAAC CTGAGAATGA TGCTAAGAAA 780
ATTAAGCAC TGCTAAACCT TCCTAGAAAC CCTTCAGTAA TAGATAAACA AGACAAGGAC 840
TGAAAGTGCT CTGAACTTGA AACTCACTGG AGAGCTGAAG GGAGCTGCCA TGTCCGATGA 900
35 ATGCCAACAG ACAGGCCACT CTTTGGTCAG CCGCTGACA AATTTAAGTG CTGGTACCTG 960
TGGTGGCAGT GGCTTGCTCT TGTCTTTTC TTTTCTTTT AACTAAGAAT GGGGCTGTTG 1020
40 TACTCTCACT TTACTTATCC TTAAATTTAA ATACATACTT ATGTTTGAT TAATCTATCA 1080
ATATATGCAT ACATGAATAT ATCCACCCAC CTAGATTTTA AGCAGTAAAT AAAACATTTT 1140
GCAAAAGATT AAAGTTGAAT TTTACAGTTA AAAAAAAAAA AAAAAAAAAA AAA 1193
45

(2) INFORMATION FOR SEQ ID NO: 260:

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(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1262 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 260:

60 GAAAAACCCA AAGATGCAGA CAATCTCTTT GAACATGAAT TGGGGGCTCT CAATATGGCT 60

	GCATTACTAC GAAAAGAAGA AAGAGCAAGT CTTCTTAGTA ATCTTGGCCC ATGTTGTAAG	120
	GCGTTGTGCT TCAGACGGGA TTCTGCAATT CGAAAGCAGC TTGTTAAAAA TGAGAAGGGC	180
5	ACCATAAAAC AAGCTTACAC GAGTSCTCCA ATGGTAGACA ATGAATTACT TCGATTGAGT	240
	CTTCGGTTAT TTAAGCGGAA GACTACTTGC CATGCTCCAG GACATGAAAA GACTGAAGAT	300
10	AATAAACTTT CACAGTCCAG TATCCAACAG GAACTGTGTG TGTCTTAAGA CCGAAGTTCA	360
	ATATGGTATT TTTGGTACTG TCTTCTTCA GCAGTGCATA TTCTTTTGCA AAGTTCTTTG	420
	GTTTGACAAG CATTAGTGAC AAAGGCAGAA AAGATTTATC AGCCATGCTA AAAGAGTGAA	480
15	GAATTTGAT CTTTAGAGAC ACTAGTTTGT GCCAACTTAA GATTTTACGT TAATTTTAC	540
	ATAGTATTTG ACACTCATGC AAAATAATGT GAAAACATCT AGATTTAGTA GTTTATTCTG	600
	CGCCTTTTGT TAAACTGAA GATTTTGGAA AATGGTTGTC ACTGCTCTTC CAGCCTATGA	660
20	ATATTTTGT GAAATGGAAC CATGGATTTA TGTCTGGATC ATCCATACAG AACCAACAAT	720
	TTTATTCAAA AACAATGTGT TCATCAAAGT AATTGCTCAC ATTGTGCAGT ACTATGTTGT	780
25	ACAGACCACG TGAAAGGGAA TGCTGGTCTA GCTGGCGTGG TATGTTTATA GGCGAATTC	840
	AGCAGAAGGA AGCCAAAATA GTTTTTCCT TTTGAAAGTT TTTTAAAAAT TATTCATGG	900
	GTCTTTTTTT TAATTAATAT GTGTGCATG TTACAATGTA TGTGGATGT CTTTGGACCC	960
30	TAAATGCTTT TTTTGTATC AGAGATTGTG TACTATTTTT ATTTTTAATA AATGTATCTT	1020
	CCCTTTCCTT GTTTAGATT TACTTTGCTC TTCGTTAATC TTATTCCTGA TGATCTAGAA	1080
35	CATTAGTCAT CAACATTACA TGTTCATGC TTCAGATATT TTACTGCTTG TGTCCTTATT	1140
	GTTGGACAGC TTAAACAGA GTTGATGGTA CTTCAATAT AGCTCATGA TACTTAAGGG	1200
40	CANCTTCCTT GGGATGTGG CTTTTTGAA GAAAAAAAT TNCCCCAAG GCAATCCCA	1260
	GT	1262

45

(2) INFORMATION FOR SEQ ID NO: 261:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1179 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

50

55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 261:

	GGCAAACTTT CCCCCAANGC TTCGAACTT GCAAGCCGAA ACCTTGAATC GTTAAAAGTT	60
	GGGTTGCGNC GGCGCCCTGG CCCGAAGAAG CGCAATGGC GTTCCGCGAA CGTTGGCCCT	120
60	CAACGGCTCG GCAGCCAGCC ATGTCCTGCA CCCAGGACAG CGGCCCTGGG CTACAAGGAC	180

	CTGGACCTCA TCTTCCTGCG CCGACCTGCG CGGGGAAGGG GAGTTTCAGA CTGTGAAGGA	240
5	CGTCGTGCTG GACTGCCTGT TGGACTTCTT ACCCGAGGGG GTGAACAAAG AGAAGATCAC	300
	ACCACTCACG CTCAAGGAAG CTTATGTGCA GAAAATGGTT AAAGTGTGCA ATGACTCTGA	360
	CCGATGGAGT CTTATATCCC TGTCAAACAA CAGTGGCAAA AATGTGGAAC TGAAATTTGT	420
10	GGATTCCTC CGGAGGCAGT TTGAATTCAG TGTAGATTCT TTTCAAATCA AATTAGACTC	480
	TCTTCTGCTC TTTTATGAAT GTTCAGAGAA CCCAATGACT GAGACATTTC ACCCCACAAT	540
15	AATCGGGGAG AGCGTCTATG GCGATTTCCT GGAAGCCTTT GATCACCTTT GTAACAAGAT	600
	CATTGCCACC AGGAATCCAG AGGAAATCCG AGGGGGAGGC CTGCTTAAAGT ACTGCAACCT	660
	CTTGGTGAGG GGCTTTAGGC CCGCCTCTGA TGAAATCAAG ACCCTTCAAA GGTATATGTG	720
20	TTCCAGGTTT TTCATCGACT TCTCAGACAT TGGAGAGCAG CAGAGAAAAC TGGAGTCCTA	780
	TTTGAGAAC CACTTTGTGG GATTGGAAGA CCGCAAGTAT GAGTATCTCA TGACCCTTCA	840
25	TGGAGTGGTA AATGAGAGCA CAGTGTGCCT GATGGGACAT GAAAGAAGAC AGACTTTAAA	900
	CCTTATCACC ATGCTGGCTA TCCGGGTGTT AGCTGACCAA AATGTCATTC CTAATGTGGC	960
	TAATGTCACT TGCTATTACC AGCCAGCCCC CTATGTAGCA GATGCCAACT TTAGCAATTA	1020
30	CTACATTGCA CAGGTTTCAGC CAGTATTCAC GTGCCAGCAA CAGACCTACT CCACTTGGCT	1080
	ACCCTGCAAT TAAGAATCAT TTAATAATGT CCTGTGGGGA AGCCATTTC AACAAGACAG	1140
35	GAGAGAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAGAGC	1179

40 (2) INFORMATION FOR SEQ ID NO: 262:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1162 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 262:

50	GGCAAACCTT CCCCCAANGC TTCGAAACTT GCAAGCCGAA ACCTTGAATC GTTAAAAGTT	60
	GGGTGCGNC GGCGCCCTGG CCCGAAGAAG CGCAATTGGC GTTCCCGGAA CGTTGGCCCT	120
	CAACGGCTCG GCAGCCAGCC ATGTCCTGCA CCCAGGACAG CGGCCCTGGG CTACAAGGAC	180
55	CTGGACCTCA TCTTCCTGCG CCGACCTGCG CGGGGAAGGG GAGTTTCAGA CTGTGAAGGA	240
	CGTCGTGCTG GACTGCCTGT TGGACTTCTT ACCCGAGGGG GTGAACAAAG AGAAGATCAC	300
60	ACCACTCACG CTCAAGGAAG CTTATGTGCA GAAAATGGTT AAAGTGTGCA ATGACTCTGA	360

	CCGATGGAGT CTTATATCCC TGTCAAACAA CAGTGGCAAA AATGTGGAAC TGAAATTTGT	420
	GGATTCCCTC CGGAGGCAGT TTGAATTCAG TGTAGATTCT TTTCAAATCA AATTAGACTC	480
5	TCTTCTGCTC TTTTATGAAT GTTCAGAGAA CCAATGACT GAGACATTTC ACCCCACAAT	540
	AATCGGGGAG AGCGTCTATG GCGATTTCCA GGAAGCCTTT GATCACCTTT GTAACAAGAT	600
10	CATTGCCACC AGGAACCCAG AGGAAATCCG AGGGGGAGGC CTGCTTAAGT ACTGCAACCT	660
	CTTGGTGAGG GGCTTTAGGC CCGCTCTGA TGAAATCAAG ACCCTTCAAA GGTATATGTG	720
	TTCCAGGTTT TTCATCGACT TCTCAGACAT TGGAGAGCAG CAGAGAAAAC TGGAGTCCTA	780
15	TTTGCAGAAC CACTTTGTGG GATTGGAAGA CCGCAAGTAT GAGTATCTCA TGACCCTTCA	840
	TGGAGTGGTA AATGAGAGCA CAGTGTGCCT GATGGGACAT GAAAGAAGAC AGACTTTAAA	900
20	CCTTATCACC ATGCTGGCTA TCCGGGTGTT AGCTGACCAA AATGTCATTCT CTAATGTGGC	960
	TAATGTCACT TGCTATTACC AGCCAGCCCC CTATGTAGCA GATGCCAACT TTAGCAATTA	1020
	CTACATGCA CAGGTTGAGC CAGTATTCAC GTGCCAGCAA CAGACCTACT CCACTTGGCT	1080
25	ACCCTGCAAT TAAGAATCAT TTAAAAATGT CCTGTGGGGA AGCCATTTC AACAAGACAG	1140
	GAGAGAAAAA NAANGAAAAG AG	1162

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(2) INFORMATION FOR SEQ ID NO: 263:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 735 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 263:

	CGGGCTGGGT ATTGCCTCG CACCATGGCG CCAAGGGCA AAGTGGGCAC GAGAGGGAAG	60
	AAGCAGATAT TTGAAGAGAA CAGAGAGACT CTGAAGTTCT ACCTGCGGAT CATACTGGGG	120
45	GCCAATGCCA TTTACTGCCT TGTGACGTTG GTCTTCTTTT ACTCATCTGC CTCATTTTGG	180
	GCCTGGTTGG CCTTGGGCTT TAGTCTGGCA GTGTATGGGG CCAGCTACCA CTCTATGAGC	240
50	TCGATGGCAC GAGCAGCGTT CTTCTGAGGA TGGGGCCCTG ATGGATGGTG GCACGAGCTC	300
	AACATGGAGC AGGCATGGC AGAGCACCTT AAGGATGTGA TCCTACTGAC AGCCATCGTG	360
	CAGGTGCTCA GCTGCTTCTC TCTCTATGTC TGGTCTTCTT GGCTTCTGGC TCCAGGCCCG	420
55	GCCCTTTACC TCCTGTGGGT GAAATGTGCTG GGCCCTGGT TCACTGCAGA CAGTGGCACC	480
	CCAGCACCAG AGCACAATGA GAAACGGCAG CGCCGACAGG AGCGGCGGCA GATGAAGCGG	540
60	TTATAGCCAT TGACATTGTG GCCACAGGCC ACTGGCCCTG GGTGGCTCTG TCAGGTGCA	600

5 CAGCCCCCTCA TGCCTGGAGC AATGAGGGTC TAGTCCAGGG GCCAAAAGCA GTCTGAGGTA 660
TTGGGTATAC TTATACTCTA TAGGGTCGTT GAATAAATGG CTTAGAATGT GAAAAAAAAA 720
AAAAAAAAA ATTTT 735

10

(2) INFORMATION FOR SEQ ID NO: 264:

15 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 783 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 264:

AAGTGCATGA GCTGCCGATG TGGTGCTTAG TGATTGCGGT TTCGGTCGCT CTCCCCTGTT 60
TCCCGGCTG GGTATTTGCC TGCACCATG GCGCCCAAGG GCAAAGTGG CACGAGAGGG 120
25 AAGAAGCAGA TATTTGAAGA GAACAGAGAG ACTCTGAAGT TCTACCTGCG GATCATACTG 180
GGGGCCAATG CCATTTACTG CCTTGTGACG TTGGTCTTCT TTTACTCATC TGCCTCATTT 240
TGGGCCTGGT TGGCCTGGGC TTTAGTCTGG CAGTGATGCG GGCCAGCTAC CACTCTATGA 300
30 GCTCGATGGC ACGAGCAGCG TTCTCTGAGG ATGGGGCCCT GATGGATGGT GGCATGGACC 360
TCAACATGGA GCAGGGCATG GCAGAGTGAG TGTCCTCCAC CGCCAGCCCA GGCACCTTAA 420
35 GGATGTGATC CTACTGACAG CCATCGTGCA GGTGCTCAGC TGCTTCTCTC TCTATGCTG 480
GTCTTCTGCG CTCTGCGCTC CAGGCGGGC CCTTTACCTC CTGTGGGTGA ATGTGCTGGG 540
CCCCCTGGTTC ACTGCAGACA GTGGCACCCC AGCACCAGAG CACAATGAGA AACGGCAGCG 600
40 CCGACAGGAG CGGCGGCAGA TGAAGCGGTT ATAGCCATTG ACGATTTKGC SACNRGCCAC 660
TGGCCCTGGG TGGCTCTGTC AGGGTGCACA GCCCCTCATG CCTGGAGCAA TGAGGGTCTA 720
45 GTCCAGGGGC CAAAAGCAGT CTGAGGTATT GGGTATACTT ATACTCTATA GGGTCGTGA 780
ATA 783

50

(2) INFORMATION FOR SEQ ID NO: 265:

55 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1638 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

60

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 265:

	GGCACGAGGC GGC GG CAGCG GTGGCGGGCG CGCCCCCGG CGGGAGCCGT NCCCTTTCCC	60
5	GTGCGGGAGC GCGGGGYCGG GGYCCAGGGG ANCCCGGGMC ACGGAGAGCG GGAAGAGGAT	120
	GGATTGCCCG GCCCTCCCC CCGGATGGAA GAAGGAGGAA GTGATCCGAA AATCTGGGCT	180
	AAGTGCTGGC AAGAGCGATG TCTACTACTT CAGTCCAAGT GGTAAAGAAGT TCAGAAGCAA	240
10	GCCTCAGTTG GCAAGGTACC TGGGAAATAC TGTGTATCTC AGCAGTTTIG ACTTCAGAAC	300
	TGGAAAGATG ATGCCTAGTA AATTACAGAA GAACAAACAG AGACTGCGAA ACGATCCTCT	360
15	CAATCAAAAT AAGGGTAAAC CAGACTTGAA TACAACATTG CCAATTAGAC AAACAGCATC	420
	AATTTTCAAA CAACCGGTAA CCAAAGTCAC AAATCATCCT AGTAATAAAG TGAAATCAGA	480
	CCCACAACGA ATGAATGAAC AGCCACGTCA GCTTTTCTGG GAGAAGAGGC TACAAGGACT	540
20	TAGTGCATCA GATGTAACAG AACAAATTAT AAAAACCATG GAACTACCCA AAGGTCTTCA	600
	AGGAGTTGGT CCAGGTAGCA ATGATGAGAC CCTTTTATCT GCTGTTGCCA GTGCTTTGCA	660
25	CACAAGCTCT GCGCCAATCA CAGGGCAAGT CTCGCTGCT GTGGAAAAGA ACCCTGCTGT	720
	TTGGCTTAAC ACATCTCAAC CCCTCTGCAA AGCTTTTATT GTCACAGATG AAGACATCAG	780
	GAAACAGGAA GAGCGAGTAC AGCAAGTACG CAAGAAATTG GAAGAAGCAC TGATGGCAGA	840
30	CATCTGTGCG CGAGCTGCTG ATACAGAAGA GATGGATATT GAAATGGACA GTGGAGATGA	900
	AGCCTAAGAA TATGATCAGG TAACTTTCGA CCGACTTTCC CCAAGAGAAA ATTCCTAGAA	960
35	ATTGAACAAA AATGTTTCCA CTGGCTTTTG CCTGTAAGAA AAAAAATGTA CCCGAGCACA	1020
	TAGAGCTTTT TAATAGCACT AACCAATGCC TTTTATAGTG TATTTTGTAT GTATATATCT	1080
	ATTATTCAAA AAATCATGTT TATTTTGAGT CCTAGGACTT AAAATTAGTC TTTTGTAATA	1140
40	TCAAGCAGGA CCCTAAGATG AAGCTGAGCT TTTGATGCCA GGTGCAATCT ACTGGAAATG	1200
	TAGCACTTAC GTAAACATT TGTTCCTCCC ACAGTTTAA TAAGAACAGA TCAGGAATTC	1260
45	TAAATAAATT TCCCAGTTAA AGATTATTGT GACTTCACTG TATATAAACA TATTTTATA	1320
	CTTTATTGAA AGGGGACACC TGTACATTCT TCCATCCTCA CTGTAAAGAC AAATAAATGA	1380
	TTATATTAC AGACTGATTG GAATTCCTTC TGTGAAAAG CACACACAAT AAAGAACCCC	1440
50	TCGTTAGCCT TCCTCTGATT TACATTCAAC TCTGATCCCG GGGCCTTAGG TTTGACATGG	1500
	GAGGTGGGAG GAAGATAGCG CATATATTTG CAGTATGAAC TATTGCCTCT GGGACGTTGT	1560
55	GAGGAATTGT GCTTTCACCA GAATTTCTAA GGATTTCTGG CTAAATATC ACCTAGCCTG	1620
	TGGTAATTTT TTTTCCCT	1638

(2) INFORMATION FOR SEQ ID NO: 266:

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 1455 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 266:

10 CGTGCCTACT GCCATGCAGG TACCGGGTCC GGAATTCCCA GGGTCGACCC ACGCGTCCGC 60
 TCAGTTGGCA AGGTACCTGG GAAATACTGT TGATCTCAGC AGTTTGTACT TCAGAACTGG 120
 15 AAAGATGATG CCTAGTAAAT TACAGAAGAA CAAACAGAGA CTGCGAAACG ATCCTCTCAA 180
 TCAAAATAAG GGTAACCAG ACTGAATAC AACATTGCCA ATTAGACAAA CAGCATCAAT 240
 TTTCAAACAA CCGGTAACCA AAGTCACAAA TCATCCTAGT AATAAAGTGA AATCAGACCC 300
 20 ACAACGAATG AATGAACAGC CACGTCAGCT TTTCTGGGAG AAGAGGCTAC AAGGACTTAG 360
 TGCATCAGAT GTAACAGAAC AAATTATAAA AACCATGGAA CTACCCAAAG GTCTTCAAGG 420
 25 AGTTGGTCCA GGTAGCAATG ATGAGACCCT TTTATCTGCT GTTGCCAGTG CTTTGCACAC 480
 AAGCTCTGCG CCAATCACAG GGCAAGTCTC CGCTGCTGTG GAAAAGAACC CTGCTGTTTG 540
 GCTTAACACA TCTCAACCCC TCTGCAAAGC TTTTATTGTC ACAGATGAAG ACATCAGGAA 600
 30 ACAGGAAGAG CGAGTACAGC AAGTACGCAA GAAATTGGAA GAAGCACTGA TGGCAGACAT 660
 CTTGTGCGCA GCTGCTGATA CAGAAGAGAT GGATATTGAA ATGGACAGTG GAGATGAAGC 720
 35 CTAAGAATAT GATCAGGTAA CTTTCGACCG ACTTTCCTCA AGAGAAAATT CCTAGAAATT 780
 GAACAAAAAT GTTCCCACTG GCTTTTGCCT GTAAGAAAAA AAATGTACCC GAGCACATAG 840
 AGCTTTTAA TAGCACTAAC CAATGCCCTT TTAGATGTAT TTTTGATGTA TATATCTATT 900
 40 ATTCAAAAAA TCATGTTTAT TTTGAGTCTT AGGACTTAAA ATTAGTCTTT TGTAATATCA 960
 AGCAGGACCC TAAGATGAAG CTGAGCTTTT GATGCCAGGT GCAATCTACT GGAAATGTAG 1020
 45 CACTTACGTA AAACATTTGT TTCCCCACA GTTTTAATAA GAACAGATCA GGAATTCTAA 1080
 ATAAATTTC CAGTTAAAGA TTATTGTGAC TTCACTGTAT ATAAACATAT TTTTATACTT 1140
 TATGAAAGG GGACACCTGT ACATTCTTCC ATCRCTACTG TAAAGACAAA TAAATGATTA 1200
 50 TATTCACAGA CTGATTGGAA TTCTTTCTGT TGAAAAGCAC ACACAATAAA GAACCCCTCG 1260
 TTAGCCTTCC TCTGATTTAC ATTCAACTCT GATCCCGGGG CCTTAGGTTT GACATGGGAG 1320
 55 GTGGGAGGAA GATAGCCAT ATATTTGCAG TATGAACTAT TGCTCTGGG ACCTTGTGAG 1380
 GAATGTGCT TTCACCAGAA TTCTAAGGA TTTCTGGCTT AAATATCACC TAGCCTGTGG 1440
 60 TAATTTTTTT TCCCT 1455

(2) INFORMATION FOR SEQ ID NO: 267:

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(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1086 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

10

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 267:

15 CGCCTGCACT ACCGGTCCGG AATTCCCGGG TCGACCCACG CGTCGCTGAC CCAGGAGAAG 60
CTGCCTGTCT ACATCAGCCT GGGCTGCAGC GCGCTGCCGC CGCGGGGCGG GCAGCTGAAC 120
TATGTGCTCT TCAGGGCGGG CACCGTGTG CATTCATCTT TGTACCCCA GCATCTAGCA 180
20 GTGTTGGCAT GTAGTAGGCA CTCAAGAAAT GTGTGTTGAA TGAACGATGC CTGTGACAAG 240
CAAGCGGACT TTATTCCTTC CTGACCCTTG CTCCTATGAC ACACCTCCTC CTGACTGCCA 300
CTGTCACTCC TTCAGAGCAG AACTCCTCTA GGAACCTGG ATGGGAAACA GCCATGGCCA 360
25 AGGACATCCT GGGTGAAGCA GGGCTACACT TTGATGAACT GAACAAGCTG AGGGTGTGG 420
ACCCAGAGGT TACCCAGCAG ACCATAGAGC TGAAGGAAGA GTGCAAAGAC TTTGTGGACA 480
30 AAATTGGCCA GTTTCAGAAA ATAGTTGGTG GTTTAATTGA GCTTGTGAT CAACTTGCAA 540
AAGAAGCAGA AAATGAAAAG ATGAAGGCCA TCGGTGCTCG GAACTTGCTC AAATCTATAG 600
CAAAGCAGAG AGAAGCTCAA CAGCAGCAAC TTCAAGCCCT AATAGCAGAA AAGAAAATGC 660
35 AGCTAGAAAG GTATCGGGTT GAATATGAAG CTTTGTGTAA AGTAGAAGCA GAACAAAATG 720
AATTTATGA CCAATTTATT TTTAGAAAAT GAACTGAAAA TTTGCTTTT ATAGTAGGAA 780
40 GGCAAAACAA AAAAAAGCCT CTCAAAACCA AAAAAACCTC TGTAGCATTC CAGCGGCTTG 840
ACCAATGACC TATGTCACAA GAGGTGGCGT GTAAGGAATG CAGCCCCCTG AAGACAGCAC 900
TACAAGTCTG GGGGAGCCAG TTTTAACATC AGTGCACAGC TGCTGCTGGT GGCCCTGCAG 960
45 TGTACGTTCT CACCTCTTAT GCTTAGTTGG AACTAAGCAG TTTGTAACT TTCATCCTTT 1020
TTTTTGTAAG TTTGGAAGGA GARGCAATAA ATTTTGTGTT TCNAAATGGC 1080
50 TTGATG 1086

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(2) INFORMATION FOR SEQ ID NO: 268:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1003 base pairs

(B) TYPE: nucleic acid

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(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 268:

5 GGCACGGGAG CAGCCGGGCT GGTCTGCTG CGAGCCGGCG GCCCGGAGTG GGGCGGCGGA 60
 GCAAACATGA ACGTTGGAGT TGCCACAGT GAAGTGAATC CAAATACCCG TGTCAATGAAC 120
 AGCCGGGGTA TGTGGCTGAC ATATGCATTG GGAGTTGGCT TGCTTCATAT TGTCTTACTC 180
 10 AGCATTC CCT TCTTCAGTGT TCCTGTTGCT TGGACTTTAA CAAATATTAT ACATAATCTG 240
 GGGATGTACG TATTTTTGCA TGCAGTGAAG GGAACACCTT TCGAACTCC TGACCAGGGT 300
 15 AAAAGCAAGG CTCCTAACTC ATTGGGAACA ACTGGACTAT GGAGTACAGT TTACATCTTC 360
 ACGGAAGTTT TTCACAATTT CTCCAATAAT TCTATATTTT CTGGCAAGTT TCTATACGAA 420
 GTATGATCCA ACTCACTTCA TCCTAAACAC AGCTTCTCTC CTGAGTGTAC TAATTCCTAA 480
 20 AATGCCACAA CTACATGGTG TTCGGATCTT TGGAAATTAAT AAGTATTGAA ATGTTTGTAA 540
 ACTGAAAAAA AATTTTACAG CTAATGAATT TCTTATAAGG AAGGAGTGGT TAGTAACTG 600
 25 CACTGTTTCT CTGATAATGT GAAATGAGAA GTATTTACAT TGGAGGGCCA ATGGCTGGTC 660
 CTTCAAGTGC TGTTTTGAAG TGCAGATTTC CATTAAATGA TGCCTCTGTT TAATACACCT 720
 GGTACATTTT TGAAGAGGGG CTTTATAAGC AGGCTGGGCA GGCCAGCTT ATAAGTTAAA 780
 30 GGGCATCACA GTGAGGGTGT AGTAGATAAA TTCAAGGAAA TAAGAGATTT GTAAGAACT 840
 AGGACCAGCT TAACTTATAA TGAATGGGCA TTGTGTTAAG AAAAGAACAT TTCCAGTCAT 900
 35 TCAGCTGTGG TTATTTAAAG CAGACTTACA TGTAACCCG AATCCTCTCT ATACAAGTTT 960
 ATTAAGATT ATTTTATTA CCGTAAAAAA AAAAAAAAAA AAA . 1003

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(2) INFORMATION FOR SEQ ID NO: 269:

(i) SEQUENCE CHARACTERISTICS:

45 (A) LENGTH: 1234 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 269:

ATCAGCATCT ACAAGTAGCA TATTTTGGAT GGTGTTGTG TGCTACTTCA AAGTAACTAG 60
 GAAAAAATAA TCCTCGCAAC ACAGGTACCT TGTCATGTCA GAATGGGGG TGTAGGTTG 120
 55 CCAGTTGTAT CAGTGTGAT TCATTTCAAT ACTTCCTACA GAGCAAACAT GAACGTTGGA 180
 GTTGCCACA GTGAAGTGAA TCCAAATACC CGTGTCTATGA ACAGCCGGG TATGTGGCTG 240
 60 ACATATGCAT TGGGAGTTGG CTGCTTCAT ATTGTCTTAC TCAGCATTC CTCTTCAGT 300

	GTTCCTGTTG CTTGGACTTT AACAAATATT ATACATAATC TGGGGATGTA CGTATTTTGT	360
5	CATGCAGTGA AAGGAACACC TTTCGAAACT CCTGACCAGG GTAAAGCAAG GCTCCTAACT	420
	CATTCGGAAC AACTGGACTA TGGAGTACAG TTTACATCTT CACGGAAGTT TTTCACAATT	480
	TCTCCAATAA TTCTATATTT TCTGGCAAGT TTCTATACGA AGTATGATCC AACTCACTTC	540
10	ATCCTAAACA CAGCTTCTCT CCTGAGTGTG CTAATTCCCA AAATGCCACA ACTACATGGT	600
	GTTCGGATCT TTGGAATTAA TAAGTATTGA AATGTTTGA AACTGAAAAA AAATTTTACA	660
15	GCTACTGAAT TTCTTATAAG GAAGGAGTGG TTAGTAACT GCACTGTTTC TGTGATAATG	720
	TGAAATGAGA AGTATTTACA TTGGAGGGCC AATGGCTGGT CCTTCAAGTG CTGTTTGTAA	780
	GTGCAGATTT CCATTAAATG ATGCTCTGT TTAATACACC TGGTACATTT CTGAAGAGGG	840
20	GCTTTATAAG CARGCTGGGC AGGCCAGCT TATAAGTTAA AGGGCATCAC AGTGAGGGTG	900
	TAGTAGATAA ATTCAAGGAA ATAAGAGATT TGTAAAGAAC TAGGACCAGC TTAACCTATA	960
25	ATGAATGGGC ATTGTGTTAA GAAAAGAACA TTTCCAGTCA TTCAGCTGTG GTTATTTAAA	1020
	GCAGACTTAC ATGTAAACCG GAATCCTCTC TATACAAGTT TATTAAAGAT TATTTTATT	1080
	ACCRACATA TTTCKCTTGT TTTATGTAAG YGGATGTATA TCCTCTGTGTT TTATACAAGC	1140
30	CAGTTCCAC TTATGAGGGT ACITTTTTTG TTTTGCTGGG CTTAATATTG TGTATTGGTC	1200
	AATGAGGCCA TTTTACANT TATTAACGTT ACAG	1234

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(2) INFORMATION FOR SEQ ID NO: 270:

- (i) SEQUENCE CHARACTERISTICS:
- 40 (A) LENGTH: 574 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

- 45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 270:

	NGAGGTGCGT TCTGAGCCGT CTGTCCTGCG CCAAGATGCT TCAAAGTATT ATTAAAAACA	60
50	TATGGATCCC CATGAAGCCC TACTACACCA AAGTTTACCA GGAGATTGG ATAGGAATGG	120
	GGCTGATGGG CTTTCATCGTT TATAAAATCC GGGCTGCTGA TAAAAGAAGT AAGGCTTTGA	180
	AAGCTTCAGC GCCTGCTCCT GGTTCATCACT AACCAATTT ACTTGAGTA CATGTGAAAG	240
55	AAAACGTCAG TCTGCCTGTA AATTTACGCA AGCCGTGTTA GATGGGGAGC GTGGAACGTC	300
	ACTGTACACT TGTATAAGTA CCGTTTACTT CATGGCATGA ATAAATGGAT CTGTGAGATG	360
60	CACTGCTACC TGGTACTGCT TTCAGTGTGT TCCCCCTCAG CCCTCCGGCG TGTGAGGCAT	420

	ACTCTGAGTA GATAATTTGT CATGCAGCGC ATGCAATCAG AATCTCACTG AGCCACCCAT	480
	CATTGTGAAA TAATTACCTC AGTTGTACAG GACTTGGTGA TCAGGATCCA GGCACCTCACT	540
5	TGTATTCTAC TGCTCAATAA ACGTTTATTA AACT	574
10	(2) INFORMATION FOR SEQ ID NO: 271:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 1731 base pairs	
	(B) TYPE: nucleic acid	
15	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 271:	
20	GCTGCAAGGT GGCCTCGTG CCGCTGCAGA TCCAGCTCAC TACCCTGGGA AATCTTACAC	60
	CTTCAAGCAC TGTGTTTTTC TGCTGTGATA TGCAGGAAAG GTTCAGACCA GCCATCAAGT	120
25	ATTTTGGGGA TATTATTAGC GTGGGACAGA GATTGTGCA AGGGGCCCGG ATTTTAGGAA	180
	TTCTGTAT TGTAAACAGAA CAATACCCTA AAGGTCTTGG GAGCACGGTT CAAGAAATG	240
	ATTTAACAGG TGTAAGACTG GTACTTCCAA AGACCAAGTT TTCAATGGTA TTACCAGAAG	300
30	TAGAAGCGGC ATTAGCAGAG ATTCCCGGAG TCAGGAGTGT TGTATTATTT GGAGTAGAAA	360
	CTCATGTGTG CATCCAACAA ACTGCCCTGG AGCTAGTTGG CCGAGGAGTC GAGGTCACA	420
35	TTGTGTCTGA TGCCACCTCA TCAAGAAGCA TGATGGACAG GATGTTTGCC CTCGAGCGTC	480
	TCGCTCRARC CNGGGATCAT AGTGACCACG AGTGNAGGCT GTTCTGCTTC AGCTGGTAGC	540
	TGATAAGGAC CATCCAAAAT TCAAGGAAAT TCAGAATCTA ATTAAGCGCA GTGCTCCAGA	600
40	GTCCGGTCTG CTTTCCAAAG TATAGGACAT TTGAAGAACT GGTATGCTAC TCACTGGTGA	660
	AGGACAGTCA GGTGAAGGAC TGTAAGCCCA CACAAGCTCT TCTTATCTCT ACTAGAATTA	720
45	AAATGTTAAG TCAAAAACGG CTCCTTTTTT GCGCCTCCTA GTGAACTTAA CCAGCTAGAC	780
	CATTTGAGTA CCAGCATTTA GTTACAAACG TCAAAGGCTT CCGGTGCTGC TTACCTTCCT	840
	TTTTTGTTAA TGTGCTTTTA TTTATTAAAA AAAATTACAA TGAAGATGCC TGTMTGTCT	900
50	CTACTGTGTA CTCTGATCGT ATCTTTCCAA AGTGCAGACT CTTGTGAAGT TTTCTTAAAT	960
	TGTTCACTTT AAAGAAAATG ACGTACCAAC AATGATTGG CTTTATATT ACTGTAAGAT	1020
55	GTTATAATGT TAATGTGGAT GTAGTGCTTT TACTTTACAG ATTGATTGGA ATAAGATTAT	1080
	TGCATATGAA TTTACCCACA GGACTCTGAA TCATGTTACC CACTCCCTC ACAATGTTGT	1140
	CCACTTAGTG AGTTGCATG ATCTATCCGT ACCAAATGAT GTTGAATAAT TACATATCTT	1200
60	TCTKGACTAT ACTGATTCT TATTTGGTC ACTATTACTA AATCTCTGTT AATACTCTCT	1260

CTTTAACTG AAAAGGGATG GGATAGAAGG GTTTCGAATG CCATATTATT GGTGGAGGGC 1320
 TGTMTTAAACA TCTTTGAAGT ATGGCTTGCT GAATATCTTT ACCAACATCT TGAATATATA 1380
 5 TTCTAGTGTC CACAAGATTT AGCAAAAAGA TAAAGCTTGG GTGGAATATC ATTTTAAAAT 1440
 GTTCATGTC TGTCTATAT TTTCTCACC TACTCTCCAA ATATTGTAAT GCAAAAAGTC 1500
 10 TCAGTAATGA TTTGGTAGTA TTAATTTTGT GGTCAATGTT TCTCTTCGAT AAATTTATTT 1560
 TCATTAAATA CTTRTTAGAG GGTTTTGAAA TGTMTTCAA ATATGTGAAA TGTGAAACTG 1620
 CTGTCTTTTA TATTAAAGTA ATTAAAGAAA ATGTATGTG ATTGAAATTA TTTGNCCTC 1680
 15 CACAAGATGG CTCTATGAGT ATTCTTCCAG GGATTCTAAT ATTTATTTAA G 1731

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(2) INFORMATION FOR SEQ ID NO: 272:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1320 base pairs
 25 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 272:

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CTGCTTAGGA AGAGAAGGTC AGAGTTCGCG GGGGCAGAGG CATTCCTGCC GCTGCCCAG 60

TCACTATGTA GTGGAGGGGC AGACACCCTC CCGCAAATTC TGAAGGTTT TTAGTCTCGA 120

35 CTAGGGCAGT AGCCCAGGAC TCCTAGTCGC CGGCTTCAGG TCACTGCCGG CTGAACGGAG 180

CTGCCGTCGC CATGTTTGGC TGCTTGGTGG CGGGGAGGCT GGTGCAAACA GCTGCACAGC 240

40 AAGTGGCAGA GGATAAATTT GTTTTGGACT TACCTGATTA TGAAAGTATC AACCATGTTG 300

TGGTMTTAT GCTGGGAACA ATCCCATTTT CTGAGGGAAT GGGAGGATCT GTCTACTTTT 360

CTTATCCTGA TTCAAATGGA ATGCCAGTAT GGMAACTCCT AGGATTTGTC ACGAATGGGA 420

45 AGCCAAGTGC CATCTTCAA AATTCAGGTC TTAATCTGG AGAAGGAAGC CAACATCCTT 480

TTGGAGCCAT GAATATTGTC CGAACTCCAT CTGTTGCTCA GATTGGAATT TCAGTGAAT 540

50 TATTAGACAG TATGGCTCAG CAGACTCCTG TAGGTAATGC TGCTGTATCC TCAGTTGACT 600

CATCACTCA GTTCACACAA AAGATGTTGG ACAATTTCTA CAATTTTGCT TCATCATTTG 660

CTGTCTCTCA GGCCAGATG ACACCAAGCC CATCTGAAAT GTTCATTCCG GCAAAATGTTG 720

55 TTCTGCAAAT GGTATGAGGC ATNTCTGTG TCCAATATTA AGGCTTTTTA TAACTGAATA 780

TCTATTTTGT CTATGAATAT ATTCCTTTT TGACATTTAA ACATATCTT TTATTGTGAA 840

60 CATCAGCACT GCATGCCATT AAAGTATGTA CTATAGAGAT CTGATGAGAA ACAGTTCTTA 900

CCCTAAATAT TTTGTTATAT TGTCGCCATT ATGAATTTAT AAAGACAGGA AAATATAGTT 960
 GCCTATGTTT TAGGGACCAC TATTAAAGCT TATAAATATT TGTGTATTTT CATTTAGAAG 1020
 5 TACCATCTAT GAGAGTAGTT TATACTGCAC TGTGTACATG AATGGCTAAT GAATCTATTT 1080
 TCCAACCTTC CCGTGTTTTA TAGATATTTT TTTTCACTTT GAGTATCCTA GAGATGGGAG 1140
 10 GATGCCTAGG AAGAGTTTGT TGAGAAGTGG TACCATGGTG TAGCATGGGA GAGCATTGGG 1200
 AATGCACTAG GTTTGAATTT GGCATAATGG TAGCTATGTG ACCCTGAGCA AATTTCTCTC 1260
 ATCTGCTCAT CTGANGAATG AGGAAATAGG AGTGAATTTG ATNTTTCCTA GGTCCNTCTA 1320
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(2) INFORMATION FOR SEQ ID NO: 273:

20 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 515 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 25 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 273:

CCCTGGAGAG GGGCTGCTGT GCCAGCTTGG GGAGGGTCTG GGATGGGGCT GCCCCTGATG 60
 30 GCCCTGATGT GGAGTACCTT GCCAGCATCT GCTGGGGTGA ACTTTATTTT AGCCCTTCCC 120
 TTGTTGYTCT TATGAAGAAC AGAGGAGGGG TGGGCAGGTC AGTGATGTCA GCAGTGAGTA 180
 35 TTCCAGCAC AGCGGCTCTG GAAGAGGCAT GAGGCATTTT TTTCAGGAAA TGRTCATTAT 240
 TCAGCCAGAA GGCATTCATT AAGTAAGTCC TGACTTTGTG CCCAGCTCTG TGTATAGGC 300
 CCTTGGCGAG ACTCAGGAGG GGCARAGGAC GCTAGKTTKT AGWTAACACG GAACCTCARA 360
 40 GGWTATATGG TCCAAGAAGA CCCGGGGGCG GTGAAAACCC TGTGGACTAA TGCTCACGGG 420
 AGCCCGAGGT CACACTTTGA CTTTGCTACC ATGGGCTGTG TCTANGNACG TATATATGCT 480
 45 GCGTAATTAT TACAGAGGCA GTCCATGTGC ATTGT 515

(2) INFORMATION FOR SEQ ID NO: 274:

50 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 2995 base pairs
 (B) TYPE: nucleic acid
 55 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 274:

60 TGACACCCAT AAGGAATCA TGAAGAAAGT AGAAGAAAAG CGAGTGGACG TTAATCAGC 60

	AGTAGCCATG GGAGAAGTCA TCCTGGCTGT CTGCCACCCC GATTGCATCA CAACCATCAA	120
	ACACTGGATC ACCATCATCC GAGCTCGCTT CGAGGAGGTC CTGACATGGG CTAAGCAGCA	180
5	CCAGCAGCGT CTTGAAACGG CCTTGTGAGA ACTGGTGGCT AATGCTGAGC TCCTGGAAGA	240
	ACTTCTGGCA TGGATCCAGT GGGCTGAGAC CACCCTCATT CAGCGGGATC AGGAGCCAAT	300
10	CCCGCAGAAC ATTGACCGAG TTAAAGCCCT TATCGCTGAG CATCAGACAT TTATGGAGGA	360
	GATGACTCGC AAACAGCCTG ACGTGGACCG GGTACCAAG ACATACAAAA GAAAAACAT	420
	AGAGCCTACT CACGCGCCTT TCATAGAGAA ATCCCGCAGC GGAGGCAGGA AATCCCTAAG	480
15	TCAGCCAACC CCTCCTCCCA TGCCAATCCT TTCACAGTCT GAAGCAAAAA ACCCAGGAT	540
	CAACCAGCTT TCTGCCCCTT GGCAGCAGGT GTGGCTGTTA GCACTGGAGC GGCAAAGGAA	600
20	ACTGAATGAT GCCTTGGATC GGCTGGAGGA GTTGAAAGAA TTTGCCAACT TTGACTTTGA	660
	TGTCTGGAGG AAAAAGTATA TGCGTTGGAT GAATCACAAA AAGTCTCGAG TGAATGATTT	720
	CTTCCGGCGC ATTGATAAGG ACCAGGATGG GAAGATAACA CGTCAGGAGT TTATCGATGG	780
25	CATTTTAGCA TCCAAGTTCC CCACCACCAA GTTAGAGATG ACTGCTGTGG CTGACATTTT	840
	CGACCAGAT GGGGATGGTT ACATGATTA TTATGAATTT GTGGCTGCTC TTCATCCCAA	900
30	CAAGGATGCG TATCGACCAA CAACCGATGC AGATAAAATC GAAGATGAGG TTACAAGACA	960
	AGTGGCTCAG TGCAATGTG CAAAAAGGTT TCAGGTGGAG CAGATCGGAG AGAATAAATA	1020
	CCGGTTCCTC CTCGGCAATC AGTTTGGGGA TTCTCAGCAG TTGCGGCTGG TCCGTATTCT	1080
35	GCGCAACCGT GATGGTTGCG GTTGGTGGAG GATGGATGGC CTTGGATGAA TTTTATAGTA	1140
	AAAATGATCC CTGCCGAGCA CGAGGTAGAA CTAACATTGA ACTTAGAGAG AAATTTCATCC	1200
40	TACCAGAGGG AGCATCCAG GGAATGACCC CCTTCCGCTC ACGGGGTCGA AGGTCCAAAC	1260
	CATCTTCCCG GGCAGCTTCC CCTACTCGTT CCAGCTCCAG TGCTAGTCAG AGTAACCACA	1320
	GCTGTACATC CATGCCATCT TCTCCAGCCA CCCAGCCAG TGAACCAAG GTTATCCCAT	1380
45	CATCAGGTAG CAAGTTGAAA CGACCAACAC CAACTTTTCA TTCTAGTCGG ACATCCCTTG	1440
	CTGGTGATAC CAGCAATTAG TTCTTCCCGG GCCTCCACAG GTGCCAAAAC TAATCGGGCA	1500
50	GACCCTAAAA AGTCTGCCAG TCGCCCTGGG AGTCGGGCTG GGAGTCGAGC CGGGAGTCGA	1560
	GCCAGCAGCC GCGGAGGAAG TGACGCTTCT GACTTTGACC TCTTAGAGAC GCATTCCTTG	1620
	TTCCGACACT TCAGAAAGCA GCGCTGCAGG GGGCCAAGGC AACTCCAGGA GAGGGCTAAA	1680
55	CAAACTTCC AAAATCCCAA CCATGTCTAA GAAGACCACC ACTGCCTCCC CCAGGACTCC	1740
	AGGTCCCAAG CGATAACACT GTCTAAGCAC CCCCAGCCA CTATCCACTT TGAATCCTGC	1800
60	TCCATACATT GGGTGTATAT TTATTCTGAA CGGAGAAGT TATATTGTTA AAAGTGTAAG	1860

	AGAATAATTG TGTATGAAG CTGCCATTAT TTTTTCCTT TTGTAAGTTA CTATTTTCAT	1920
	GTGAATATTT ATGTAGATAA AATTTCCTC CTGGTAACCC TGTAATGGAT GGGGCCCAGA	1980
5	AATGAAATAT TTGAGAAAA CAAGTGAAAA GGTCAAGATA CAAATGTGTA TTAAAAAAA	2040
	AAAAGCCTAT TAATAGGGTT TCTGCGCGGT GCAGGGTTGT AAACCTGCTT TATCTTTTAG	2100
10	GATTATTCCT AAATGCATCT TCTTTATAAA CTTGACTTGC TATCTCAGCA AGATAAATTA	2160
	TATTAATAAA ATAAGAATCC TGCAGTGTCT AAGGAATCT TTTTGTGTA ATCACGGACA	2220
	CCTCAATTAG CAAGAACTGA GGGGAGGGCT TTTCCATTG TTTAATGTTT TGTGATTTT	2280
15	AGCTAAAGAG AGGGAACCTC ATCTAAGTAA CATTTGCACA TGGATACAGC AAAAGGAGTT	2340
	CATTGCAATA CTGTCTTGG ATATTGTTT AGTACTGGT GTTTAAAGGA CAAATAGCTG	2400
20	CTAGAATTCA GGGGTAAATG TAAGTGTTC GAAAACGTCA GAACATTTGG GTTTAAAC	2460
	TGATTTGTTG CTCCTATCC AGCCTAGACA CCAGTAACTC TTGTGTTTAC CAGGACCCAG	2520
	ACCCCTGGCA AGGATAGGC TCGTTGGTGA CATTGTGAAT TTCAGATTG TTTTATCCAC	2580
25	TTTTTTTGCT ATTTATTTAA ATGGTCGATC AACTTCCAC AAAGTGAAG ATGAATTCCA	2640
	CGAGCCTGTT CTGAAATGT GGACGTAAGA CAAACACGTG CTCGTCTTT AATGGAGTTC	2700
30	ACCAGCACAC TTGTTAACCA GTCCTGTTT CTTCGTCTT TTTTGTGCG TAATAAAGTC	2760
	AACTGACCAA GTGACCATGA AAAGGGGCTG TCTGGGCTC CTGTTTTTA GCTGCTGTT	2820
	TTGAGTCCG ACCATGTTG TGTGTGATTA TCTCAATTG TTTTAATTGA GGCAGAACT	2880
35	GAAGCTCTAC CAATGAAGT TTTAGAAACA AGACACACTT TTGTATTAAA ATTGCTTGCA	2940
	GTAACAAAA AAAAAAAAAA AAAAAAAAAA AAAAACTCG AGGGGGGCC GGTAC	2995

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(2) INFORMATION FOR SEQ ID NO: 275:

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(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1990 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 275:

	GGGACCCCG CGSCTCCCG GGATGGTGAG CAAGGCGCTG CTGCNWCCTG TCTGCCGTCA	60
	ACCGCAGAGG ATGAAGCTG TGCTGGGCAT CGCCTTGCTG GCCTACGTCG CCTCTGTTG	120
55	GGGCAACTTC GTTAATATGA GGTCTATCCA GGAAAATGGT GAACTAAAA TTGAAAGCAA	180
	GATTGAAGAG ATGGTTGAAC CACTAAGAGA GAAAATCAGA GATTTAGAAA AAAGCTTTAC	240
60	CCAGAAATAC CCACCACTAA AGTTTTTATC AGAAAAGGAT CGGAAAAGAA TTTTGAWTAA	300

	CAGGAGGGCG AGGTTTCGTG GGCTCCCATC TKAAC TGACA AACTCATGAT GGACGGCCAC	360
5	GAGGTGACCG TGGTGGACAA TTTCTTCACG GGCAGGAAGA GAAACGTGGA GCACTGGATC	420
	GGACATGAGA ACTTCGAGTT GATTAAACCAC GACGTGTGGG AGCCCCCTCTA CATCGAGGTT	480
	GACCAGATAT ACCATCTGGC ATCTCCAGCC TCCCCCTCAA ACTACATGTA TAATCCTATC	540
10	AAGACATTAA AGACCAATAC GATTGGGACA TTAAACATGT TGGGGCTGGC AAAACGAGTC	600
	GGTGCCCGTC TGCTCCTGGC CTCCACATCG GAGGTGTATG GAGATCCTGA AGTCCACCCCT	660
15	CAAAGTGAGG ATTACTGGGG CCACGTGAAT CCAATAGGAC CTCGGGCCTG CTACGATGAA	720
	GGCAAACGTG TTGCAGAGAC CATGTGCTAT GCCTACATGA AGCAGGAAGG CGTGGAAGTG	780
	CGAGTGGCCA GAATCTTCAA CACCTTTGGG CCACGCATGC ACATGAACGA TGGGCGAGTA	840
20	GTCAGCAACT TCATCCTGCA GGCCTCCAG GGGGAGCCAC TCACGGTATA CGGATCCGGG	900
	TCTCAGACAA GGGCGTCCA GTACGTCAGC GATCTAGTGA ATGGCCTCGT GGCTCTCATG	960
25	AACAGCAACG TCAGCAGCCC GGTCAACCTG GGAACCCAG AAGAACACAC AATCCTAGAA	1020
	TTTGCTCAGT TAATTAAAAA CCTGTGTTGGT AGCGGAAGTG AAATTCAAGTT TCTCTCCGAA	1080
	GCCCAGGATG ACCCAGAGAA AAGAAAACCA GACATCAAAA AAGCAAAGCT GATGCTGGGG	1140
30	TGGGAGCCCG TGGTCCCGCT GGAGGAAGGT TTAAACAAAG CAATTCACTA CTTCCGTAAA	1200
	GAACTCGAGT ACCAGGCAAA TAATCAGTAC ATCCCCAAAC CAAAGCCTGC CAGAATAAAG	1260
35	AAAGGACGGA CTCGCCACAG CTGAACTCCT CACTTTTAGG ACACAAGACT ACCATTGTAC	1320
	ACTTGATGGG ATGTATTTTT GGCTTTTTTT TGTGTGCTT TAAAGAAAGA CTTTAACAGG	1380
	TGTCATGAAG AACAACTGG AATTTCAATC TGAAGCTTGC TTTAATGAAA TGGATGTGCC	1440
40	TAAAGCTCC CCTCAAAAAA CTGCAGATTT TGCCTTGCAC TTTTGAATC TCTCTTTT	1500
	TGTAATAATAG CGTAGATGCA TCTCTGCGTA TTTTCAAGTT TTTTATCTT GCTGTGAGAG	1560
45	CATATGTTGT GACTGTGCTT GACAGTTTTA TTTACTGGTT TCTTTGTGAA GCTGAAAAGG	1620
	AACATTAAGC GGGACAAAAA ATGCCGATTT TATTTATAAA AGTGGGTACT TAATAAATGA	1680
	GTCGTTATAC TATGCATAAA GAAAAAYCCT AGCAGTATTG TCAGGTGGTG GTGCGCCGGC	1740
50	ATTGATTTTA GGCAGATAA AAGAATTCTG TGTGAGAGCT TTATGTTTCT CTTTAAATTC	1800
	AGAGTTTTTC CAAGGTCTAC TTTTGAGTTG CAAACTTGAC TTTGAAATAT TCCTGTGTT	1860
55	CATGATCAAG GATATTTGAA ATCACTACTG TGTTTGCTG CGTATCTGGG GCGGGGCGAG	1920
	GTTGGGGGGC ACAAAGTTAA CATATTCCTG GTTAACCATG GTTAAATATG CTATTTTAAT	1980
	AAAATATTGA	1990
60		

(2) INFORMATION FOR SEQ ID NO: 276:

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(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2436 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 276:

	AACTTCGCTT AGCTCTCCAG GGTNAAACGG GTGAGNCCTT AAAACAGAA GAGAACAAGA	60
15	TTTAAAGTCC GTTGCAATTGA AAATAACAAA CAATATCAAT GTTTTAATCA AGGATCTCTT	120
	CCACATTCCCT CCTTCTTATA AGAGCACAGT AACACTATCC TGGAAACCTG TACAAAAGGT	180
	TGAGATTGGG CAAAAGAGAG CCAGTGAAGA TACAACTTCA GGTTCACCAC CCAAGAAATC	240
20	TTCAGCAGGA CAAAAAGAG ATGCCAGGCA GATTTATAAC CCTCCCAGTG GGAAATATAG	300
	CAGCAATTG GGCAACTTTA ATTATGAGCA GAGAGGAGCC TTCAGGGGAA GTAGAGGTGG	360
25	CCGAGGTGG GGCACACGAG GAAATCGTAG TCGGGGAAGA CTCTACTGAA TAAGACATCA	420
	GCATTCTTCA GCATTGTGAT GAGCTTAATA TACTTAAATT CTACTACTCA TTGGATTGCC	480
	GGGATGTCC CTTTAAACAG ACTGCTGCCT TCAGCTAAAA ACTTAATGTT CTTTATACCT	540
30	TTGTATGTAT GACCTACTTT TGTAAACAGAC CATGGTTGTG TCCAAGGTAA AACCACAGTG	600
	ATATTTTGG ATGCTTTGTC TGCAATCTTG ACTTGTTTT GCAGTATCAT TATTCAGACT	660
35	TCAAATGTG AATCTTTTAA ACATCTTGAT AATTTGTTGT TGAGAGCTGT TCATTCTAAA	720
	ATGTAATGAA ATTCAGTCTA GTCTGTCTGA TAAAGATCAT CAGTTTGTAA AGGTTACTGA	780
	TTTTCTCTT CCTCTTAGT TTTTACCCA ATATATGGAG AAGAGTAATG GTCAATCTTA	840
40	ACATTTTGTT TTAATTGTTT AATAAAGCTG CTGGGCAGTG GTGCAGCATT CCTACCTAGT	900
	GTCATAAAAG CAAATACTT ACATAGCTTT CTTAAATAT AGGAATGACA TTACATTTT	960
45	AGGAGAAAGT AAGTTGCTTT GCACCGCCTA CTTAATTCCT TTCCATATAT TGTGATACAA	1020
	ACTTTTGAAT ATGGAATCTT ACTATTTGAA TAGAAATGTG TATGTATAAT ATACATACAT	1080
	ACATAAGCAT ATATGTGTGT GTGTGTGTGT ATATATATAT ATATGCATGC TGTGAACTT	1140
50	GACTACACAA CATAAATCAC TTTTAAATT CCAGGAACGG GTAGTCTGAC ACGGTGATTA	1200
	TCCTTTTGAG GCTGAATCCG TTATTAACCT GTTATTTAGG TTTTACTCC CAGTAGCAAG	1260
55	GGATTCCTAAG TTAGTTGCAC TTACATGATT ATTGTTATTT AAACTAAGA ATAAAGGCTG	1320
	CATTTTCAAA GATAAATTGG AATTGCTGTT GGTGAAATAA CAACCAAAAT ACTGAATCTG	1380
60	ATGTACATAC AGGTTTCTAC AGGAAGAGAT GGTATAATTT ACAATTTGGA GATTTAATAA	1440

	CCAGGGCTAC CCAGAAAAAG TGA	CTTGATA ACATGGTACC AATAAGTAAG GGATGCTCTC	1500
	TCGGTTTGCT TTTGCCACTT TCAAGATTTT	AACCTCTCAG GTTATTAATC AAAATTATTG	1560
5	TATAAGTTAG CCAATAGAAT TTTAGGTTA	AAACAACAGA TGGGGGGTTT GTGGAGTGT	1620
	TAATGTCATG GGCATTTTTA GTAGCATAGA	CCCTTTGTTC TGCATTTGAA TGTTCGTAT	1680
10	ATTTTGTGTT CACAGTTAAT CTTCCTCCC	CAAGTTTGCT ATTCAAATCA ACTGCCTGAA	1740
	TGACATTTC AGTAGTCTGA TGTATTTTC	TGAGGAATAG TTTGTGATTC CAATGCAGGT	1800
	GTCTTCATTA CCATTACCTC TACACTGCAG	AAGAAGCAAA ACTCCTTTAT TAGAATTACT	1860
15	GCACATGIGT ATGGGGAAAA TAGTCTGAA	AGGCTAGAAT GATACAAGTG AGCAAAAGTT	1920
	GGTCAGCTG GCTATGGAGT GGTGGCAATA	ATCTCTAAAC ATTCCAAAAG ACCATGAGCT	1980
20	GAACCTAAAC TCCCTTGGAA TCTGAACAAA	GGAATATAAA ATTGCCATTT GAAACTGAC	2040
	CAGCTAATCT GGACCTCAGA GATAGATCAG	CCAGTGGCCC AAAGCCATTT CAAGTACAGA	2100
	AATTATAGAG ACTACAGCTA AATAAATTG	AACATTAAAT ATAATTTTAC CACTTTTGT	2160
25	CTTTATAAGC ATATTGTAA ACTCAGAACT	GAGCAGAACT GACTTTACTT TCTCAAGTTT	2220
	GATACTGAGT TGA	CTGTTCC CTTATCCCTC ACCCTTCCCC TTCCCTTTCC TAAGGCAATA	2280
30	GTGCACAACT TAGGTTATTT TTGCTTCCGA	ATTTGAATGA AAACTTAAT GCCATGGATT	2340
	TTTTCTTTT GCAAGACACC TGTATCAT	CTTGTTTAAA TGTAATGTC CCCTTATGCT	2400
	TTTGAAATAA ATTTCCCTTTT GTAATTTTAA	AAAAAA	2436
35			

(2) INFORMATION FOR SEQ ID NO: 277:

- 40 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 782 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- 45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 277:

	GCCACTGACT TCTCCACCC TTCTGTCTCC	CCCATAATAG TTTATTTGGT TGGTCTGGAC	60
50	TCACTTGTGG CCTTTRATTA AATTCCTAAG	GGGCTGAAG AAGACATTTT TACTGCAGAG	120
	GGTTAGAGGC ACTTGAGCAA GGCCCCACA	TCCCAACTCT GGGAGTTGTG GTGGAGGAG	180
55	GCACTTCTGG GGGATAGGAC CAGACAAGAT	AACAGGAGCT CACATGNNAA GCAGAAGCTG	240
	TGACAAGTTT AGTAGTCCCA AAATGGGTTA	TATCCCTTCC CCCTTTACAT CAGAATCTTG	300
	TGAAATGGGA AAACAACAGA AGGAGGGGAT	CAAAGATAGC TGATCTCACA TGCTTCCAG	360
60	GCAGGGCARG GGTGGGAGTC AAACCCGGGT	GACAGGTGGG TGGAGAGCCC TGTTTGAGGT	420

TGTGGCTGAT CCCTCTCTGG TATTAGTTTT TCCCTGGGA GCAGGAAGCC CTAGGAAGAG 480
 GGGACTGCAG GGTCCCCRGG GGATCTTTCC TCCCTCCCCT GCATGAGGCA GAGGCAAGCT 540
 5 GCCTGCCAAC CCCCTCCCTC AAGGAATGGC CTTGCCCAGG AATGCCACAC ACACATACCC 600
 TCTCTTTTTT TTCTAGTCAA ACTCTTGTTT ATTCTTGGC TTGCCTCCCT CCTTCCTCCC 660
 10 CTCTCAACCT TTACTTCTGA TTCTATTTT ATGGAATTG GGATTGAAGT TAAACTACAA 720
 CAGTGCCGCC AACACCAAGT CTGTCAGGAA AAAAATACAA AGAAATTAA CAAAAAAAAA 780
 AA 782
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20 (2) INFORMATION FOR SEQ ID NO: 278:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 961 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 278:

GAGTCCCGC TGGAGACCCG TGCTCTGGGC CGGCGCCTTC ACCATGGCCT CGGCAGAGCT 60
 30 GGAATACACC ATCGAGATCC CGGATCAGCC CTGCTGGAGC CAGAAGAACA GCCCAGCCC 120
 AGGTGGGAAG GAGGCAGAAA CTCGGCAGCC TGTGGTGATT CTYTTGGGCT GGGGTGGCTG 180
 35 CAAGGACAAG AACCTTGCCA AGTACAGTGC CATCTACCAC AAAAGGGGCT GCATCGTAAT 240
 CCGATACACA GCCCCGTGGC ACATGGTCTT CTCTCCGAG TCACTGGGTA TCCCTTCACT 300
 TCGTGTTTTG GCCCAGAAGC TGCTCGAGCT GCTCTTTGAT TATGAGATTG AGAAGGAGCC 360
 40 CCTGCTCTTC CATGCTTCA GCAACGGTGG CGTCATGCTG TACCGCTACG TGCTGGAGCT 420
 CCTGCAGACC CGTCGCTTCT GCCGCTGCG TGTGGTGGGC ACCATCTTTG ACAGCGCTCC 480
 45 TGGTGACAGC AACCTGGTAG GGGCTCTGCG GGCCCTGGCA GCCATCCTGG AGCGCCGGGC 540
 CGCCATGCTG CGCCTGTTGC TGCTGGTGGC CTTTGCCCTG GTGGTCGTCC TGTTCACGT 600
 CCTGCTTGCT CCCATCACAG CCCTCTTCCA CACCCACTTC TATGACAGGC TACAGGACGC 660
 50 GGGCTCTCGC TGGCCCGAGC TCTACCTCTA YTCGAGGGCT GACGAAGTAG TCCTGGCCAG 720
 AGACATAGAA CGCATGGTGG AGGCACGCCCT GGCACGCCGG GTCTGGCGC GTTCTGTGGA 780
 55 TTTCGTGICA TCTGCACAGC TCAGCCACCT CCGTGACTAC CCTACTTACT ACACAAGCCT 840
 CTGTGTCGAC TTCATGCGCA ACTGCGTCCG CTGCTGAGGC CATGCTCCA TCTCAMCTCT 900
 GCTCCAGAAA TAAATGCCTG ACAMCTCCCC AAAAAAAAAA AAAAAAAAAA ACTCGAGGGG 960
 60

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961

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(2) INFORMATION FOR SEQ ID NO: 279:

(i) SEQUENCE CHARACTERISTICS:

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- (A) LENGTH: 1228 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 279:

CGCGCTTTGC AGTTGGGTCT CCTGGTGATC GGCCAACGCC AAGTAGGGGA TTGCGTTCCC	60
TCCAGTCGCA GCCCTATCAG ATTTGGATAT GTCTTCATA TTTGATTGGA TTTACAGTGG	120
TTTCAGCAGT GTGCTACAGT TTTTAGGATT ATATAAGAAA ACTGGTAAAC TGGTATTTCT	180
TGGATTGGAT AATGCAGGAA AAACAACATT GCTACACATG CTAAGAAGTG ACAGACTTGG	240
ACAACATGTC CCAACATTAC ATCCCACTTC CGAAGAAGTG ACCATTGCTG GCATGACGTT	300
TACAACTTTT GATCTGGGTG GACATGTTCA AGCTCGAAGA GTGTGGAAAA ACTACCTTCC	360
TGCTATCAAT GGCATTGTAT TTCTGGTGGA TTGTGCAGAC CACGAAAGGC TGTTAGAGTC	420
AAAAGAAGAA CTTGATTAC TAATGACAGA TGAAACCAAT GCTAATGTGC CTATACTGAT	480
TCTTGGGAAT AAGATCGACA GACCTGAAGC CATCAGTGAA GAGAGGTTGC GAGAGATGTT	540
TGGTTTATAT GGTACAGCAA CAGGAAAGGG GAGTATATCT CTGAAAGAAC TGAATGCCCG	600
ACCCTTAGAA GTTTTCATGT GTAGTGTGCT CAAAAGACAA GGTACGGAG AAGGCTTCGG	660
CTGGATGGCA CAGTACATTG ATTAACACAA ACTCACATTG GTTCCAGGTC TCAACGTTCA	720
GGCTTACTCA GAGATTGAT TGCTCAACAT GCATAACTTG AATCAATAG ACTTTTGCTG	780
GTATATAAAC AGATGTTTTT TAGATTATTA ATATTAAATC AACTTAATTT GAATGAGAAT	840
TGAAACTGA TTCAAGTAAG TTTGAGTATC ACAATGTTAG CTTTCTAATT CCATAAAAGT	900
ACTTGGTTTT TACAGTTTTAT AATCTGACAT CACCCAGCG CCATTTGTAA AGAGCAACTT	960
TCCAGCAGTA CATTTGAAGC ACTTTTAAAC AACATGAAAC TATAAACCAT ATTTAAAAGC	1020
TCATCATGTT AAATTTTTTA TGTAATTTTC TGGAAGTAGT TTTTAAATTT TAGATTATAT	1080
GTCCACCTAT CKTAAGTGTA CAGTTAATAA TTAGCTTATT CAATGATTGC ATGATGCCTT	1140
ACAGTTTTCA ATAACTTTTT TTCATTATGA AACGTCATGC AATAAAACAA ACTCTAATGT	1200
TTGGCAAAAA AAAAAAAAAA AAANTCGA	1228

60

(2) INFORMATION FOR SEQ ID NO: 280:

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 1327 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 280:

10 TCTCGGGTCT CGGGACAGGT GAGCACCTG ATGAAGGCCA CGGTCTGAT GCGGCACCTG 60
 GCGGGGTGCA GGAGATCGTG GCGGCCCTCC GCAAGGGCGS CGGAGACCGG TTACAGGTGA 120
 15 TTTCTGATTT TRACATGACC TTGAGCAGGT TTGCATATAA TGGAAAGCGA TGCCCTTCTT 180
 CTTACAATAT TCTGGATAAT AGCAAGATCA TCAGTGAGGA GTGTCGGAAA GAGCTCACAG 240
 CGCTCCTTCA CCACTATTAC CCAATTGAGA TCGACCCACA CCGGACCGTC AAGGAGAAGC 300
 20 TACCTCATAT GGTGGAATGG TGGACCAAAG CGCACAATCT CCTATGTCAG CAGAAGATTC 360
 AGAAGTTTCA GATAGCCCAG GTGGTTAGAG AGTCCAATGC AATGCTCAGG GAGGGATATA 420
 25 AGACCTTCTT CAACACACTC TACCATAACA ACATTCCCCT TTTCATCTTT TCTGCGGGCA 480
 TTGGTGATAT CCTGGAAGAA ATTATCCGAC AGATGAAAGT GTTCCACCCC AACATCCACA 540
 TCGTGTCTAA CTACATGGAT TTTAATGAAG ATGGTTTCTT CCAGGGATTT AAGGGCCAGC 600
 30 TGATACACAC ATACAACAAG AACAGCTCTG TGTGTGAGAA CTGTGGTTAC TTCCAGCAAC 660
 TTGAGGGCAA AACCAATGTC ATCCTGCTGG GAGACTCTAT CGGGGACCTC ACCATGGCCG 720
 35 ATGGGGTTCC TGGTGTGCAG AACATTCTCA AAATGGGCTT CCTGAATGAC AAGGTGGAGG 780
 AGCGGCGGGA NCGCTAACAT GGACTCCTAT GACATCGTGC TGGAGAAGGA CGAGACTCTG 840
 GATGTGGTCA ACGGGCTACT GCAGCACATC CTGTGCCNAG GGGGTCCAGC TGGAGATGCA 900
 40 AGGCCCCTGA AGGCGCAGGC TCCNAAGKCC SCTGCAGGCC GTGGTGAGGA GGGGCGCCTC 960
 CCCAGAGTCT GCTCCCCCGT GAACACAGAG CAGAGCCAGG GTGGCCAGCA GTGGCTGGGT 1020
 45 CCTTCCGGCG CCTTCCGTCC TCCTTTCCCT GAGCACCTTC ATCACCAGAG GCTTGAAGGA 1080
 ACCCGGCCAT GTGGCAGGGC ACAGGCACTG TTCCTGGTGA ACCTTGGACC ACAGCATGTC 1140
 AGTGCTCTAG GGATTGTCTA CTCCAGGGAT TTTCTTCAAA ATTTTTAAAC ATGGGAAGTT 1200
 50 CAAACAAATA TAATGTGTGA AACAGATCAA AATTTTAAAC ATGAAAAAAA AGCTGCTCTG 1260
 ATTCAGGGGA TGTGGGTCGG GGTAGAACCT GGACCTCTTG GCCTGGGGGC ACATGGGATG 1320
 55 CTTCTAG 1327

60 (2) INFORMATION FOR SEQ ID NO: 281:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 799 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 281:

10 TCACCCCTGCC TACAGCGTGG AGCTCAGATG ACTGCCGCCCT CCACGGTCAC TGTGAGCAGG 60
 TGGTATTAC AGCCTGCATG ACCCTCACGG CCAGCCCTGG GGTGTTCCCC GTCACTGTGT 120
 15 GGCTTTGGCT GAAGCCTAAT TCCACAGCTC CTGTGTTTTT GAGAGAGACT GAGAGAACCA 180
 TAATCCTTGC CTGCTGAACC CAGCCTGGGC CTGGATGCTC TGTGAATACA TTATCTTGCG 240
 ATGTGGGGTT ATTCCAGCCA AAGACATTTC AAGTGCCTGT AACTGATTTG TACATATTTA 300
 20 TAAAAATCTA TTCAGAAATT GGTCCAATAA TGCACGTGCT TTGCCCTGGG TACAGCCAGA 360
 GCCCTTCAAC CCCACCTTGG ACTTGAGGAC CTACCTGATG GGACGTTTCC ACGTGTCTCT 420
 AGAGAAGGAT TCCTGGATCT AGCTGGTCAC GACGATGTTT TCACCAAGGT CACAGGAGCA 480
 25 TTGCGTCGCT GATGGGGTTG AAGTTGGTT TGGTTCTTGT TTCAGCCCAA TATGTAGAGA 540
 ACATTTGAAA CAGTCTGCAC CTTTGATACG GTATTGCATT TCCAAAGCCA CCAATCCATT 600
 30 TTGTGGATTT TATGTGTCTG TGGCTTAATA ATCATAGTAA CAACAATAAT ACCTTTTTCT 660
 CCATTTTGCT TGCAGGAAAC ATACCTTAAG TTTTTTTTGT TTGTGTTTGT TTTTTTTGTT 720
 35 TTTTGTITTC CTTTATGAAG AAAAAATAAA ATAGTCACAT TTTTAATACY AAAAAATGGA 780
 CAAAAAAGT CGAGGGGGG 799

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(2) INFORMATION FOR SEQ ID NO: 282:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2196 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 282:

50 AAAGACTCTA ACATCCATGA GCTTGAACAT GAGCAAGAGC CTACTTGTGC CKSCCAGATG 60
 GCTGAGCCCT TCCGTACCTT CCGAGATGGA TGGGTCTCCT ACTACAACCA GCCTGTGTTT 120
 55 CTGGCTGGCA TGGGTCTTGC TTTCCTTTAT ATGACTGTCC TGGGCTTTGA CTGCATCACC 180
 ACAGGGTACG CCTACACTCA GGGACTGAGT GGTTCATCC TCAGTATTTT GATGGGAGCA 240
 60 TCAGCTATAA CTGAATAAT GGAAGTGA GCTTTTACTT GGCTACGTCG AAAATGTGGT 300

	TTGGTTCGGA CAGGTCTGAT CTCAGGATTG GCACAGCTTT CCTGTTTGAT CTTGTGTGTG	360
	ATCTCTGTAT TCATGCCTGG AAGCCCCCTG GACTTGTCCG TTTCTCCTTT TGAAGATATC	420
5	CGATCAAGGT TCATTCAAGG AGAGTCAATT ACACCTACCA AGATACCTGA AATTACAAC	480
	GAAATATACA TGTCTAATGG GTCTAATTCT GCTAATATTG TCCCGGAGAC AAGTCCTGAA	540
10	TCTGTGCCCC TAATCTCTGT CAGTCTGCTG TTTGCAGGCG TCATTGCTGC TAGAATCGGT	600
	CTTTGGTCCT TTGATTTAAC TGTGACACAG TTGCTGCAAG AAAATGTAAT TGAATCTGAA	660
	AGAGGCATTA TAAATGGTGT ACAGAACTCC ATGAACTATC TTCTTGATCT TCTGCATTT	720
15	ATCATGGTCA TCCTGGCTCC AAATCCTGAA GCTTTTGGCT TGCTCGTATT GATTTCAGTC	780
	TCCTTTGTGG CAATGGGCCA CATTATGTAT TTCCGATTTC CCCAAAATAC TCTGGGAAAC	840
20	AAGTCTTTTG CTTGCGGTCC TGATGCAAAA GAAGTTAGGA AGGAAAATCA AGCAAATACA	900
	TCTGTTGTTT GAGACAGTTT AACTGTTGCT ATCCTGTTAC TAGATTATAT AGAGCACATG	960
	TGCTTATTTT GTACTGCAGA ATTCCAATAA ATGGCTGGGT GTTTTGCTCT GTTTTACCA	1020
25	CAGCTGTGCC TTGAGAACTA AAAGCTGTTT AGGAAACCTA AGTCAGCAGA AATTAACTGA	1080
	TTAATTTCCC TTATGTTGAG GCATGGAAAA AAAATTGGAA AAGAAAACT CAGTTTAAAT	1140
30	ACGAGACTA TAATGATAAC ACTGAATTCC CCTATTTCTC ATGAGTAGAT ACAATCTTAC	1200
	GTAAAAGAGT GGTTAGTCAC GTGAATTCAG TTATCATTG ACAGATCTT ATCTGTACTA	1260
	GAATTCAGAT ATGTCAGTTT TCTGCAAAAC TCACTCTTGT TCAAGACTAG CTAATTTATT	1320
35	TTTTTGATC TTAGTTAATT TTAANAACAA ATTCTTCAAG TATGAAGACT AAATTTTGAT	1380
	AACTAATATT ATCCTTATTG ATCCTATGA TCTTAAGGTA TTTACATGTA TGTGGAAAA	1440
40	CAAAACACTT AACTAGAAAT CTCTAATAAG GTTTATGGTT TAGCTTAAAG AGCACCTTTG	1500
	TATTTTTATT ATCAGATGGG GCAACATATT GTATGAAGCA TATGTAGCAC TTCACAGCAT	1560
	GGTTATCATG TAAGCTGCAG GTAGAAGCAA AGCTGTAAAG TAGATTATC ACACAATGAC	1620
45	TGCATACAGA CTTCAAATAT GTCAATAGTT TGGTCATAGA ACCTAGAAGC CAAAAGCCAC	1680
	ACAGAAGGGC AAGAATCCCA ATTTAACTCA TGTTATCATC ATTAGTGATC TGTGTTGTAG	1740
50	AACATGAGGG TGTAAGCCTT CAGCCTGGCA AGTTACATGT AGAAAGCCCA CACTTGTGAA	1800
	GGTTTGTGTT TACAAATCAC TTGATTTAAC AACTCAGGT AGAATATTTT TATTTTACT	1860
	GTTTTATACC CAGAAGTTAT TTCTACATTG TTCTACAGCA AGAATATTCA TAAAAGTATC	1920
55	CCTTTCAAAT GCCTTTGAGA AGAATAGAAG AAAAAAGTT TGTATATATT TTAATAAATT	1980
	GTTTTAAAG TCAGTTTGCA ACATGTCTGT ACCAAGATGG TACTTTGCCT TAACCGTTTA	2040
60	TATGCACTTT CATGGAGACT GCAATACGTT GCTATGAGCA CTTTCTTTAT CCTTGGAGTT	2100

TAATCCTTTG CTTCATCTTT CTACAGTATG ACATAATGAT TTGCTATGTT GTAAAAATCTT 2160
 TGTAATAAAT TTCTATATAA AATATTTGAA ACTTAA 2196

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(2) INFORMATION FOR SEQ ID NO: 283:

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(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1185 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 283:

GCAGTTAAGG CTTCTGATAA GGAAAGAGAG TCTGAACAGA GCACACACAT CTGGAGCTCC 60
 20 AGGAGTGGGG GATGCAGCAT CAGATTCCAT CTTGAATTTC TGCTAAAATA CTTTGTACTC 120
 ATAATGGATC TCAACAAAGA TCTGTATTTT ATCTGTGGCT CCATCTTCCC TCTGGGTCAA 180
 GTAGATGTTA AGCTGGACCT TGGCAGCCT CTTAACATGA AGAGATCTAG CTAGACAGAC 240
 25 AGACTCCCCC ATTTATGGGA ACAAGAATTC AATTTATTCT CTATTTATAA AACATTTTTT 300
 TAAAGTGCCT TGGGTATAAA AATCTAAATG TCTGCGGTGT GATCAGTCAG GAGCACGTAA 360
 30 CTATCACTCT TCGCATCCTT TGGTCACTGG GAGATCCTTT GGGGGCTGGG AGGTCTTCT 420
 GTCCAGGCT AAAGGAAAAG CTTACAAGG GTAAGAGCCA CAGAACCCTC GGCAAGAAAG 480
 GCCGTCAGG GAGAATGAAT GGTACAGAGA GGAAAGGAAG GAAAGGGGT GGAACAGAGG 540
 35 TAGAAGGCAA GGAAGGATG CCGCACTGGA GACCGATGGG GACACTCTAA TTGTGCAAGA 600
 GGGAGGATCT TCCTTCTTGA ATGCTGAACA CAGCTAGTCT GAACCTTCCT TGGAAAGTCC 660
 40 AGCTGTTTGC CCATGCATAG GGCCAACCTC CCCTGCAAAG CAGCAAATGT GGCTTCTATC 720
 AGGAAGGAAA AGTATCCATC AGTGTGACAA GAGGTCACCT TCGAACTTGC ATGAACTCCT 780
 TGCGCAGCCA CAAAGAGTCC TGGTAGAAGT GAGGATCGCC TAGTCTTACG GCTGTCCGTT 840
 45 TATAGAAGTA GCAGTACAAC ACTGCTGCTA GTCTCTGGAA TACAAACAGC ATTTGAAGTC 900
 CATCTGTCCA TATGAAGCTG TTGGAGTTT TCCAGCGTAA GTTCATGACC CAGACATGAA 960
 50 GGGAGATGCT GAGGGCAAAG TACACAGCTG TCAGGATGAT GGTCCCTTTG AACTTATGGA 1020
 ATAGAGGTTT GACCAGGCCA GCCTGGAAGA CGAAGGTGTT GAAGAACATG AGGAAAATGA 1080
 TGATGATGTT GAAGAGGACT GCAATATCCT GGATGCACTG AGGGAGAGGY TTCTAGTTCC 1140
 55 TTTGAATGAG AGCTGTTTCC CTTGCTCTAA GGCAAGCACC TCCAA 1185

60

(2) INFORMATION FOR SEQ ID NO: 284:

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 1634 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 284:

10 AGGGAAAGGG GAGGGTAGCG GGAGGGTAGC AGGTGAGTTC CTAGGGCTGG AAGGTTTAGC 60
AGCAGCCTGG TGCAGTGCCC TGTCAATCAAG ACAAACCCAC GGTCCCTMCTG GGTGCCTACC 120
15 AAGCTTGSTT TGTACAAAAG CAAGGTGGGA GTCTATTTT GTACATGAGA TACATCACAC 180
TTACCTGTGG GCCAGTATTG TGAAGTGAGT CTGAGTTGTT TACACTGATG CCTTCCCTGC 240
CCACCACAAA TTGTGTACAT AGTCTTCAGA TGATACCACC CCTTCCCTCA GCTCCCAACC 300
20 AAGAGCTGGT TCTAGGCCCTG TGTATATGT CATATTTAGC STTTTATAT ATGACCTTTG 360
ATTTCTGTTG TTTGTATTTT AGCACAGTGT ATGCACCTTC ATTTAAATAC ATCTGTGTGC 420
25 ATACAGATAC GCATATATGT GTGTGCGTAT GCATATATCT CTCATCTGTA GTTCCAAGA 480
GTTCACTGA AGCAGATGGA GTCCTGCAGC CCAGGAGACA CCCTGCATCC CTGCTAATAG 540
TGTTTGCCAC AAGTATTAGT GAGTCTTCCT TATTAATATT TTCATTTTCA AAGACTGAAG 600
30 CAAAGCTGAT AGTGTGCTGCT GTTCTTTTGG CAGCTAAGTG AGGGTCTTGG GATGACTTGC 660
TGTGTTCTCT AAGCTGCACT TTGGGGCCAT CTCTGCAGTA TTAGCCCCCT TTTTGCTTGG 720
35 TGGTACTCTG TCTGTGCCCTG TGTGTGTGTG TGATAGTCAC TCTTGCAATG CTCCATGTC 780
TGGTTTGTGG CATTTGGGGA TAAGGTGCTG AAGCCAGAGC ATTTGCAGTT TGTGAGGC 840
CTCGTTGCCA ATGATAGATC ACTCTGTGTG ACCTGGTATG TCTGCTTGCT TGCTGCTTTT 900
40 CCTTGCTTTC TCTTGAAGA GGAAAGGACT CTGGTCAGGC CCAGGCTGAG TGAGATGAGC 960
TGCAGCTGGC TCATGGCCTT CTAGAGCAG AGAGAGGAGT ATGTCATTTT ACTAAGTTCC 1020
45 TAAACAAACA TTTATGCAGG CAACACTCCT TGCAGATCCA GAAACTGAGG CACAATAGGG 1080
TTATGACTTG CTCAAGAATA TGTAGCTGCT AGGGGGTAAA TCAAGGCATC ACAATTTCTG 1140
TTCAGCGGGC AGGAATAGGC TGTGAATTGC TAGCACTTTT TTTTTTTAAG CAATTACTTT 1200
50 TTGACTTGTT CCTCTGAAAG TGCAAGAGGC GTACACCTTT CCCAAATGTA GACTAGAATC 1260
TGCAGGATGC CACCCACTGT ATAGTTCTGC TTTCCAGAG AGGAAGAACT TTTAGAAACC 1320
55 AAATGATCTT AATTGTTATT GCCCACCCTT GGCTTTTCCG GGTAGAAAAT TCACAGTAGG 1380
AATGATTGTT AAGAGAGAGT GCTTGGAACC ATGGGTAAAC AGGAAAGGCT ACCTAACTTC 1440
ACATATCTGC AACCAGAGCA GCCACCAAGC ATTACTTAGC AGCAGGAAAA TGATTGTATT 1500
60

TGAGTTCCTG TGTGTCCAAA ACTGAGGCAC CATGTTCTTT GAAAACATGC CACCTCAAGG 1560
 CTGGGCGCGG TGGCTCACAC CTGTAATCCC AGCAYTTTGG GGAGGCCSAG GCGGGGCGG 1620
 5 KTTACCGGG GGTG 1634

10 (2) INFORMATION FOR SEQ ID NO: 285:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1795 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 285:

20 TTCCCCCAG GTTGGCTTCC TTCGATTCCT TTTCTTGGTA TCAACGTTG ATTGAAGAA 60
 CAACCCCTC TTTGTCAACC TCAATAATGA GCTCACTGTG GAGGAGCAGC TCGGCGACAG 120
 CTCMCCGYA TGGTCATTGT TACCCCCCAA GACCGCAAAA ACTCTGTGTG GACACAGGAT 180
 25 GGACCCCTCAG CCCAGATCCT GCAGCAGCTT GTGGTCCTGG CAGCTGAAGC CCTGCCCATG 240
 TTAGAGAAGC AGCTCATGGA TCCCCGGGGA CCTGGGGACA TCAGGACAGT GTTCCGGCCG 300
 30 CCCTTGGACA TTTAGACAGT GCTGATTCGC CTGTYTCCTC GCCATATCCC GCGGCACCGC 360
 AGGCTTGTGG ACTCGCCAGY TGCCTCCTTC TGCCGGGGCC TGCTCAGCCA GCCGGGGCCC 420
 TCATCCCTGA TGCCCGTGCT GGGTNATGAT CCTNCTCAGC TCTATCTGAC GCAGCTCAGG 480
 35 GAGGCCTTIG GGGATCTGGC CCTTTCTTC TATGACCAGC ATGGTGGAGA GGTGATTGGT 540
 GTCTCTGGA AGCCACCCAG CTTCCAGCCG CAGCCCTTCA AGGCCTCCAG CACAAAGGGG 600
 40 CGCATGGTGA TGTCTCGAGG TGGGGAGCTA GTAATGGTGC CCAATGTTGA AGCAATCCTG 660
 GAGGACTTIG CTGTGCTGGG TGAAGGCCTG GTGCAGACTG TGGAGGCCCG AAGTGAGAGG 720
 TGGACTGTGT GATCCAGCT CTGGAGCAAG CTGTAGACGG ACAGCAGGAC ATTGGACCTC 780
 45 TAGAGCAAGA TGTCAGTAGG ATGACCTCCA CCCTCCTTGG ACATGAATCC TCCATGGAGG 840
 GCCTGCTGGC TGAACATGCT GAATCATCTC CAACAAAACC CAGCCCCAAC TTTCTCTCTG 900
 50 ATGCTCCAGC ATTGGGGCAG GGCATGGTG GCCCATGTAG TCTCCTGGGC CTCACCATCC 960
 CAGAAGAGGA GTGGGAGCCA GCTCAGAGAA GGAAGTGAAC CCAGGAGATC CATCCACCTA 1020
 TTAGCCCTGG GCCTGGACCT CCTGCGATT TCCACTCCT TTCTTAGTCT TCTTCCAGAA 1080
 55 ACAGAGAAGG GGATGTGTGC CTGGGAGAGG CTCTGTCTCC TTCTGCTGC CAGGACCTGT 1140
 GCCTAGACTT AGCATGCCCT TCACTGCAGT GTCAGGCCTT TAGATGGGAC CCAGCGAAAA 1200
 60 TGTGCCCTT CTGAGTCACA TCACCGACAC TGAGCAGTGG AAAGGGGCTA TATGTGTATG 1260

AATAGACCAC ATTGAAGGAG CACAATGCCC TCCTGTGTG ATGCCACTTC CCAGGGTGGA 1320
 GACAGTGGAA AAGAACCGAG GACAGGAAAG GATTGGGTAG GTGAAGGGGT CAGGGGACTG 1380
 5 GTAGTCACCC AATCTTGGAG AGGTGCAAAA AGCACTGGGG GCTACCCGTT AGCTGCATCT 1440
 GCCCTGGCTG TTTGCCCGTT CATGTCACAA ACTGCCACTA CTATGTACCT GCAGTGGGGT 1500
 10 TGCAGAGATG GGGGAGACTC AAGTCTTACT CCCCAGGAGC TCCCAGGGCC CAAGGAGGAG 1560
 AATGCTGCCT CCTTTCAGTC TGGTCTACAC CCACCTTCTG GTAGCCTCTC TGCTTCCTGT 1620
 AATCTCTGGCT GTTTTTCAG ACTCAGCTCA AATAGTGGCC CTCCTTAAGC CCATCCCTCG 1680
 15 CCCCCAGCCT GAGGTGATCT TTCCCTCCTC TGAATATTA GAGCAGTTAC TGTCTGTTC 1740
 GTTCGTTTGG CAGGCACACA CAGTGGCATA AATCTATTTG TTTTGAACCT TGATT 1795
 20

(2) INFORMATION FOR SEQ ID NO: 286:

25 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 858 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 30 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 286:
 TCTGCTTTCG GTGCTGCGTG TACTGCTGGG CGGCTTCTTC GCGCTCGTGG GGTGGCCAA 60
 35 GCTCTCGGAG GAGATCTCGG CTCCAGTTTC GGAGCGGATG AATGCCCTGT TCGTGCAGTT 120
 TGCTGAGGTG TTCCCGCTGA AGGTATTTGG CTACCAGCCA GATCCCCTGA ACTACCAAAT 180
 40 AGCTGTGGGC TTTCTGGAAC TGCTGGCTGG GTTGTGCTG GTCATGGGCC CACCGATGCT 240
 GCAAGAGATC AGTAACTTGT TCTTGATTCT GCTCATGATG GGGGCTATCT TCACCTTGGC 300
 AGCTCTGAAA GAGTCACTAA GCACCTGTAT CCCAGCCATT GTCTGCCTGG GGTTCCTGCT 360
 45 GCTGCTGAAT GTCGGCCAGC TCTTAGCCCA GACTAAGAAG GTGGTCAGAC CCACTAGGAA 420
 GAAGACTCTA AGTACATTCA AGGAATCCTG GAAGTAGAGC ATCTCTGTCT CTTTATGCCA 480
 TGCAGCTGTC ACAGCAGGAA CATGGTAGAA CACAGAGTCT ATCATCTTGT TACCAGTATA 540
 50 ATATCCAGGG TCAGCCAGTG TTGAAAGAGA CATTTTGTCT ACCTGGCACT GCTTCTCTTT 600
 TTTAGCTTTA CTACTCTTTT GTGAGGAGTA CATGTTATGC ATATTAAAT TCCTCATGTC 660
 55 ATATGAAAAT ACAAATAAG CAGAAAAGAA ATTTAAATCA ACCAAAATTC TGATGCCCCA 720
 AATAACCACT TTTAATGCCT TGGTGTAAAT ATACCTCTGA ACTTTTCTCT GTGCCTTTAA 780
 60 ACAGATATAT ATTTTCTTTT AATGAAAATA AAACCATATA TCCTATTTTA TTTCTCTCTT 840

TTAAAACCTT ATAAACTA

858

5

(2) INFORMATION FOR SEQ ID NO: 287:

(i) SEQUENCE CHARACTERISTICS:

10

- (A) LENGTH: 915 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 287:

15

GAATTCGGCA CGAGCGCGGC CATGGCGCTC CTGCTTTCGG TGCTGCGTGT ACTGCTGGGC 60

GGCTTCTTCG CGCTCGTGGG GTTGGCCAAG CTCTCGGAGG AGATCTCGGC TCCAGTTTCG 120

20

GAGCGGATGA ATGCCCTGTT CGTGCAGTTT GCTGAGGTGT TCCCCTGAA GGTATTTGGC 180

TACCAGCCAG ATCCCCTGAA CTACCAAATA GCTGTGGGCT TTCTGGAACT GCTGGCTGGG 240

TTGTGCTGG TCATGGGCCC ACCGATGCTG CAAGAGATCA GTAAC TTGTT CTTGATTTCTG 300

25

CTCATGATGG GGGCTATCTT CACCTTGGCA GCTCTGAAAG AGTCACTAAG CACCTGTATC 360

CCAGCCATTG TCTGCCTGGG GTTCTCTGCTG CTGCTGAATG TCGGCCAGCT CTTAGCCCAG 420

30

ACTAAGAAGG TGGTCAGACC CACTAGGAAG AAGACTCTAA GTACATTCAA GGAATCCTGG 480

AAGTAGAGCA TCTCTGTCTC TTTATGCCAT GCAGCTGTCA CAGCAGGAAC ATGGTAGAAC 540

ACAGAGTCTA TCATCTTGTT ACCAGTATAA TATCCAGGT CAGCCAGTGT TGAAAGAGAC 600

35

ATTTTGTCTA CCTGGCACTG CTTTCTCTTT TTAGCTTTAC TACTCTTTTG TGAGGAGTAC 660

ATGTTATGCA TATTAACATT CCTCATGTCA TATGAAAATA CAAAATAAGC AGAAAAGAAA 720

40

TTTAAATCAA CAAAATTCT GATGCCCCAA ATAACCACTT TTAATGCCTT GGTGTAAGTA 780

TACCTCTGAA CTTTTTCTG TGCCTTTAAA CAGATATATA TTTTTTTTWA ATGAAAATAA 840

AACCATATAT CCTATTTTAT TTCCTCCTTT TAAAACCTTA TAAACTATAA MAAAAAAAAA 900

45

AAAAAAAAAA CTCGA 915

50

(2) INFORMATION FOR SEQ ID NO: 288:

(i) SEQUENCE CHARACTERISTICS:

55

- (A) LENGTH: 1517 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 288:

60

	CCTTGTGGCA ACTAGTGGGT CCCCGGGCT GCAGNAATTC GGGCAGTGGT TCTGNGTCTG	60
	AAGATACTCT GAGTTCTCT GAGAGATCCA AAGGCTCCGG GAGCAGACCC CCAACCCCCA	120
5	AAAGCAGCCC TCAGAAGACC AGGAAGAGCC CTCAGGTGAC CAGGGGTAGC CCTCAGAAGA	180
	CCAGCTGTAG COCTCAGAAG ACCAGGCAGA GCCCTCAGAC GCTGAAGCGG AGCCGAGTGA	240
10	CCACCTCACT TGAAGCTTTG CCCACAGGAC AGTGCTGACA GACAAGAGTG GCGACAGTG	300
	GAAGCTGAAG TCCTTCCAGA CCAGGGACAA CCAGGGCATT CTCTATGAAG CTGCACCCAC	360
	CTCCACCCTC ACCTGTGACT CAGGACCACA GAAGCAAAAG TTCTCACTCA AACTGGATGC	420
15	CAAGGATGGG CGCTTGTTC AATGAGCAGAA CTCTTCCAG CGGGCCGCCA AGCCTCTGCA	480
	AGTCAACAAG TGAAGAAGC TGTACTCGAC CCCACTGCTG GCCATCCCTA CCTGCATGGG	540
20	TTTCGGTGT CACCAGGACA AATACAGGTT CTGGTGTGA CCCAGCCTGG GGAGGAGCCT	600
	TCAGTCGGCC CTGGATGTCA GCCCAAAGCA TGTGCTGTGC AGAGAGGTCT GTGCTGCAGG	660
	TGGCCTGCCG GCTGCTGGAT GCCCTGGAGT TCCTCCATGA GAATGAGTAT GTTCATGGAA	720
25	ATGTGACAGC TGAAAATATC TTTGTGGATC CAGAGGACCA GAGTCAGGTG ACTTTGGCAG	780
	GCTATGGCTT CGCNTTCCGC TATTGCCCAA GTGGCAAACA CGTGGCCTAC GTGGAAGGCA	840
30	GCAGGAGCCY TCACGAGGGG GACCTTGAGT TTCATTAGCA TGGACCTGCA CAAGGGATGC	900
	GGGCCCTCCC GCCGCRGYGA CCTCCAGAGC CTGGGYTAMT GCATGCTGAA GTGGYTCTAM	960
	GGGTTTCTGC CATGGACAAA TTGCCTTCCA AMAMTGAGGA CATCATGAAG CAAAAACAGA	1020
35	AGTTGCCTTG GGATTCATTT TAATGTAAGC TKGACTTTGT CATGCCAGAA ACAAGGCTCG	1080
	GTCACCGTCA GCAGTTTGCA GTTTTCCACC TCCWCCAGT TCCTCCGTGT GGTTGACCCA	1140
40	GATATCTCCG TTAGCAGCC GCCTCCGGGG GACCACCTCC CTCCCTTTGA GTCAGCCACA	1200
	GACAGCCTAC TTGACGGCCC CGCTGGCCCC CACATTCCAC TGAAGTGTGC GGATGCCACA	1260
	GTGACCCCT CTCAGGCACA GCATGACCTC CTGAAGTCGA GCCTGCTTGC TTTGAACCTA	1320
45	CCAGTTAAAA TCTCCTCAAA ATGTTTGGAT ACCGCCCATT GGCCCTCAC AGCCACGAGC	1380
	TCCCTGACCA GTGTGCGTGT GTGTGTGTGT GTGTGTCTGT GTGTGTGCTT GGGACGGGTG	1440
50	GGGAGGTCAC CTTTGGGTGT GCGGTGTGCC CCCAGGACCT GTAAGTAATA AAATCTTTAT	1500
	TTCCAAAAA AAAAAA	1517

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(2) INFORMATION FOR SEQ ID NO: 289:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 3865 base pairs

(B) TYPE: nucleic acid

60

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 289:

5	TGGAGGGGGG GAGCTTCCTT GAGCAGTGGG CCCAGGCCCTG GCCCTCCACA CTTCATTCTC	60
	TGACCTTTCT CTCTCCTCAT TTCGGTGCAT GTCCTTTCTG CAGCTGCCTT TCAGCACAGG	120
10	TGGTTCCACT GGGGGCAGCT AACCGTGAGT GACAAGGATG GGAAGCCACA GGTGCATTTT	180
	ACTCAAGTCT TCTCTAGTCA ATGAGGGGCA CCCAGTGCTT CTAGGGCAGG CTGGGTGGTG	240
	GTCCCTTAGG TATCAGCCTC TCTTACTGTA CTCTCCGGA ATGTTAACCT TTCTATTTTC	300
15	AGCCTGTGCC ACCTGTCTAG GCAAGCTGGC TTCCCATTTG GCCCCGTGGG GTCCACAGCA	360
	GGGTGGCTSC CCCCCAGGGC CACCGCTTCT TTCTTGATCC TCTTTCTTA ACAGTGACTT	420
20	GGGCTTGAGT CTGGCAAGGA ACCTTGCTTT TAGCTTCACC ACCAAGGAGA GAGGTTGACA	480
	TGACCTCCCC GCCCCCTCAC CAAGGCTGGG AACAGAGGGG ATGTGGTGAG AGCCAGGTTT	540
	CTCTGGCCCT CTCCAGGGTG TTTTCCAATA GTCACTACTG TCTTCTCCTT GTAGCTAATC	600
25	AATCAATATT CTTCCCTTGC CTGTGGGCAG TNGGAGAGTG CTGCTGGGTG TACGCTGCAC	660
	CTGCCCACTG AGTTGGGGAA AGAGGATAAT CAGTGAGCAC TGTTCCTCTC AGAGCTCCTG	720
30	ATCTACCCCA CCCCCTAGGA TCCAGGACTG GGTCAAAGCT GCATGAAACC AGGCCCTGGC	780
	AGCAACCCTG GGAATGGCTG GAGGTGGGAG AGAACCTGAC TTCTCTTTCC CTCTCCCTCC	840
	TCCAACATTA CTGGAACCTT ATCCTGTTAG GATCTTCTGA GCTTGTTTCC CTGCTGGGTG	900
35	GGACAGAGGA CAAAGGAGAA GGGAGGTCTT AGAAGAGGCA GCCCTTCTTT GTCTCTGGG	960
	GTAAATGAGC TTGACCTAGA GTAAATGGAG AGACCAAAAG CCTCTGATTT TTAATTTCCA	1020
40	TAAAATGTTA GAAGTATATA TATACATATA TATATTTCTT TAAATTTTGT AGTCTTTGAT	1080
	ATGTCTAAAA ATCCATTCCC TCTGCCCTGA AGCCTGAGTG AGACACATGA AGAAAAGTGT	1140
	GTTTCATTTA AAGATGTTAA TTAAATGATT GAAACTTGGC TGTGGCTACT GCTTCTTAAT	1200
45	GTGGGGGGGA CAGGCAGTG GTCTGGGCCC ACATTTAGAA GGGAAAATGT TTTGCCTGCT	1260
	GCACACATTG GACCCAAGTA TGGGCTCTTT CTGCCTAGTA CTGCCAAAGG GACTGTTAAG	1320
50	GTGTCTGTGC CATCTTCTAC CCCCCACCCC CCATTACGGG TAAAGGRAAC CCCAGACTAG	1380
	GTGAGGGGCC AGCAGCTGCC TCACATGTG TTCTCTCTG AGATGGTCCA GCTCACATCC	1440
	AGACACCTTG TTCAGACATT TTATTTGAAT TTATGACAGT GATGGGGATT TGAAGTGAAT	1500
55	GCCTTATGGA GAAGTACCCC ACCCTCTATG AAGACAGAAT CACTCTCTGC CATTCATTCT	1560
	GCCTGATGCT AACAACACGC AGCTGATTTA GGGAGTGTCC CAGCCTAGCT GGATCAAGGG	1620
60	AAATTCCAGG AGCCCTGGGG CAGGCCCTGG NCCCCAGTGC CAAGCCTCAG AGTAAGCAGA	1680

	CATTGGGAAA GTTGCCAACC ACTTGGTAGA CCACTAGGTT CTCTGTTTTT CCTTCCCTTT	1740
5	CCTTTTCAAA TCCCACAGTT TCCTGTTGGG GAGAAGCTGT AATTAGCCTA GTCCAGGTAC	1800
	CAGATCCCAG CTAGGGGCGC AGCTGNCTTG GATAACTCCA AGAAAACCTG GGCACCAGTA	1860
	TTTTTCCAAT TATAAGGACT GTGGCATAAA TTTTAAATG AGTTATATG AAACCAGATT	1920
10	TCTCCAGCTG CCAAGGGAAG AAGGTAGGGC TGGACTCCCT GCTGTGGCCC AGCCCTTGTT	1980
	AGGGGTGGT CTCTCACTGC AGCCAGACAG GATGATCCTG GGTTCGGGG AGGGTAAGCT	2040
15	GCCCCGTGCC GAGTTCTGCA CCGAATAAAG AGTCCAAACC CGCTGCTTCC GTGTCTGAG	2100
	AGATGGGTAA ATGGGTGATG GATGGAGCAG ACTGAAGAGA CAGCAGATGA CTCAGTGGTG	2160
	GAAGAAGGGG GGAAGATGCT GGGCTGGCTA GCTAATGTTT CCCCTTTTCA GCGATTTACA	2220
20	GGAAATGGAG CCCAGCTTGG TCATGAAGTT GGTTCGCTTC CACTGTGCGA TGCACCTCTC	2280
	AGAAATTTTG AAGTCAGCCT GCAACTTCTC GAAGACTTTC TTCTTGGGCT TGAGCTCCTC	2340
25	ATCTGGTTGG CCTTTTTCAT AGCCCTTCAC AAACACGTGC TCACCAGGAG CAGAGCCTGC	2400
	CGGAGGGTCC AGAGGTCAA CTGGCGGTTT ATCCCTTCTA TAGAAGCACA CAGAAGCATG	2460
	CCTTGGGACT CGACTCCTCT CATCTTCTGG GGTTCAGGT TGCACAGCAC CACTACCAGC	2520
30	CTGTCTGCA GTTCTCTCTT GGGCACGAAC TGTACCAGGC CGCTCACCAC AGTCCGTGGT	2580
	TCAGCTTCCC CCACGTCAAT CTTCTCTACA TACAGGCTGT CTGCATCTGG GTGCTTCTCC	2640
35	ACAGTGATGA TTTTCCCCAC ACGGATATCC AGCCGGGATG GGATGACCTC CTCTGGTTCT	2700
	GAATCTTTGG CAGGCCTTTG GCCATGGCT TCTGCTTTGA GGGATCTGGG TAGGCAGCGC	2760
	TGGCCAGTTT TTTTCAAGGCA GGGGTATTAA ACTTTTCCCG GATTGGATCC AGCAACTTGT	2820
40	TCAGTGCAC TTCAACAGAA TTCTTCAGGT CTCAGGATG TACAACCTCA GCAGCAAAGT	2880
	CCTTTTCCAG GTCCACGTAA GCTGTGTAGG TTTTGTTC ACCCATTTT TCATCTCGTA	2940
45	GGATCACAAA CTCGACTTA AGGGGAAAAA GGACATGCTT GATGAAGGAC AGAACCCCAT	3000
	TGTTCTCCAC ATTTCTTGGC TCACAGAAGG CCTTCTTCAG TTTTTCCTTC ACATCCTCCT	3060
	TCCGATCAAG GAGATCAATC TTGGACTCCT CTTCTGAAGA GCTCATTTTG CTGCCTGTTA	3120
50	ATCCTGGAAC CATAGGATTC ATCAGATGGA CCGTTTGTGA ATAGCCAAGT GCAGGGAGGT	3180
	ACTTCTCTGC AAAGGTGAAA ATCTTCTCTT GATCAATGCC TCCAAATTGG GCATCTACTT	3240
55	TTAAATACTC TTTCATCCAA GCCTGCAGTC CGGGGTATAA GAGGCCACTC AGCAAAGGGT	3300
	GCTCCACCTG CTTTACCACC TCAGCTCCAG CCTTCTTGA ATCGTGCTGT GTGACCACGG	3360
	AGGAGAGTCT GTACACATCT AGTGTGTACT CTTTGTCTGAG CTGGTAATCA GTGCCTTTGA	3420
60	TGAACITGAG CTTCTCCAAG GGCACACCAA TGCTCTCCAG CATTGCTTTG ATCACATCTT	3480

CATAGTAACT GACTCGGAGT TCTAGAAGTT CCCATGGGGC TTTCATGTTA TCCAGGTATG 3540
 CGTGGAGGTC CGCAAACAGA ATTGTTACCT CACACCCTGC CTTTAAGAAG TCTGCAATCT 3600
 5 TTGACATGGG CACAAAGTAA GCCACATGTG GTTTGCCCGT GGTGCGCGTT CCCAGTAAA 3660
 TTTTAAGTTC CCGCTCCTTC AGTATCTCCT TCAGCTTCTC TTCCCCCAGA ACCTCCTGCA 3720
 10 GGTTCGCGGT GATAAGGTGC AGTTTCTCTT CAGGCTGGG AGCGTCCCC ATGGTCCGCT 3780
 ACCCCTGCTT CCCCCTCTCA GCCCGGCACC AGAGCCCCCT CCTGGGTCAC CGTCGCCGCC 3840
 GCGTGCCGGG AACTGTCACG CGAGT 3865
 15

20 (2) INFORMATION FOR SEQ ID NO: 290:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1910 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 290:

AGGGAGAGGA GGAGAGGGGG TCTGCGCGCG GCCGCTACCC AGAAGCCAGC GGACGGCAGC 60
 30 ACGGAGTGGG CTGTCCCCGA GCCCAGCCCC GAGCGAGCCC CCCCCCGCC CCCGMAGGAC 120
 GCGCTYCCA GCCAGCCCGA CTCCTAGGAG GAGGGGAGGC GGGAAAGCAG CTCAAGCCTC 180
 35 ACCCACC GCC CTGCCCCCAG CCCC GCCACT CCCAGGCTCC TCGGGACTCG GCGGGTCCTC 240
 CTGGGAGTCT CGGAGGGGAC CGNCTGTGCA GACGCCATGG AGTTGGTGCT GTCTTCCTC 300
 TGCAGCCTGC TGGCCCCCAT GTCTCTGGCC AGTGCAGCTG AAAAGGAGAA GGAAATGGAC 360
 40 CCTTTTCATT ATGATTACCA GACCTGAGG ATTGGGGGAC TGGTGTTCGC TGTGGTCCTC 420
 TTCTCGGTG GGATCCTCCT TATCCTAAGT CGCAGGTGCA AGTGCAGTTT CAATCAGAAG 480
 45 CCCC GGCCCC CAGGAGATGA GGAAGCCAG GTGGAGAACC TCATCACC GC CAATGCAACA 540
 GAGCCCCAGA AAGCAGAGAA CTGAAGTGCA GCCATCAGGT GGAAGCCTCT GGAACCTGAG 600
 GCGGCTGCTT GAACCTTTGG ATGCAAATGT CGATGCTTAA GAAAACCGGC CACTTCAGCA 660
 50 ACAGCCCTTT CCCCAGGAGA AGCCAAGAAC TTGTGTGTCC CCCACCCTAT CCCCTCTAAC 720
 ACCATTCTC CACTGATGA TGCAACTAAC ACTTGCCTCC CCACTGCAGC CTGCGGTCTT 780
 55 GCCCACCTCC CGTGATGTGT GTGTGTGTGT GTGTGTGTGT GACTGTGTGT GTTTGCTAAC 840
 TGTGGTCTTT GTGGCTACTT GTTGTGGAT GGTATTGTGT TTGTTAGTGA ACTGTGGACT 900
 CGCTTTCCCA GGCAGGGGCT GAGCCACATG GCCATCTGCT CCTCCCTGCC CCCGTGGCCC 960
 60

	TCCATCACCT TCTGCTCCTA GGAGGCTGCT TGTTCGCCGA GACCAGCCCC CTCCCCTGAT	1020
	TTAGGGATGC GTAGGGTAAG AGCACGGGCA GTGGTCTTCA GTCGTCTTGG GACCTGGGAA	1080
5	GGTTTGACGC ACTTTGTCAT CATCTTTCAT GGACTCCTTT CACTCCTTTA ACAAAAACCT	1140
	TGCTTCCTTA TCCCACCTGA TCCAGTCTG AAGGTCTCTT AGCAACTGGA GATACAAAGC	1200
10	AAGGAGCTGG TGAGCCCAGC GTTGACGTCA GGCAGGCTAT GCCCTTCCGT GGTTAATTTT	1260
	TTCCCAGGGG CTTCACGAG GAGTCCCCAT CTGCCCCGCC CCTTCACAGA GCGCCCGGGG	1320
	ATTCCAGGCC CAGGGCTTCT ACTCTGCCCC TGGGAATGT GTCCCCTGCA TATCTTCTCA	1380
15	GCAATAACTC CATGGGCTCT GGGACCTAC CCCTTCCAAC CTCCCTGCT TCTGAGACTT	1440
	CAATCTACAG CCCAGCTCAT CCAGATGCAG ACTACAGTCC CTGCAATGG GTCTCTGGCA	1500
20	GGCAATAGTT GAAGGACTCC TGTTCGTTG GGGCCAGCAC ACCGGGATGG ATGGAGGGAG	1560
	AGCAGAGGCC TTTGCTTCTC TGCCTACGTC CCCTTAGATG GGCAGCAGAG GCAACTCCCG	1620
	CATCCTTTGC TCTGCCTGTC GGTGGTCAGA GCGGTGAGCG AGGTGGGTTG GAGACTCAGC	1680
25	AGGCTCCGTG CAGCCCTTGG GAACAGTGAG AGGTTGAAG TCATAACGAG AGTGGAAGT	1740
	CAACCAGAT CCCGCCCTC CTGTCTCTG TGTTCCTCGG GAAACCAACC AAACCGTGCG	1800
30	CTGTGACCCA TTGCTGTCTC CTGTATCGTG ATCTATCTC AACACAACA GAAAAAAGGA	1860
	ATAAATATC CTTGTTCM TAAAAA AAAAAGGGGG	1910

35

(2) INFORMATION FOR SEQ ID NO: 291:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 3276 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 291:

40	GCGACCGTCG TTTGAGTCGT CGCTGCCGCT GCCGCTGCCA CTGCCACTGC CACCTCGCGG	60
	ATCAGGAGCC AGCGTTGTTC GCCGACGCC TCGCTGCCG TGGGAGGAAG CGAGAGGGAA	120
50	GCCGCTTGCG GGTTCGTCG CGCTGCTCGC CCACCGCTG GAAGAGCCGA GCCCCGCCCC	180
	AGTCGGTCG TTAGCACCGC TCGTAGCCGT TACCCGCGG CCGCCACAGC CGCCGGCCG	240
55	GAGAGGCGCG CGCCATGGCT TCTGGAGCCG ATTCAAAAGG TGATGACCTA TCAACAGCCA	300
	TTCTCAAACA GAAGAACGT CCCAATCGGT TAATTGTTGA TGAAGCCATC AATGAGGACA	360
	ACAGTGTGGT GTCCTTGTC CAGCCCAAGA TGGATGAATT GCAGTTGTTC CGAGGTGACA	420
60	CAGTGTTCCT GAAAGGAAAG AAGAGACGAG AAGCTGTTTG CATCGTCCTT TCTGATGATA	480

	CTTGTTCTGA TGAGAAGATT CCGATGAATA GAGTTGTTTCG GAATAACCTT CGTGTAACGCC	540
	TAGGGGATGT CATCAGCATC CAGCCATGCC CTGATGTGAA GTACGGCAAA CGTATCCATG	600
5	TGCTGCCCCAT TGATGACACA GTGGAAGGCA TTAAGGTAA TCTCTTCGAG GTATACCTTA	660
	AGCCGTACTT CCTGGAAGCG TATCGACCCA TCCGAAAGG AGACATTTT CTGTGTCGTG	720
10	GTGGGATGCG TGCTGTGGAG TTCAAAGTGG TGGAAACAGA TCCTAGCCCT TATTGCATG	780
	TTGCTCCAGA CACAGTGATC CACTGCGAAG GGGAGCCTAT CAAACGAGAG GATGAGGAAG	840
	AGTCCTTGAA TGAAGTAGGG TATGATGACA TTGGTGGCTG CAGGAAGCAG CTAGCTCAGA	900
15	TAAAGGAGAT GGTGGAAGT CCCCTGAGAC ATCCTGCCCT CTTTAAGGCA ATTGGTGTGA	960
	AGCCTCCTAG AGGAATCCTG CTTTACGGAC CTCCTGGAAC AGGAAAGACC CTGATGCTC	1020
20	GAGCTGTAGC AAATGAGACT GGAGCCTTCT TCTTCTTGAT CAATGGTCCT GAGATCATGA	1080
	GCAAATTGCG TGGTGTAGTCT GAGAGCAACC TTCGTAAAGC CTTTGAGGAG CTTGAGAAGA	1140
	ATGCTCCTGC CATCATCTTC ATTGATGAGC TAGATGCCAT CGCTCCCAA AGAGAGAAAA	1200
25	CTCATGGCGA GGTGGAGCGG CGCATTGTAT CACAGTTGTT GACCTCATG GATGGCCTAA	1260
	AGCAGAGGGC ACATGTGATT GTTATGGCAG CAACCAACAG ACCCAACAGC ATTGACCCAG	1320
30	CTCTACGGCG ATTTGGTTCG TTTGACAGGG AGGTAGATAT TGGAAATCCT GATGCTACAG	1380
	GACGCTTAGA GATTCTTCAG ATCCATACCA AGAACATGAA GCTGGCAGAT GATGTGGACC	1440
	TGGAACAGTA GCCAATGAGA CTCACGGGCA TGTGGGTGCT GACTTAGCAG CCCTGTGCTC	1500
35	AGAGGCTGCT CTGCAAGCCA TCCGCAAGAA GATGGATCTC ATTGACCTAG AGGATGAGAC	1560
	CATTGATGCC GAGGTCATGA ACTCTCTAGC AGTTACTATG GATGACTTCC GGTGGGCCTT	1620
40	GAGCCAGAGT AACCCATCAG CACTGCGGGA AACCGTGGTA GAGGTGCCAC AGGTAACCTG	1680
	GGAAGACATC GGGGGCTAG AGGATGTCAA ACGTGAGCTA CAGGAGCTGG TCCAGTATCC	1740
	TGTGGAGCAC CCAGACAAAT TCCTGAAGTT TGGCATGACA CCTTCCAAGG GAGTTCTGTT	1800
45	CTATGGACCT CCTGGCTGTG GGAAAACTTT GTTGGCCAAA GCCATTGCTA ATGAATGCCA	1860
	GGCCAACTTC ATCTCCATCA AGGGTCCTGA GCTGCTCACC ATGTGGTTTG GGGAGTCTGA	1920
50	GGCCAATGTC AGAGAAATCT TTGACAAGGC CCGCCAAGCT GCCCCTGTG TGCTATTCTT	1980
	TGATGAGCTG GATTCGATTG CCAAGGCTCG TGGAGGTAAC ATTGGAGATG GTGGTGGGGC	2040
	TGCTGACCGA GTCATCAACC AGATCCTGAC AGAAATGGAT GGCATGTCCA CAAAAAAAAA	2100
55	TGTGTTTCATC ATTGGCGCTA CCAACCGGCC TGACATCATT GATCCTGCCA TCCTCAGACC	2160
	TGGCCGTCTT GATCAGCTCA TCTACATCCC ACTTCCTGAT GAGAAGTCCC GTGTTGCCAT	2220
60	CCTCAAGGCT AACCTGCGCA AGTCCCCAGT TGCCAAGGAT GTGGACTTGG AGTTCCTGGC	2280

	TAAATGACT AATGCTTCT CTGGAGCTGA CCTGACAGAG ATTTGCCAGC GTGCTTGCAA	2340
5	GCTGGCCATC CGTGAATCCA TCGAGAGTGA GATTAGGCGA GAACGAGAGA GGCAGACAAA	2400
	CCCATCAGCC ATGGAGGTAG AAGAGGATGA TCCAGTGCCT GAGATCCGTC GAGATCACTT	2460
	TGAAGAAGCC ATGCGCTTTG CGCGCCGTTT TGTCACTGAC AATGACATTC GGAAGTATGA	2520
10	GATGTTTGCC CAGACCCCTC AGCAGAGTCG GGGCTTTGGC AGCTTCAGAT TCCCTTCAGG	2580
	GAACCAGGGT GGAGCTGGCC CCAGTCAGGG CAGTGGAGGC GGCACAGGTG GCAGTGTATA	2640
15	CACAGAAGAC AATGATGATG ACCTGTATGG CTAAGTGGTG GTGGCCAGCG TGCACTGAGC	2700
	TGGCTGCCT GGACCTTGT CCGTGGGGT GGGGGCGCTT GCCCAGGAGA GGGACCAGGG	2760
	GTGCGCCAC AGCCTGCTCC ATTCTCCAGT CTGAACAGTT CAGCTACAGT CTGACTCTGG	2820
20	ACAGGGGGTT TCTGTTGCAA AAATACAAAA CAAAAGCGAT AAAATAAAG CGATTTTCAT	2880
	TTGGTAGGCG GAGAGTGAAT TACCAACAGG GAATTGGGCC TTGGGCTATG CCATTTCTGT	2940
25	TGTAGTTTGG GGCAGTGCAG GGGACCTGTG TGGGGTGIGA ACCAAGGCAC TACTGCCACC	3000
	TGCCACAGTA AAGCATCTGC ACTTGACTCA ATGCTGCCCG AGCCCTCCCT TCCCCCTATC	3060
	CAACCTGGGT AGSTGGGTAG GGGCCACAGT TGCTGGATGT TTATATAGAG AGTAGGTTGA	3120
30	TTTATTTTAC ATGCTTTTGA GTTAATGTTG GAAACTAAT CACAAGCAGT TTCTAAACCA	3180
	AAAAATGACA TGTGTAAAA GGACAATAAA CGTTGGGTCN AAATGGGWRA AAAAAAAAAA	3240
35	AAAAAAGGGG GGCCCCCTCTA AAGNNCCANN CTTCGT	3276

40 (2) INFORMATION FOR SEQ ID NO: 292:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1695 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 292:

50	TTGCAATGGT TGAATTCCTC TCCTCAGGCC AGCCTAGGAG AAGAAGTTCT TAGTCCCAGA	60
	GGTGAGGCAG GAGGCGGCAG TTCTTGCGCG GTGAGGGCGG AGCTGAAGTG ACACCGGAGG	120
	CGGAAGCAAC GGTCCGTGGG GCGGAGAAGG GGGCTGGCCC CAGGAGGAGG AGGAAACCTT	180
55	TCCGAGAAAA CAGCAACAAG CTGAGCTGCT GTGACAGAGG GGAACAAGAT GCGGCGCCG	240
	AAGGAGCCT CTGGGTGAGG ACCCACTGG GGCTCCCGCC GCTGCTGCTG CTGACCATGG	300
60	CCTTGGCCGG AGGTTGGGG ACCGCTTCGG CTGAAGCATT TGAATCGGTC TTGGGTGATA	360

CGGCGTCTTG CCACCGGGCC TGTCAGTTGA CCTACCCCTT GCACACCTAC CCTAAGGAAG 420

AGGAGTTGTA CGCATGTCAG AGAGGTTGCA GGCTGTTTTC AATTGTGCAG TTGTGGATG 480

5 ATGGAATTGA CTTAAATCGA ACTAAATTGG AATGTGAATC TGCATGTACA GAAGCATATT 540

CCCAATCTGA TGAGCAATAT GCTTGCCATC TTGGTTGCCA GAATCAGCTG CCATTGCTG 600

AACTGAGACA AGAACAACCTT ATGTCCCTGA TGCCAAAAT GCACCTACTC TTTCCTCTAA 660

10 CTCTGGTGAG GTCATTCTGG AGTGACATGA TGGACTCCGC ACAGAGCTTC ATAACCTCTT 720

CATGGACTTT TTATCTTCAA GCCGATGACG GAAAAATAGT TATATTCCAG TCTAAGCCAG 780

15 AAATCCAGTA CGCACCACAT TTGGAGCAGG AGCCTACAAA TTTGAGAGAA TCATCTCTAA 840

GCAAAATGTC CTATCTGCAA ATGAGAAATT CACAAGCGCA CAGGAATTTT CTGAAGATG 900

GAGAAAGTGA TGGCTTTTTA AGATGCCTCT CTCTTAATC TGGGTGGATT TTAAC TACAA 960

20 CTCTTGCTCT CTGGTGATG GTATTGCTTT GGATTTGTTG TGCAACTGTT GCTACAGCTG 1020

TGGAGCAGTA TGTTCCCTCT GAGAAGCTGA GTATCTATGG TGACTTGGAG TTTATGAATG 1080

25 AACAAAAGCT AACAGATAT CCAGCTTCTT CTCTTGTTGGT TGTTAGATCT AAAACTGAAG 1140

ATCATGAAGA AGCAGGGCCT CTACCTACAA AAGTGAATCT TGCTCATTTCT GAAATTTAAG 1200

CATTTTTCTT TTAAAAGACA AGTGTAATAG ACATCTAAAA TTCCACTCCT CATAGAGCTT 1260

30 TTAAAATGGT TTCATTGGAT ATAGGCCTTA AGAAATCACT ATAAAATGCA AATAAAGTTA 1320

CTCAAACTCG TGAAGACTGT ATTTGCTATA ACTTTATTGG TATTGTTTTT GTAGTAATTT 1380

35 AAGAGGTGGA TGTTTGGGAT TGTATTATTA TTTTACTAAT ATCTGTAGCT ATTTTGT TTTT 1440

TTGCTTTGGT TATTGTTTTT TTCCCTTTTC TTAGCTATGA GCTGATCAIT GCTCCTTCTC 1500

ACCTCTGCC ATGATACTGT CAGTTACCTT AGTTAACAAG CTGAATATTT AGTAGAAATG 1560

40 ATGCTTCTGC TCAGGAATGG CCCACAAATC TGTAATTTGA AATTTAGCAG GAAATGACCT 1620

TTAATGACAC TACATTTTCA GGAAGTGAAG TCATTAAAAT TTTATTTGAA TAATTAAAAA 1680

45 AAAAAAAAAA AANCT 1695

50 (2) INFORMATION FOR SEQ ID NO: 293:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1501 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 293:

60 CACTTTCAGC AGTCCTTTGC TCTCTTGCT TCTACCTCAA ATAGCCCCAG GAGTGGGCTT 60

	TAGTCTCCAA TATGGAGCAT CTCAAGCTTC TCCTGGGGGA TGGGGATTGG GATGGGCAGA	120
5	ATCTGTTTTG GWTCTCCGGG TTATTTCCAG TGGGTGTAAA AGCAGAGCTG GGCCTTTCCC	180
	TCCTTTATCC CTGAGGGTGG GTAAGAAGGA CTGTATCTAC ACCTGTTCTT CCCTACCTTC	240
	TCTTTTGTTA GGGAGGCCTC ATTCTAAGTT CCTCAAGAGA GTCCITGGCT TAAAGCTGTA	300
10	GCAAGGGTGT GCTAGGTGGG GGATTTGGAG CAAAACCGTC GAGTAGGCAT GATACTGGTA	360
	TGGAGTGGG CTGCAAAATC AGACAGAAAT GGCTTGAGAA GCCGCAGGG AGCATGCCTG	420
15	TCTCTCAGTG ATAGAGTATG GGAGGGACCT CCCTAGCTTG GAAAATGAGA ATTGAAGGGG	480
	TTATGAACAA ATAGGATGCC TAGTTGAGGA TGTTCCTCAA GTTTTGTCCA ATCTTATCAT	540
	TAGTAGATTT TATAAGCCAC AGAGACAAAC CAGAAACGGA ATAATGTTAC TTTGGATGCT	600
20	TTATTTTTTT GTTCTAGGTG TGGCTTTGTA CATGCAGAAG AATGCTATAT GCTGCACATT	660
	TTGCCTTTAA AGTCTTACGA CTTTCCCAT TTTAGTCTAA TGGGAAGATA CAGATGTGCA	720
25	AGTCTGCTTT TTTGTTTTTT GTTATTATTT TTTTTTTTTT GCTCTGTGTT ATGGACATTT	780
	TCAGACATGC ACAGAAGTGG AGAGGATGGT CCTTGGACCC MATGTGTCCA TCACCTAGCT	840
	GCATCACTTA TCAGCTATGG TCAACCTGGT TTCATCTGTA TCTCTCTCTT TTCACCTGTA	900
30	TTGTTTATTT AAAATCCAAG ACACTATGCC AATGCAACCG TGACTIONTT GGGAGATTGG	960
	TAGTCTCTTT TGATGGTGAT AGTGATGGG TGCATATCA TAATCACATC AGGTCTGCTT	1020
35	TTTGCTTTTA ATGTTAACTA ATGAAGTTC AGAGATGGGC CTTAGAAATG TGTTTTAAGA	1080
	ATTAACAAGG AGTCTCAAAA AGAAATGAGA GGGATGCTTC CTTTNCCTT GCATCTACAA	1140
	AACMAGAGAG AGACTGTTCT GTTGTAATAAC TCTTTCAAAA ATTCTGATAT GGTAAAGTAC	1200
40	TTGAGACCC CTACACAGAT GTCAATCTTT TTTTCTGTGT AACATGGAAA CTTGTGTGAC	1260
	CATTAGCATT GTTATCAGCT TGTACTGGTC TCATAACTCT GGTTTTGGAA GAATAATTG	1320
45	GAAATTGTTG CTGTGTTCTG TGAAAATAAC CTCCCCAAAA TAATTAGTAA CTGGTTGTTT	1380
	TACTTGGTAA TTTGACACCC TGTTAATAAC GCAATTATTT CTGTGTTCTT AAACAGTATA	1440
	AATAGTTGTA AGTTTGCATG CATGATGGAA AAATAAAAAC CTGTATCTCT GTTAAAAAAA	1500
50	A	1501

55 (2) INFORMATION FOR SEQ ID NO: 294:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2683 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

60

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 294:

5	TGANTGTGGT CCCGGGTGCN GATTGGCAGN GCCTCCGCCG CGGCTCGTGG TTGTCCCGCC	60
	ATGGCACTGT CGCGGGGGCT GCCCGGGAG CTGGCTGAGG CGGTGGCCGG GGGCCGGGTR	120
10	CTGGTGGTGG GGGCGGGCGG CATCGGCTGC GAGCTCCTCA AGAATCTCGT GCTCACCGGT	180
	TTCTCCACCA TCGACCTGAT TGATCTGGAT ACTATTGATG TAAGCAACCT CAACAGACAG	240
	TTTTTGTTC AAAAGAAACA TGTGGAAGA TCAAAGGCAC AGGTGCCAA GGAAAGTGTA	300
15	CTGCAGTTTT ACCCGAAAGC TAATATCGTT GCCTACCATG ACAGCATCAT GAACCTGAC	360
	TATAATGTGG AATTTTTCCG ACAGTTTATA CTGGTTATGA ATGCTTTAGA TAACAGAGCT	420
20	GCCCGAAACC ATGTTAATAG AATGTGCCTG GCAGCTGATG TTCTCTTTAT TGAAAGTGGA	480
	ACAGCTGGGT ATCTTGGACA AGTAACTACT ATCAAAAAGG GTGTGACCGA GTGTTATGAG	540
	TGTCATCCTA AGCCGACCCA GAGAACCTTT CCTGGCTGTA CAATTCGTAA CACACCTTCA	600
25	GAACCTATAC ATTGCATCGT TTGGGCAAAG TACTTGTTC ACCAGTTGTT TGGGAAGAA	660
	GATGCTGATC AAGAAGTATC TCCTGACAGA GCTGACCTG AAGCTGCCTG GGAACCAACG	720
30	GAAGCCGAAG CCAGAGCTAG AGCATCTAAT GAAGATGGTG ACATTAAACG TATTTCTACT	780
	AAGGAATGGG CTAAATCAAC TGGATATGAT CCAGTTNAAA CTTTTTACCA AGCTTTTAA	840
	AGATGACATC AGGTATCTGT TGACAATGGA CAACTATGG CGGAAAAGGA AACCTCCAAT	900
35	TCCGTTGGAC TGGGCTGAAG TACAAAGTCA AGGAGAAGAA ACGAATGCAT CAGATCAACA	960
	GAATGAACCC CAGTTAGGCC TGAAAGACCA GCAGTTCTA GATGTAAAGA GCTATGCACG	1020
40	TCTTTTTTCA AAGAGCATCG AGACTTTGAG AGTTCATTTA GCAGAAAAGG GGGATGGAGC	1080
	TGAGCTCATA TGGGATAAGG ATGACCCATC TGCAATGGAT TTTGTACACT CTGCTGCAAA	1140
	CCTCAGGATG CATATTTTCA GTATGAATAT GAAGAGTAGA TTTGATATCA AATCAATGGC	1200
45	AGGGAACATT ATTCTGCTA TTGCTACTAC TAATGCAGTA ATTGCTGGGT TGATAGTATT	1260
	GGAAGGATTG AAGATTTTAT CAGGAAAAAT AGACCAAGTC AGAACAATTT TTTTGAATAA	1320
50	ACAACCAAAC CCAAGAAAGA AGCTTCTTGT GCCTTGTGCA CTGGATCCTC CCAACCCCAA	1380
	TTGTATGTA TGTGCCAGCA AGCCAGAGGT GACTGTGCGG CTGAATGTCC ATAAAGTGAC	1440
	TGTTCTCACC TTACAAGACA AGATAGTGAA AGAAAAATTT GCTATGGTAG CACCAGATGT	1500
55	CCAAATTGAA GATGGGAAAG GAACAATCCT AATATCTTCC GAAGAGGGAG AGACGGAAGC	1560
	TAATAATCAC AAGAAGTTGT CAGAATTGG AATTAGAAAT GGCAGCCGGC TTCAAGCAGA	1620
60	TGACTTCCTC CAGGACTATA CTTTATGAT CAACATCCTT CATAGTGAAG ACCTAGGAAA	1680

	GGACGTTGAA TTTGAAGTGT TTGGTGATGC CCCGAAAAA GTGGGSCCA AACAAGCTGA	1740
	AGATGCTGCC AAAAGCATAA CCAATGGGCA GTGATGATGG AGCTCAGCCC TCCACCTCCA	1800
5	CAGCTCAAGA GCAAGATGAC GTTCTCATAG TTGATTGCGA TGAAGAAGAT TCTTCAAATA	1860
	ATGCCGACGT CATGAAGAAG AGAGAAGCCG CAAGAGGAAA TTAGATGAGA AAGAGAATCT	1920
10	CAGTGCAAAG AGGTCACGTA TAGAACAGAA GGAAGAGCTT GATGATGTCA TAGCATTAGA	1980
	TTGAACAGAA ATGCCTCTAA ACAGAACCCT CTTACTATTT AGTTTATCTG GGCAGAACCA	2040
	GATTGTTATG TCCTTTGTTC CAAAGGGAAA AAATTGACAG CAGTGACTTG AAAATGATTC	2100
15	TGCTCCCTTT GAAAGCATTC ATTTTGCTAG AACTGTTAGA CACATTGCAG TATGCTGTAT	2160
	TGAAAGTAGG AATATAGTTT TAAAAACCCT TTGAACAAAG TGTGTGCATA ACCAGTCATG	2220
20	AGATAAAACA ACACAATGCA TGTTCCTTTT TTAATGTAAA TACCCTTAGG TATCATTAAT	2280
	AGTTTCAAAA TATTGTGGTT TAGTAAAGTT GATACCTGGT TATAAATATT ATGCCTTTAT	2340
	TTTTGGCTAG AAGAAGAATT ATTTTGTAGC TAGATCTAAC CATTTTCATA CTCTTAACTG	2400
25	ATTGAAACAG ATTCAAAGAA GTATCGAGTG CTATGCATTG AAACCTGTPTT TTAAATGTTA	2460
	GATGGCACTA TGTATATTAA TGTAACAACA TGTTAATTTA CTCAAGTTT CAGTTTGTAC	2520
30	CGCCTGGTAT GTCTGTGTAA GAAGCCAATT TTTGTGTATT GTTACAGTTT CAGGTTATTT	2580
	ATATTCGATG TTTTGTAAAA CTCAAATAAC GACTATACTT ATGGACCAA TAAATGGCAY	2640
35	TGCATTCTKG TKAAAAAAN NACAGAAAAA AAAAAAACA AGA	2683

(2) INFORMATION FOR SEQ ID NO: 295:

- 40 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1454 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- 45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 295:

	GGACTCGGGG TGGCTCTAAG GGCAGGGAT AGGGCTGGGG AGCGCCGGCC TGTGGCCCTG	60
50	ACCAGCCCCT TCTCGTGCAG GTTCCACCCC GATGCAGGTG GTCACGTGCT TGACGCGGGA	120
	CAGCTACCTG ACGCACTGCT TCCTCCAGCA CCTCATGGTC GTGCTGTCCT CTCTGGAACG	180
55	CACGCCCTCG CCGGAGCCTG TTGACAAGGA CTTCTACTCC GAGTTTGGGA ACAAGACCAC	240
	AGGGAAGATG GAGAACTACG AGCTGATCCA CTCTAGTCGC GTCAAGTTTA CCTACCCAG	300
	TGAGGAGGAG ATTGGGGACC TGACGTTTAC TGTGGCCCAA AAGATGGCTG AGCCAGAGAA	360
60	GGCCCCAGCC CTCAGCATCC TGCTGTACGT GCAGGCCTTC CAGGTGGGCA TGCCACCCCC	420

	TGGGTGCTGC AGGGGCCCC TGCGCCCCAA GACACTCCTG CTCACCAGCT CCGAGATCTT	480
5	CCTCCTGGAT GAGGACTGTG TCCACTACCC ACTGCCCGAG TTTGCCAAAG AGCCGCCGCA	540
	GAGAGACAGG TACCGGCTGG ACGATGGCCG CCGCGTCCGG GACCTGGACC GAGTGCTCAT	600
	GGGTACCAG ACCTACCCGC AGCCCTCACC CTCGTYTTCG ATGACGTGCA AGGTCATGAC	660
10	CTCATGGGCA GTGTCACCCCT GGACCACTTT GGGGAGGTGC CAGGTGGCCC GGCTAGAGCC	720
	AGCCAGGGCC GTGAAGTCCA GTGCAGGTG TTTGTCCCCA GTGCTGAGAG CAGAGAGAAG	780
15	CTCATCTCGC TGTGGCTCG CAGTGGGAG GCCCTGTGTG GCCTGAGCTG CCTGTCGAGC	840
	TCACCGGCTA GCCCAGGCCA CAGCCAGCCT GTCGTGCCA GCCTGACGCC TACTGGGGCA	900
	GGGCAGCAGG CTTTGTGTT CTCTAAAAAT GTTTTATCCT CCCTTTGGTA CCTTAATTTG	960
20	ACTGTCTCG CAGAAATGTG AACATGTGTG TGTGTTGTGT TAATTCCTTC TCATGTTGGG	1020
	AGTGAGAATG CCGGGCCCT CAGGGCTGTT CGGTGTGCTG TCAGCCTCCC ACAGGTGGTA	1080
25	CAGCGTGCA CACCAGTGC GTGTCTGCTG TTGTGGGACC GTTGTAAACA CGTGACACTG	1140
	TGGGTCTGAC TTTYTCTTCT ACACGTCTT TCCTGAAGTG TCGAGTCCAG TCCTTTGTTG	1200
	CTGTTGCTGT TGCTGTGCT GTTGCTGTTG GCATCTTGCT GCTAATCCTG AGGCTGGTAG	1260
30	CAGAAATGCAC ATTGGAAGCT CCCACCCCAT ATTGTTCTTC AAAGTGGAGG TCTCCCCTGA	1320
	TCCAGACAAG TGGGAGAGCC CGTGGGGGCA GGGGACCTGG AGCTGCCAGC ACCAAGCGTG	1380
35	ATTCTGCTG CCTGTATTCT CTATTCCAAT AAAGCAGAGT TTGACACCGW MAAAAAAAAA	1440
	AAAAAAAAA AACN	1454

40

(2) INFORMATION FOR SEQ ID NO: 296:

(i) SEQUENCE CHARACTERISTICS:

45

- (A) LENGTH: 828 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 296:

50

ACCTTGCCAT GCCCACAAA CAGATCACCA GCCAGCTTAC ACAGGCATTA ACTCTCCTCA	60
ATGAGGAAGA ATCATTACA ACTGAGCAAG ACATTCATAT GATCATTTAA GGAAGTGTTC	120
55 CCCTTATGTG TTAGCAAGTA TAATCGGCTA ACTCTAAAT CCCAATGAAT AGTCCTAGGC	180
TGGACAGCAA TGGGCTGCAA TTAGGCAGAT AAAGACATCA GTCCAGTAA ATGAATCCAT	240
60 AGACTCATCT AGCACCAACT ACCATTAGCA CTATGTTAGG AGCTGCAAGG CCCCAGTA	300

GAAGATGTGC ATAATGTCTG CTCCTGTGTA GCTCAGGAGA CAATTCCAGC ACAGACACTA 360
 CAGTTAACGC TGAAGTCAG CTGCAAGTAA TAGCA#GAAC AGTCAGAAAA ATACCTTATG 420
 5 AGGGGGCAGG GCTGAAGCTG GGCCTTGAAG GATGGATGAA ATTTGGATAG AGAATGAGGA 480
 AGACAGAGGG NCTCCAAGTG AGAGAAGCAT GAAAAATGAG CARGGGCCTG GATCAGTGGG 540
 GTGTATTTCAG AGCACCTYTC CAGATGCACC ATGCATGCTC ACAGTCCCTT GCCTATGTGT 600
 10 GGCAGAGTGT CCCAGCCAGA TGTGTGCCCC CACCCCATGT CCATTTACAT GTCCTTCAAT 660
 GCCCACCTCA AAAGGYACYT CTTCTGTAAA GCTTTCCCTK GGTATCAGGA ATCAAAATTA 720
 15 ATCAGGGATC TTTCACACT GCTGTTTTT CCTCTTGGT CCTTCTATCA CTAAAACTCA 780
 TCTCATTCAG CCTTACAGCA TAACTAATTA TTGTTTTCC TCACTACA 828

20

(2) INFORMATION FOR SEQ ID NO: 297:

(i) SEQUENCE CHARACTERISTICS:
 25 (A) LENGTH: 2416 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 297:

TCAATTTCCTA TTAAGTCAGA TCAGCCATG TGATTCACCA TTTGTCAGGC TCTCAGGTTT 60
 AACAAAACCT ACTATCACCA TCATCCTTCA ACAGCCACAG TCTGAATTGA GCCAACATTT 120
 35 TTTTTTCTTT GAGAAAGAAG TGGACTGGG CACAACTTT AGTCTGAGG GAGCTAGTGG 180
 AAATCTAGAC AATAGAAGTC ATCGATAGCA GCTTTTCTC AAATGTGTGA CTCCTCAGGG 240
 40 GCTAAACTGC TCTTAGCTTA GAATTATGCT TTAGTAGAGA TCTAGCAGAT AAGTGGGTTA 300
 ATCACTACCA TCCTGTAACT AGTTATATAG CTTCACAGCA TGAGGGAGAC ATCAAAACAGG 360
 GATGGAAGCA ACCCCAAGGA TATGCAAGAA GGGCATGATG AACCCCTTC CCTCTGGCAG 420
 45 GAGAACAAGG CCAACCAAGG GACAGACTGG AAAGCACTTA GATGTTTAAG GAGGAGAAAG 480
 GGAAGCTTT GACCAGTCTT TGCCTTTTGC CAAGTTTCTC CAGTTCTCCG CTGCTTGCAA 540
 50 CCTCTAGCGC AGTAACATTT GCAGAATTGC AGATTTTCCC CCAGATACTA GGAGGAAAGG 600
 GACTTTGGGG GGTGGGGAAG GGTTCGTGGT GTTTTAAAAG CATAAGTTAC CTGTTTGCAC 660
 TGTTTAAAGA TAGGAAAAAA AAATAGTGGG CAAGGTGAAC ATCAGACGTA AATTTGTGTG 720
 55 TTTTTATTTT GTCATGCTCT TGAAAATGTT TGACCATTTG TAGTATACAC AGTGAACTT 780
 GATTCTCTGT TGCATAAAAC ACTATATTTT TTTGGAAATG TTAGTGTTCA AAAGCCTCTT 840
 60 CCTCCCTTT CCTTTTCTTA TGTACTTCTT TCATACTTGC TTTACTGATC AGCCAGGCAA 900

	TAGCCATCCA AGAGCTAGAG CATGAAACAG GGCCCTTTCC AAGTAGGCTC TGGGTGTCCT	960
5	AAGCCAGCGT GTGCCCTCTG GTTTAGTGAG TGTAAATAGAG TCCCTGGCAC CTTTCTTTGC	1020
	AAATGAGGCT AACAGACCAG ACTGCAGCAA GTTATCAGAT TCCTCAATCA GATGCACTAG	1080
	GAGTGAGGAG CCCAGGGATG GAGGGGGTTC CTGAAGTATT GCAGTTGGCT GTAGTAGCTG	1140
10	AGTTCTTTTC CATGTTACCG AAATGTAGC CAGTTACAGT TTAATCAGGA AAACGGTAGA	1200
	TCAATTCAGC CATGGTAGTG CTGGTTGGCA GGGATTGGTA ACGGAGAGAA CTGCTCATCA	1260
15	GCCAAACTC AAGCCTTGCC TTTTAGGAGG CCACCAGCAG AGGGACTTGG TCCTCCTTGT	1320
	CTGGTACTTG TGTACATGCC GGTGACCTGA GGACTCCACT CACACTGGCG AGCAAAAAGG	1380
	GAGCAGTGAT TCTCTTTTCT CTCCCCACCC CCTGCCCTTT GTTACCAACA CCAGTTTCCC	1440
20	AGGGGGTACA TGAGTTTCTG AATTTTAA AATGTMTT GGTMTGGMTT TTCTGGGGAC	1500
	TGATAAGTGC TTTAAGCAAT GTCCATACCC CGTCAAGACT CCCAGCTTAG TCATTTTCTT	1560
25	GTATTTTCT GTTCACAGTA TTTGTGTGTG TGCTTGTMTT GGCAGCTCAT TTGGCTGTA	1620
	TTATATATTG AGTGATGAAT TGATCCTCTT TTTTCCCTAA GGGATATGAA TTGTMTTCT	1680
	TGTGTATAT TCTGCTTGTG AATAGCTGGA GCAAACCTGG GGCTGACACG CGTAAGSTAG	1740
30	GGCTGCAAR CGAGAAGAGA GCCGGTGGAG TGTACTTGTG CCTGACAGGC TGACCTACCT	1800
	GAGTCTCTGA GCTTTTCAGT CCAATCTTT GCAAGGCTCA AAATGCCACA GAACCTCTCC	1860
35	TCTTCTCCC ACTCCCCTG GCAGGGACCG GACCATCCCT ACATGCAACA TGCTGTTCCT	1920
	CCAGCCCCCT CATTGCCAT GGCAAAACAG GTACCTTTGG GGCATGGGG CATTACATGG	1980
	GATGCTTGTG TAATCGACCA CCTAGCCTTC TCTCTCCCT CCCGTCTCC CCCAGAATCA	2040
40	CTTCCTAGGA CACCCGAGCT GCTTGCCCAG GGTCTGTTT CCCTGCTAAC TCCAGAGAAG	2100
	CATCCAGGG CTMTGTGACA GTCTCTAATT CCCTTCCCT CTCGTTAAGA ATCATATTGT	2160
45	ATAGTAGCTT TCAGACCATA CAGTATTCAT TGGGTACTC CTATTATTAT CAAGTAGCTG	2220
	GAATTGTGAA GGTGGGAGTA GTTAGATCTT TAGCTTTTAT TCCTTATTIT TTGTATTAC	2280
	TCTCCATGTG TATAAATTAT TGATCATGTT GCTGGCTTTT ATAACTCTA AGCGAAGGAG	2340
50	GAGCACTGCC TCAGCCTTTG CACATGGTAA TGAAGCACTG TTTTAAATA AAAGRGRGAA	2400
	MCMCCAAAAA AAAAAA	2416

55

(2) INFORMATION FOR SEQ ID NO: 298:

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(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 545 base pairs

(B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 298:

	GAATTCGGCA CGAGCCATGC YTGGCCTCTC CTGTATTCCTT ACAGTCACCTT TGTGGCTGT	60
	TTCTGACTCA GCAGCTACCT GCATTGTGGC CAAAGGATGA CCTATTCCTT CTCAGGAGGG	120
10	CAAAAATGTG GAATAGTGTC TGTCCATGCC TCTCCTCATG GGCTACCACC TCTGCCACCG	180
	TGGTTAATCA GTAACAACCA GGAGAGAAGC TGCTGGAAC TACCTCTGGG AACTCCCTGG	240
15	ATGGTTTGGT GCAGGAATGT AGTAGGCATA CACGTGGMTG CGTGGATCTG GGCCCTCCTG	300
	ATGTGAGTAG AGAGGTAAAA GGSCACCATC TCCTTGACCT YTGGGGAAC CATCCACAAA	360
	GAAGATGTTT CCAAGATGCT TCTGAAGATT GSCTAAAAAT AGCCGGTTTC CACCCCGTG	420
20	AATGCATCCA TTCTAGAATG CTCTTCACC AGGACCAGAG AACTGATTTA CAGAAGTGAC	480
	ATGAAAACAT TCCATCCCAG AATTTGCANT ACCTCAAATT NAATTCTAC CTATTAAAA	540
25	NAAAA	545

30 (2) INFORMATION FOR SEQ ID NO: 299:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1530 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 299:

40	GGCTCTGCTG GGCATCATAC TTGTCACTGG GTAAACAGTT TGCCCACTTA CCGCAGATGA	60
	AGCTGCTTGC CAGGCTCTC CGGCTCTGTG AGTTTGGGAG GCAGGCATCT TCCAGGAGGC	120
	TGGTGGCTGG CCAGGGATGT GTGGGGCCCC GCGGAGGGTG CTGCGCTCCC GTCCAGGTGG	180
45	TTGGGCCCAG GGCTGATCTC CCACCTGTG GAGCCTGCAT TACTGGAAG ATCATGCGGC	240
	CAGATGATGC CAACGTGGCC GGCAATGTCC ACGGGGGGAC CATCCTGAAG ATGATCGAGG	300
50	AGGCAGGCGC CATCATCAGC ACCCGGCATT GCAACAGCCA GAACGGGGAG CGCTGTGTGG	360
	CCGCCCCGGC TCGTGTGAG CCGACCGACT TCCTGTCTCC CATGTGCATC GGTGAGGTGG	420
	CGCATGTCAG CGCGGAGATC ACCTACACCT CCAAGCACTC TGTGGAGGTG CAGGTCAACG	480
55	TGATGTCCGA AAACATCCTC ACAGGTGCCA AAAAGCTGAC CAATAAGGCC ACCCTGTGGT	540
	ATGTGCCCTT GTCGCTGAAG AATGTGGACA AGGTCCTCGA GGTGCCTCCT GTGTGTATT	600
60	CCCGGCANGA GCAGGAGGAG GAGGGCCGGA AGCGGTATGA AGCCAGAAG CTGGAGCGCA	660

	TGGAGACCAA GTGGAGGAAC GGGGACATCG TCCAGCCAGT CCTCAACCCA GAGCCGAACA	720
5	CTGTCAGCTA CAGCCAGTCC AGCTTGATCC ACCTGGTGGG GCCTTCAGAC TGCACCCTGC	780
	ACGGCTTTGT GCACGGAGGT GTGACCATGA AGCTCATGGA TGAGGTCGCC GGGATCGTGG	840
	CTGCACGCCA CTGCAAGACC AACATCGTCA CAGCTTCCGT GGACGCCATT AATTTTCATG	900
10	ACAAGATCAG AAAAGGCTGC GTCATCACCA TCTCGGGACG CATGACCTTC ACGAGCAATA	960
	AGTCCATGGA GATCGAGGTG TTGGTGGACG CCGACCCTGT TGTGGACAGC TCTCAGAAGC	1020
15	GCTACCGGGC CGCCAGTGCC TTCTTCACCT ACGTGTGCT GAGCCAGGAA GGCAGGTCGC	1080
	TGCTGTGCC CCAGCTGGTG CCCGAGACCG AGGACGAGAA GAAGCGCTTT GAGGAAGGCA	1140
	AAGGGCGGTA CCTGCAGATG AAGGCGAAGC GACAGGGCCA CGCGGAGCCT CAGCCCTAGA	1200
20	CTCCCTCCTC CTGCCACTGG TGCTCGAGT AGCCATGGCA ACGGGCCCAG TGTCCAGTCA	1260
	CTTAGAAGTT CCCCCCTTGG CCAAAAACCC AATTCACATT GAGAGCTGGT GTTGTCTGAA	1320
25	GTTTTCTGAT CACAGTGTA ACCTGTACTC TCTCTGCAA ACCTACACAC CAAAGCTTTA	1380
	TTTATATCAT TCCAGTATCA ATGCTACACA GTGTTGTCCC GAGCGCCGGG AGGCGTTGGG	1440
	CAGAAACCTT CGGGAATGCT TCCGAGCACG CTGTAGGTA TGGGAAGAAC CCAGCACCAC	1500
30	TMATAAAGCT GNTGCTTGGC TGGGAAGNA	1530

35 (2) INFORMATION FOR SEQ ID NO: 300:

(i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 997 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 300:

45	AGGTAGTGAG AGACACATTA CACCTAACCA ACAAGAAGAA GGATCCTCCC CCTTATAATT	60
	TAACTATGTT TACAGGGAAT GCGTACATTG TGGCTTCCCG AGNATTTCTG CCAACATGTT	120
50	TTGAAGAACC CTAAATCCCA ACAACTGATT GAATGGGTAA AAGACACTTA TAGCCCAGAT	180
	GAACACCTCT GGGCCACCCT TCAGCGTGCA CGGTGGATGC CTGGCTCTGT TCCCAACCAC	240
	CCCAAGTACG ACATCTTCAG ACATGACTTC TATTGCCAGG CTGGTCAAGT GGCAGGGTCA	300
55	TGAGGGAGAC ATCGATAAGG GTGCTCCTTA TGCTCCCTGC TCTGGAATCC ACCAGCGGGC	360
	TATCTGCGTT TATGGGGCTG GGGACTTGAA TTGGATGCTT CAAAACCATC ACCTGTTGGC	420
60	CAACAAGTTT GACCCAAAGG TAGATGATAA TGCTCTTCAG TGCTTAGAAG AATACCTACG	480

TTATAAGGCC ATCTATGGGA CTGAACCTTG AGACACACTA TGAGAGCGTT GCTACCTGTG 540
 GGGCAAGAGC ATGTACAAAC ATGCTCAGAA CTGCTGGGA CAGTGTGGGT GGGAGACCAG 600
 5 GGCTTTGCAA TTCGTGGCAT CCTTTAGGAT AAGAGGGCTG MTATTAGATT GTGGSTAAGT 660
 AGATCTTTTG CCTTGCAAAT TGCTGCCTGG GTGRATGCTG CTGTCTCTCT CACCCCTAAC 720
 10 CCTAGTAGTT CCTCCACTAA CTTCTCACT AAGTGAGAAT GAGAACTGCT GTGATAGGGA 780
 GAGTGAAGGA GGGATATGTG GTAGAGCACT TGATTTCAGT TGAATGCCTG CTGGTAGCTT 840
 TTCCATCTG TGGAGCTGCC GTTCCTAATA ATTCCAGGTT TGGTAGCGTG GAGGAGAACT 900
 15 TTGATGGAAA GAGAACCCTC CCTTCTGTAC TGTAACTTA AAAATAAATA GCTCCTGATT 960
 CAAAGTAAGG AAAAAA AAAAGAAAAA AACTCGA 997

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(2) INFORMATION FOR SEQ ID NO: 301:

25 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 2345 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 301:

TTGAGGCCGA CGCTAGGGGC CCGGAAGRAA ACTGCGAGGC GAAGGTGACC GGGGACCGAG 60
 CATTTICAGAT CTGCTCGGTA GACCTGGTGC ACCACCACCA TGTGCGTGC AAGGCTGGTG 120
 35 TGCTCCGGA CACTACCTTC TAGGGTTTTC CACCAGCTT TCACCAAGGC CTCCCCTGTT 180
 GTGAAGAATT CCATCAGGAA GAATCAATGG CTGTTAACAC CTAGCAGGGA ATATGCCACC 240
 40 AAAACAAGAA TTGGGATCCG GCGTGGGAGA ACTGGCCAAG AACTCAAAGA GGCAGCATG 300
 GAACCATCGA TGGAAAAAAT ATTAAAAATT GATCAGATGG GAAGATGGTT TGTGCTGGA 360
 GGGGCTGCTG TTGGTCTTGG AGCATTGTGC TACTATGGCT TGGGACTGTC TAATGAGATT 420
 45 GGAGCTATTG AAAAGGCTGT AATTGGCCT CAGTATGTCA AGGATAGAAT TCATTCCACC 480
 TATATGTACT TAGCAGGGAG TATGGTTTA ACAGCTTTGT CTGCCATAGC AATCAGCAGA 540
 50 ACGCCTGTTT TCATGAACTT CATGATGAGA GGCTCTTGGG TGACAAATTGG TGTGACCTTT 600
 GCAGCCATGG TTGGAGCTGG AATGCTGGTA CGATCAATAC CATATGACCA GAGCCACGGC 660
 CCAAAGCATC TTGCTTGGTT GCTACATTCT GGTGTGATGG GTGCAGTGGT GGCTCCTCTG 720
 55 ACAATATTAG GGGGTCTCT TCTCATCAGA GCTGCATGGT ACACAGCTGG CATTGTGGGA 780
 GGCTCTCCA CTGTGGCCAT GTGTGCGCCC AGTGAAAAGT TTCTGAACAT GGGTGCACCC 840
 60 CTGGGAGTGG GCCTGGGTCT CGTCTTTGTG TCCTCATTGG GATCTATGTT TCTTCCACCT 900

	ACCACCGTGG CTGGTGCCAC TCTTTACTCA GTGGCAATGT ACGGTGGATT AGTTCTTTTC	960
5	AGCATGTTCC TTCTGTATGA TACCCAGAAA GTAATCAAGC GTGCAGAAGT ATCACCAATG	1020
	TATGGAGTTC AAAAATATGA TCCCATTAAC TCGATGCTGA GTATCTACAT GGATACATTA	1080
	AATATATTTA TCGAGTTGC AACTATGCTG GCAACTGGAG GCAACAGAAA GAAATGAAGT	1140
10	GACTCAGCTT CTGGCTTCTC TGCTACATCA AATATCTTGT TTAATGGGGC AGATATGCAT	1200
	TAAATAGTTT GTACAAGCAG CTTTCGTTGA AGTTTAGAAG ATAAGAAACA TGTATCATA	1260
15	TTTAAATGTT CCGGTAATGT GATGCCTCAG GTCTGCCTTT TTTTCTGGAG AATAAATGCA	1320
	GTAATCCTCT CCCAAATAAG CACACACATT TTCAATTCTC ATGTTTGAGT GATTTTAAAA	1380
	TGTTTTGGTG AATGTGAAAA CTAAGTTTG TGTCATGAGA ATGTAAGTCT TTTTCTACT	1440
20	TTAAATTTA GTAGGTTTAC TGAGTAACTA AAATTTAGCA AACCTGTGTT TGCATATTTT	1500
	TTTGGAGTGC AGAATATTGT AATTAATGTC ATAAGTGATT TGGAGCTTTG GTAAAGGGAC	1560
25	CAGAGAGAAG GAGTCACCTG CAGTCTTTTG TTTTTTTAAA TACTTAGAAC TTAGCACTTG	1620
	TGTTATTGAT TAGTGAGGAG CCAGTAAGAA ACATCTGGGT ATTTGGAAAC AAGTGGTCAT	1680
	TGTTACATTC ATCTGCTGAA CTTAACAAAA CTGTTTATCC TGAACAGGC ACAGGTGATG	1740
30	CATTCTCCTG CTGTGCTTC TCAGTGCTCT CTTTCCAATA TAGATGTGGT CATGTTTGAC	1800
	TTGTACAGAA TGTTAATCAT ACAGAGAATC CTTGATGGAA TTATATATGT GTGTTTACT	1860
35	TTTGAATGTT ACAAAGGAA ATAACTTTAA AACTATTCTC AAGAGAAAAT ATTCAAAGCA	1920
	TGAAATATGT TGCTTTTCC AGAATACAAA CAGTATACTC ATGATTGCTA AGTGTTTTTT	1980
	TATTTTGCAT TATTTATTGA ACTGTCTAAT TGAATACAGC TTGCTCTTGT CACCTCTTCA	2040
40	AGCTTTCAAG CCTTTATAGA AAAGCTTCTT TGTGGCTTAC ACTGGAAATT ATGAAAGCAG	2100
	TTTTTCTCCT AAGACTTTTG GTTCTCGCA TTGCCTCTCA GACTAAGCAC TAAAAAGCAA	2160
45	AGCAAAACAG AACTAGTNCT GTCTTAATGA AATATATCAA CCCAAAAGTG TAATGAGGAA	2220
	AATGCTTCAT TAGTTTCCCC TAGCAGACTT TPACTTCTCT TACACTGCTA CACCATTACT	2280
	TTCTTGAGAC ATTTGTAAGT CCTTGATAC AGAAGAGTGA TATTTAGGAG GNCPTTAATG	2340
50	AAGGG	2345

55 (2) INFORMATION FOR SEQ ID NO: 302:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2369 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

60

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 302:

5	TTTTTTTTTT TTTTTTTTTT TTTTNCNCAAG ATCATTGTTT ATTTATTACT TCAGATAAAA	60
	AGATAGTATA CATATTAGGG AATCCCTTAA AATCAACTC TAGAGTTATA CACCATCTAG	120
	TACTTTTGCA ATGAATGTTA ACAACAACAA AAAAAATCTC TAAACACCTG AAAGCCCCAC	180
10	TATTAACATG GACTATGGTA ATAAAAAATT TTGACATTTA ATTTGTTCAA CATATAGTAT	240
	TTACATTATG AAACCAATGG TGATGATACA ATAAAGTGAT AAAGAAATAG TAAAAATAAA	300
15	CTTTAAAAAG CAAAGGTTTA TAGTCTGACA ATGCTAATTA TCCTAATTGT ATATAAAAAA	360
	TTAAACATA GAGCTTTCTG TTACAAAAAT CTTAATCCTC TGGGTTGTAA TCATTACTTG	420
	CTACCAATTT ACATGCAACA TCTGCTAGGA CTGACATTTG ATTTTTTTTCC CCAAGAATGT	480
20	GTGAGTAGAT AAATGACATT TCAGAGCAGA TATTAATTTA CTTGTGGACA GAAAAAGAAA	540
	CTCAAGATTG TACTGGTCA CAAGCCTCTT CCCAATAGAA ATTATAAAAA CAGTAAGATA	600
25	AAATTTAAAA AAAATCTAAA AAGGGGATGC ATAGGCAAAG AGTACCATAA ATGGCACAGC	660
	TCAAAAAATC CCAGGACCAA TCAGACACAC ATCTTTTCTC TCTCCTTCAG CGACAAGAGG	720
	TCGATTTTGC CATCAAATAA CCATGATTGA AGCAAGCGAG GGGCACCAGG TGTACAACTG	780
30	ATTAGATCTT GCAAAATACT AAGATGGGAG CAGGGGTGGC CAGAAGAAGG GGTAAATTTAT	840
	ATATAATTCA AACTATATAC AGCATAAATG GAATGCAGCC CATCCCAAAC TGGCTCTGIG	900
35	AAACAATTGG ACCTTTATAG TTAATAATTAT AACAAAGTGA ATAATACAAT AGATTTACAT	960
	GGGAAGCAAA ATCCAAGGGA CATTTTATAT TAAGTATTTA CTGTGCTGTT TCAATTTAAA	1020
	AATAATTTTG CTAAGTATAC ATCTCAACTG AAGTCTATGT AAAAAATGTC CTAATAGATA	1080
40	CAGATATTTA CCTTTGGTGA GTTGAAGGCC TTTTGTGAC TTCTGTCTGA ACTGTAGGCA	1140
	GAATGCTAGA TGTACATGCA CATATGGAGA AACTCAAGCT GAGGTCATCC AAAAGCTGTG	1200
45	CGTATGAGGA GGCTGGAGGT ACTTTGAAAG TCAAAGTAGA CCAGAAACCC AAAACAGGTA	1260
	ACAGTGAGGA TGGCAACAGG GAATGGAATG CCAATATGGC AGTAAAACTT TTTTAAAAAA	1320
	CAGAAAGAGG AAGGCCTCTC GTACCAGCAG AATCCTGTAC ACGTACAAA AAGAAAAAGC	1380
50	CACCCACCAT TTTGTAAAC AGAAGCCAAT TATAGTGTGG GAAAGTACAA ATTACAGAAA	1440
	ACCAGAAGTC AACAGAAGAA AACTACTGG TTTACTTGAG AGAAAGGAGA ATGGTTCACC	1500
55	CCGAGCAGAG TTAATTGGTG AACGCCCCA CCACGCCCA CAGAACCTCA TTGGTGTGG	1560
	CCTTCAGACA TTCCACTTCA GGTCTAAGT CGAGAARNIG CCGCACTCTC TTGGTAGCCA	1620
60	AATCATACTG CTCGTCCAGA AGAGGAGCAA AAGCATTTCTC CAGGACGTCC GAGGCATGAG	1680

CCAGGTAAAT GAGGGCCAGC AAGCGCCTGT CCATGCGGTG AGGGTCATTC ACCCATTTGT 1740
 CAAGAACGCG TTCTGTACT TTCTTGATGA GCGCTGCTT AATGTTGTTA TTGGTGAGGG 1800
 5 GATGTGTGT CATGTCAAAA AGTAGGAAGT TCTGTTTCTC TGTGTCAAT ACACCCTTTT 1860
 CCACCAGGTT TTTAGCTAAT CGTCCCGTA CATTTCCTAA CTGATAATGC AATTTTAATG 1920
 GATTCATGT CTCACCACTA AGTAATTCAA TCCAGTTCTG GACCGTTTCT GGAGGCTGAG 1980
 10 TTTCCCTAAC ATGCTTCAGA GCTTCATCAA GAAGAACATC CCCTGTTGGA GCATCTGACT 2040
 TACAGATTAC CTTTCTTGTT AATAGACTTT TACGTCTCAT TCCACAAGCC TCTAGTTGTA 2100
 15 ACCTTCCTCT CAATGCTAAT TCAATTAACA TACAGCCACG TAATCCAGAT GATATACAGT 2160
 CATTCAAAA TGATGTGTAA ACCTTCGCGG TCCTTGAGGC CCAGCAGGAG CACTTCCTCC 2220
 ATCAGGGTCA GCCCGGTTTC CTGGAGTGC CCCTTGTCGT CGTCGTCTG CTCGTGCGG 2280
 20 CGGCTCTGCG CGTCGTCTC GCTGCTAGCC GCGCCGCCG CCGCCGCCG CTCCTTGTCG 2340
 GCGGCGTTGC GGGAGGCCTC GGTGCGCCG 2369

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(2) INFORMATION FOR SEQ ID NO: 303:

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- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1181 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 303:

GGGACGTGTG GTTTCAGCTC GTGCGCCTCC CCGTGGGTTT GCGACGTTTA GCGACTATTG 60
 40 GCGCTGCGCC ACGCCGGCTG CGAGACTGGG GCGGTGGYTG CTGGTCCCGG GTGATGCTAG 120
 GCGGCTCCCT GGGCTCCAGG CTGTTGCGGG GTGTAGGTGG GAGTCACGA CGGTTGGGG 180
 CCCGAGGTGT CCGCGAAGGT GCGGCACATG GCGGCAGGG GAGAGCATGG CTCAGCGGAT 240
 45 GGTCTGGGTG GACCTGGAGA TGACAGGATT GGACATGAG AAGGACCAGA TTATTGAGAT 300
 GGCCTGTCTG ATAACTGACT CTGATCTCAA CATTTTGGCT GAAGGTCTTA ACCTGATTAT 360
 50 AAAACAACCA GATGAGTTGC TGGACAGCAT GTCAGATTGG TGTAAAGGAG ATCACGGGAA 420
 GTCTGGCCTT ACCAAGGCAG TGAAGGAGAG TACAATTACA TTGCAGCAGG CAGAGTATGA 480
 ATTTCTGTCC TTTGTACGAC AGCAGACTCC TCCAGGGCTC TGTCACCTTG CAGGAAATTC 540
 55 AGTTCATGAA GATAAGAAGT TTCTTGACAA ATACATGCCC CAGTTCATGA AACATCTTCA 600
 TTATAGAATA ATTGATGTGA GCACTGTTAA AGAACTGTGC AGACGCTGGT ATCCAGAAGA 660
 60 ATATGAATTT GCACCAAGA AGGCTGCTTC TCATAGGGCA CTTGATGACA TTAGTGAAAG 720

CATCAAAGAG CTTCAGTTTT ACCGAAATAA CATCTTCAAG AAAAAAATAG ATGAAAAGAA 780
 5 GAGGAAAATT ATAGAAAATG GGGAAAATGA GAAGACCGTG AGTTGATGCC AGTTATCATG 840
 CTGCCACTAC ATCGTTATCT GGAGGCAACT TCTGGTGGTT TTTTTCCTC ACGCTGATGG 900
 CTGGGCAGAG CMCTTCGGTT AACTTGCAATC TCCAGATTGA TTACTCAAGC AGACAGCACA 960
 10 CGAAATACTA TTTTTCCTCT AATATGCTGT TTCCATTATG ACACAGCAGC TCCTTTGTAA 1020
 GTACCAGGTC ATGTCCATCC CTGGGTACAT ATATGCATTT GCTTTTAAAC CATTTCTTTT 1080
 GTTTAAATAA ATAAATAAGT AAATAAAGCT AGTTCATTG AAATGCAAAA AAAAAAAAAA 1140
 15 AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA N 1181

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(2) INFORMATION FOR SEQ ID NO: 304:

(i) SEQUENCE CHARACTERISTICS:

25

- (A) LENGTH: 1537 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 304:

30

CTTTTGTGT TCCGGCCGAT CCCACCTCTC CTCGACCTG GACGTCTACC TTCCGGAGGC 60
 CCACATCTTG CCCACTCCGC GCGCGGGGCT AGCGCGGGTT TCAGCGACGG GAGCCCTCAA 120
 35 GGGACATGGC AACTACAGCG GCGCCGGCGG GCGCGCCCG AANATGGAGC TGGCCCGGAA 180
 TGGGGAGGGT TCGAAGAAAA CATCCAGGGC GGAGGCTCAG CTGTGATTGA CATGGAGAAC 240
 ATGGATGATA CCTCAGGCTC TAGCTTCGAG GATATGGGTG AGCTGCATCA GCGCCTGCGC 300
 40 GAGGAAGAAG TAGACGCTGA TGCAGCTGAT GCAGCTGCTG CTGAAGAGGA GGATGGAGAG 360
 TTCCTGGGCA TGAAGGGCTT TAAGGGACAG CTGAGCCGGC AGGTGGCAGA TCAGATGTGG 420
 45 CAGGCTGGGA AAAGACAAGC CTCAGGGCC TTCAGCTTGT ACGCCAACAT CGACATCCTC 480
 AGACCCCTACT TTGATGTGGA GCCTGCTCAG GTGCGAACAG GGCTCCTGGA GTCCATGATC 540
 CCTATCAAGA TGGTCAACTT CCCCAGAAA ATGTCAGGTG AACTCTATGG ACCTCTCATG 600
 50 CTGGTCTTCA CTCTGGTTGC TATCCTACTC CATGGGATGA AGACGTCTGA CACTATTATC 660
 CGGGAGGGCA CCCTGATGGG CACAGCCATT GGCACCTGCT TCGGCTACTG GCTGGGAGTC 720
 55 TCATCCTTCA TTTACTTCCT TGCCCTACCTG TGCAACGCC AGATCACCAT GCTGCAGATG 780
 TTGGCACTGC TGGGCTATGG CCTCTTTGGG CATTCATTG TCCTGTTTAT CACCTATAAT 840
 60 ATCCACCTCC ACGCCCTCTT CTACCTCTTC TGGCTGTGG TGGGTGGACT GTCCACACTG 900

CGCATGGTAG CAGTGTGGT GTCTCGGACC GTGGGCCCCA CACAGCGGCT GTCCTCTGT 960
GGCACCTGG CTGCCCTACA CATGCTCTTC CTGCTCTATC TGCATTTTGC CTACCACAAA 1020
5 GTGNTAGAGG GGATCCTGGA CACACTGGAG GGCCCCAACA TCCCGCCCAT CCAGAGGGTC 1080
CCCAGAGACA TCCCTGCCAT GTCCTCTGCT GCTCGGCTTC CCACCACCGT CCTCAACGCC 1140
10 ACAGCCAAAG CTGTTGGGT GACCCTGCAG TCACACTGAC CCCACCTGAA ATTCTTGGCC 1200
AGTCCTCTTT CCGCAGCTG CAGAGAGGAG GAAGACTATT AAAGGACAGT CCTGATGACA 1260
TGTTTCGTAG ATGGGGTTTG CAGCTGCCAC TGAGCTGTAG CTGCGTAAGT ACCTCCTTGN 1320
15 AGCTGTGGC ACTTCTGAAA GCACAAGGCC AAGAACTCCT GGCCAGGACT GCAAGGCTCT 1380
GCAGCCAATG CAGAAAATGG GTCAGCTCCT TTGAGAACCC CTCCCCACCT ACCCCTTCCT 1440
TCCTCTTTAT CTCTCCACA TTGTCTTGCT AAATATAGAC TTGGTAATTA AAAAAAAAAA 1500
20 AAAAAAAAAA AAAAAAAAAA AAAAAAGGGG GGNCCCC 1537

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(2) INFORMATION FOR SEQ ID NO: 305:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1493 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 305:

35

TGCATGCCAA AACCAATGCC TGCCAAACAA AATCTTAGAC ATCCCAATAT AATATGTTAG 60
TTATATTTCT ATTACATCA TTATTGAAAA TACCCAGCTC AGTGCCTGGC TTAATAAATG 120
40 TTTAATTCCC TTACCTACTC TTGCTCTATT TTTTATTG AAATGGAGAT GAGCAAAATA 180
ACACATTCAT GGCTGAAGCA ATTTTMTGGA CATTTCTTGT TACCAAAAGA TCTATAATCA 240
GGATGATCCT GAGCTGTTCA AACAAGCTGT ATATAACAG ACAATGAAAC TCTTTGCAGA 300
45 GCTGGAAATT AAAAGGAAAG AGAGAGAAGC CAAAGAGATG CATGAAAGGA AACGACAAAG 360
GGAAGAAGAG ATTGAAGCTC AAGAAAAAGC CAAACGGGAA AGAGAGTGGC AGAAAACTT 420
50 TGAGGAAAGT CGAGATGGTC GTGTGGACAG CTGGCGAAAC TTCCAAGCCA ATACGAAGGG 480
GAAGAAAGAG AAGAAAAATC GGACCTTCCT GAGACCACCG AAAGTAAAAA TGGAGCAACG 540
TGAGTGACCG CCCAAGGTCA CAGGCACAGA ACCTTTCCCC TGCTATCTCC CTTCCTGCTT 600
55 CGAAGGACTC ATTCTTTCCT CCCACTTCCA CCCCAACATA GAGTAGTATT TGCTTTTATG 660
TCCATTTTGT TTTCAATACG ATTTAATATC GATCAGAGTA ATTCTTTTGT ACATTGAAAT 720
60 GAGGGGCTTG GTTTAAAAA AGACCTTTCC CTCTCCCTGC CCCTAGAACA ACCAGTATTA 780

GAAGGTGCCA CCATGGGTGC TGCCTTCTCT TCCCACAGCC TGTAAGTCAG TGTTTTGTAC 840
 TTCACTGAAT TGTGATGGTT AGAAACTTCG TGGATAGTTT GTGGAAATCA TCCAATTAAA 900
 5 CATACTGCTT AAAACAGTGT TGCTGTGACT TCAGAGACAA GCCTGGAAGG GGCACCTTAG 960
 GAAGCCOCTT CGCTTCAGTT GCTCGCTTCT GGGTGTGCTC CCTTCGAAGG CCCAGATAAG 1020
 10 ACAGGGAACA CTTGTGAGCA CACAGAGCAG CATCTGATGC CCTGTGGTGT TTGGCATGTG 1080
 CCCCCTGTCT ACTGACCAAT CAGTGTGGCA TGAGGCCAC GCCACCCAAA CCTTTCACCT 1140
 TCCAAAGAGC TAGCCGTCCT CCACCCAGTA CCATGTCCTA GCCTGTCTGC ATTGTGTAGT 1200
 15 GGTAATATTC TTTATGTATA ATAAATTTTT ATACCCAAGC CATTGATGTA CTTTTCTTG 1260
 TACTCTCCCT TGTGGGTCCC TTGTCTGGCT TGGCTGAACC CAAAATGCT TTGGGGTTGG 1320
 20 ACAGACCTGG CTGAACCTTA GTTCTTTCAT CTATGAAATG GGAATATGAA TTACTGCAGC 1380
 AGCTTTTAGG GCAGATTTC CATGGCATAT ACAAGGTAAC TACCATAGTG CTCCTTGGGT 1440
 25 ATTGCCAATA TCCTATTATT TCTGTGTAAA ATGAAGATAC TGATTGTTTT GAG 1493

30 (2) INFORMATION FOR SEQ ID NO: 306:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 577 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 306:

AATTCGGCAG AGGNATTATA TACACTATAC TGGCATTTC TGTTCACCC AGCCCGGAAA 60
 40 GTCAGAGATG TATATTGGAA AATTTACAAC TCCATCTACA TTGGTTCCCA GGACGCTCTC 120
 ATAGCACATT ACCCAAGAAT CTACAACGAT GATAAGAACA CCTATATTCT TTATGAACTT 180
 45 GACTATATCT TATAATTTTA TTGTTTATTT TGTGTTTAAT GCACAGCTAC TTCACACCTT 240
 AAACTTGCTT TGATTGGTG ATGTAACTT TTAACATTG CAGATCAGTG TAGAACTGGT 300
 CATAGAGGAA GAGCTAGAAA TCCAGTAGCA TGATTTTAA ATAACCTGTC TTTGTTTTTG 360
 50 ATGTTAAACA GTAAATGCCA GTAGTGACCA AGAACACAGT GATTATATAC ACTATACTGG 420
 AGGGATTTC TTTTAAATTC ATCTTTATGA AGATTAGAA CTCATTCTTT GTGTTTAAAG 480
 55 GGAATGTTTA ATTGAGAAAT AAACATTTGT GWACAAAATG YTAACAAAAA AAAAAAAA 540
 AAAAAAAA AAAAAAAA AAAAAAAA AACTCGA 577

60

(2) INFORMATION FOR SEQ ID NO: 307:

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 2860 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 307:

10 GTGTGACCG CTCTCNCAAT ATGGCTCCCC CGGCTGGCA GRWRKTCRGT CWCKRGTGGC 60
 TAGCCTGTCC TGACAGGGGA GAGTTAAGCT CCCGTTCTCC ACCGTGCCGG CTGGCCAGGT 120
 15 GGGCTGAGGG TGACCGAGAG ACCAGAACCT GCTTGCTGGA GCTTAGTGCT CAGAGCTGGG 180
 GAGGGAGGTT CCGCCGCTCC TCTGCTGTCA GCGCCGGCAG CCCCTCCCGG CTTCACTTCC 240
 20 TCCCGCAGCC CCTGCTACTG AGAAGCTCCG GGATCCACG AGCCGCCACG CCCTGGCCTC 300
 AGCCTGCGGG GCTTCCAGTC AGGCCAACAC CGACGCGCAC TGGGGAGGAA GACAGGACCC 360
 TTGACATCTC CATCTGCACA GAGGTCCTGG CTGGAACCGA GCAGCCTCCT CCTCCTAGGA 420
 25 TGACCTCACC CTCAGCTCT CCAGTTTCA GGTGGAGAC ATTAGATGGA GGCCAAGAAG 480
 ATGGCTCTGA GCGGACAGA GGAAAGCTGG ATTTTGGGAG CGGGCTGCCT CCCATGGAGT 540
 30 CACAGTTCCA GCGCAGGAC CGGAAATTCG CCCCTTCAGA TAAGAGTCAA CCTCCAATA 600
 CCGAAAGGGA ACAGGTGCCA GTCAGCCGGA TCCAAACCGA TTTGACCGAG ATCGGCTCTT 660
 CAATGCGGTC TCCCGGGGTG TCCCGGAGGA TCTGGCTGGA CTTCCAGAGT ACCTGAGCAA 720
 35 GACCAGCAAG TACCTCACCG ACTTCGAAA TACACAGAGG GCTCCACAGG TAAGACGGCC 780
 TGATGAAGGC TGTGCTGAAA CCTTAAGGAC GGGGTCAATG CCTGCATTCT GCCACTGCTG 840
 40 CAGATCGACC GGGACTCTGG CAATCCTCAG CCCCTGGTAA ATGCCAGTG CACAGATGAC 900
 TATTACCGAG GCCACAGCGC TCTGCACATC GCCATTGAGA AAGAGGAGTC TGCAGTGTGT 960
 GAAGCTCCTG GTGAGAATG GGGCCAATGT GCATGCCCCG GTCTGCGGCG ACTTCTTCCA 1020
 45 GAAGGGCCAA GGGACTTGCT TTTATTTCGG TGAGCTACCC CTCTCTTTGG CCGCTTGCAC 1080
 CAAGCAGTGG GATGTGGTAA GCTACCTCCT GGAGAACCCA CACCAGCCCG CCAGCCTGCA 1140
 50 GGCCACTGAC TCCAGGGCA ACACAGTCCT GCATGCCCTA GTGGATGATC TCGGACAACT 1200
 CAGCTGAGAA CATTGCACTG GTGACCAGCA TGTATGATGG GCTCTCCAA GCTKGGGSCC 1260
 SCCYTCTGCC CTACCGTGCA GCTTGAGGAC ATCCGCAACC TGCAGGATCT CACGCCCTCTG 1320
 55 AAGCTGGCCG CCAAGGAGGG CAAGATCGAG ATTTTCAGGC ACATCCTGCA GCGGGAGTTT 1380
 TCAGGACTGA GCCACCTTTC CCGAAAGTTC ACCGAGTGGT GCTATGGGCC TGTCCGGGTG 1440
 60 TCGCTGTATG ACCTGGCTTC TGTGGACAGC TGTGAGGAGA ACTCAGTGCT GGAGATCATT 1500

	G CCTTTCATT GCAAGAGCCC GCACCGACAC CGAATGGTCG TTTTGGAGCC CCTGAACAAA	1560
5	CTGCTGCAGG CGAAATGGGA TCTGCTCATC CCCAAGTTCT TCTTAACTT CCTGTGTAAT	1620
	CTGATCTACA TGTTTCATCTT CACCGCTGTT GCCTACCATC AGCCTACCCT GAAGAAGCAG	1680
	GCCGCCCCTC ACCTGAAAGC GGAGGTTGGA AACTCCATGC TGCTGACGGG CCACATCCTT	1740
10	ATCCTGCTAG GGGGGATCTA CCTCCTCGTG GGGCCAGCTG TGGTACTTCT GCGGGCGCCA	1800
	CGTGTTCATC TGGATCTCGT TCATAGACAG CTACTTTGGA AATCCTCTTC CTGTTCCAGG	1860
15	CCCTGCTTCA CAGTGGTGTC CCAGGTGCTG TGTTCCTGG GCCATCGAGT GGTACCTGCC	1920
	CCTGCTGTG TCTGCGCTGG TGGCTGGGCT GGCTGAACCT GCTTTACTAA TACACGTGGC	1980
	GTTCCAGCAC ACAGGCAGTC TACAGTTTCA TGWTCCTGA AGCCCTGGTG AGCCTGAGCC	2040
20	AGGAGGCTTG GCGCCCCGAA GCTCCTACAG GCCCAATGC CACAGAGTCA GTGCAGCCCA	2100
	TGGAGGGACA GGAGGACGAG GGCAACGGGG CCCAGTACAG GGTATCCTG GAAGCCTCCT	2160
25	TGGAGCTCTT CAAATTCAAC ATCGGCATGG GCGAGCTGGC CTTCCAGGAG CAGCTGCACT	2220
	TCCGCGGCAT GGTGCTGCTG CTGCTGCTGG CCTACGTGCT GCTCACCTAC ATCCTGCTGC	2280
	TCAACATGCT CATCGCCCTC ATGAAGCGAA CGTCACAGTG TCGCCACTGA CAGCTGGAGC	2340
30	ATCTGGAAGC TGCAGAAAGC CATCTCTGTC CTGGAGATGG AGAATGGCTA TTGGTGGTGC	2400
	AGGAAAAAGC AGCGGGCAGG TGTGATGCTG ACCGTTGGCA CTAAGCCCAG ATGGCAGCCC	2460
35	CGATGAGCGC TGGTGTCTCA GGGTGGAGGA GGTGAAGTGG GCTTCATGGG GAGCAGACGC	2520
	TGCCTACGCT GTGTGAGGAC CCGTCAGGGG CAGGTGTCCC TCGAACTCTC GAGAACCCTG	2580
	TCCTGGCTTC CCCTCCCAAG GAGGATGAGG ATGGTGCCTC TGAGGAAAAC TATGTGCCCCG	2640
40	TCCAGTCTCT CCACTCCAAC TGATGGCCCA GATGCAGCAG GAGGCCAGAG GACAGAGCAG	2700
	AGGATCTTTC CAACCACATC TGCTGGCTCT GGGGTCCCAG TGAATTCTGG TGGCAAATAT	2760
45	ATATTTTCAC TAACTCAAAA AAAAAAAAAA AAAAAAAAAA AAAAVGAGGG GGGGCCGKGT	2820
	ASCCAAWTTT GCCCTATAAG TGAGTGCCWA TTACGATAAA	2860

50

(2) INFORMATION FOR SEQ ID NO: 308:

(i) SEQUENCE CHARACTERISTICS:

55

- (A) LENGTH: 876 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

60

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 308:

	CTGCTTGIGT CTGCGCTGGT GCTGGGCTGG CTGAACCTGC TTTACTATAC ACGTGGCTTC	60
	CAGCACACAG GCATCTACAG TGTCTATGATC CAGAAGCCCT GGTGAGCCTG AGCCAGGANN	120
5	TTGGCGCCCC GAAGCTCCTA CAGGCCCAA TGCCACAGAG TCAGTGCAGC CCATGGAGGG	180
	ACAGGAGGAC GAGGGCAACG GGGCCAGTA CAGGGGTATC CTGGAAGCCT CCTTGGAGCT	240
10	CTTCAAATTC ACCATCGGCA TGGCGAGCT GGCCTTCCAG GAGCAGCTGC ACTTCCGCGG	300
	CATGGTGCTG CTGCTGCTGC TGGCCTACGT GCTGCTCACC TACATCCTGC TGCTCAACAT	360
	GCTCATCGCC CTCATGNAGC GAGACCGWCA ACAGTGTCCG CACTGACAGC TGGAGCATCT	420
15	GGAAGCTGCA GAAAGCCATC TCTGTCTCTGG AGATGGAGAA TGGCTATTGG TGGTGCAGGA	480
	AGAAGCAGCG GGCAGGTGTG ATGCTGACCG TTGGCACTAA GCCAGATGGC AGCCCCGATG	540
20	AGCGCTGGTG CTTTCAGGGTG GAGGAGGTGA ACTGGGCTTC ATGGGAGCAG ACGCTGCCTA	600
	CGCTGTGTGA GGACCCGTCA GGGGCAGGTG TCCCTCGAAC TCTCGAGAAC CCTGTCTCTGG	660
	CTTCCCCCTCC CAAGGAGGAT GAGGATGGTG CCTCTGAGGA AAACATATGTG CCCGTCCAGC	720
25	TCCTCCAGTC CAACTGATGG CCCAGATGCA GCAGGAGGCC AGAGGACAGA GCAGAGGATC	780
	TTTCCAACCA CATCTGCTGG CTCTGGGGTC CCAGTGAATT CTGGTGGCAA ATATATATTT	840
30	TCACTAAMMM AAAAAAAAAA AAAAAAAAAA ACTCGA	876

(2) INFORMATION FOR SEQ ID NO: 309:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 2025 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 309:

45	CATGACCCGC CTGATGCGAT CCCGCACAGC CTCTGGTTCC AGCGTCACTT CTCTGGATGG	60
	CACCCGCAGC CGCTCCACA CCAGCGAGGG CACCCGAAGC CGCTCCACA CCAGCGAGGG	120
	CACCCGCAGC CGCTCGACA CCAGCGAGGG GGGCCACCTG GACATCACCC CCAACTCGGG	180
50	TGCTGCTGGG AACASGCCGG GCCCAAGTCC ATGGAGGTCT CTGCTAGGC GGCCTGCCCA	240
	GCTGCCGCCC CCGGACTCTG ATCTCTGTAG TGGCCCCCTC CTCCCCGGCC CCTTTTCGCC	300
55	CCCTGCCTGC CATACTGCGC CTAACCTGGT ATTAATCCAA AGCTTATTTT GTAAGAGTGA	360
	GCTCTGGTGG AGACAAATGA GGTCTATTAC GTGGGTGCCC TCTCCAAAGG CGGGGTGGCG	420
	GTGGACCAA GGAAGGAAGC AAGCATCTCC GCATCGCATC CTCTTCCATT AACCAGTGCC	480
60	CGGTGCCAC TCTCTCCCC TCCCTCAGAG ACACCAAAC GCAAAAACA AGACGCGTAC	540

	AGCACACACT TCACAAAGCC AAGCCTAGGC CGCCTGAGC ATCCTGGTTC AAACGGGTGC	600
	CTGGTCAGAA GGCCAGCCGC CCACTTCCCG TTTCTCTTTT AACTGAGGAG AAGCTGATCC	660
5	AGTTTCCGGA AACAAAATCC TTTTCTCATT TGGGGAGGGG GGTAAATAGT ACATGCAGGC	720
	ACCTCTTTTA AACAGGCAAA ACAGGAAGGG GGAAAAGGTG GGATTCATGT CGAGGCTAGA	780
10	GGCATTTGGA ACAACAAATC TACGTAGTTA ACTTGAAGAA ACCGATTTTTT AAAGTTGGTG	840
	CATCTAGAAA GCTTTGAATG CAGAAGCAAA CAAGCTTGAT TTTTCTAGCA TCCTCTTAAT	900
	GTGCAGCAAA AGCAGGCRAC AAAATCTCCT GGCTTTACAG ACAAAAATAT TTCAGCAAAC	960
15	GTTGGGCATC ATGGTTTTTG AAGGCTTTAG TTCTGCTTTC TGCTCTCCT CCACAGCCCC	1020
	AACCTCCAC CCCTGATACA TGAGCCAGTG ATTATTCTTG TTCAGGGAGA AGATCATTTA	1080
20	GATTTGTTTT GCATTCCCTA GAATGGAGGG CAACATTCCA CAGCTGCCCT GGCTGTGATG	1140
	AGTGTCTTG CAGGGGCCG AGTAGGAGCA CTGGGGTGGG GCGGAATTG GGGTTACTCG	1200
	ATGTAAGGA TTCTTGTTG TTGTGTGAG ATCCAGTGCA GTTGTGATTT CTGTGGATCC	1260
25	CAGCTTGGTT CCAGGAATTT TGTTGTGATTG GCTTAAATCC AGTTTTCAT CTTCGACAGC	1320
	TGGGCTGGAA CGTGAACCTA GTAGCTGAAC CTGTCTGACC CGGTCACGTT CTTGGATCCT	1380
30	CAGAACTCTT TGCTCTTGTC GGGGTGGGG TGGGAACCTA CGTGGGGAGC GTGGGCTGAG	1440
	AAAATGTAAG GATTCTGGAA TACATATTCC ATGGGACTTT CCTTCCCTCT CTGCTTCCT	1500
	CTTTTCTGC TCCCTAACCT TTCGCCAAT GGGGCAGCAC CACTGACGTT TCTGGGCGGC	1560
35	CAGTGGGCT GCCAGTTCC TGTACTACTG CCTGTACTT TTCATTTTGG CTCACCGTGG	1620
	ATTTTCTCAT AGGAAGTTG GTCAGAGTGA ATTGAATATT GTAAGTCAGC CACTGGGACC	1680
40	CGAGGATTC TGGGACCCG CAGTTGGGAG GAGGAAGTAG TCCAGCCTC CAGGTGGCGT	1740
	GAGAGGCAAT GACTCGTTAC CTGCCGCCA TCACCTTGGA GGCCTTCCCT GGCCTTGAGT	1800
	AGAAAAGTCG GGGATCGGG CAAGAGAGGC TGAGTACGGA TGGGAAACTA TTGTGCACAA	1860
45	GTCTTCCAG AGGAGTTTCT TAATGAGATA TTTGTATTTA TTTCCAGACC AATAAATTTG	1920
	TAACTTTGCA AAAAAAAAA AAAAAAAAA AAAAAAAAA AAAAAAAAA AAAAAAACTC	1980
50	GAGGGGGGCC CGTACCCAAT TCGCCGTATA TGATCGTAAA CAATC	2025

55 (2) INFORMATION FOR SEQ ID NO: 310:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 3026 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

60

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 310:

5	TAGGCAGCAC TGAAATATCC TAACCCCTA AGCTCCAGGT GCCCTGTGGN ACGAGCAACT	60
	GGACTATAGC AGGGCTGGGC TCTGTCTTCC TGGTCATAGG CTCACTCTTT CCCCCAAATC	120
	TTCTCTGGA GCTTTGCAGC CAAGGTGCTA AAAGGAATAG GTAGGAGACC TCTTCTATCT	180
10	AATCCTTAAA AGCATAATGT TGAACATTCA TTCAACAGCT GATGCCCTAT AACCCCTGCC	240
	TGGATTCTTT CCTATTAGGC TATAAGAAGT AGCAAGATCT TTACATAATT CAGAGTGGTT	300
15	TCATTGCCTT CCTACCTCTCT CTAATGGCCC CTCCATTATAT TTGACTAAAG CATCACACAG	360
	TGGCACTAGC ATTATACCAA GAGTATGAGA AATACAGTGC TTTATGGCTC TAACATTACT	420
	GCCTTCAGTA TCAAGGCTGC CTGGAGAAAG GATGGCAGCC TCAGGGCTTC CTTATGTCCT	480
20	CCACCACAAG AGCTCCTTGA TGAAGGTCAT CTTTTTCCCC TATCCTGTC TCCCCCTCCC	540
	CGCTCCTAAT GGTACGTGGG TACCCAGGCT GGTTCCTGGG CTAGGTAGTG GGGACCAAGT	600
25	TCATTACCTC CCTATCAGTT CTAGCATAGT AAACACGGT ACCAGTGTGA GTGGGAAGAG	660
	CTGGGTTTTT CTAGTATACC CACTGCATCC TACTCCTACC TGGTCAACCC GCTGCTTCCA	720
	GGTATGGGAC CTGCTAAGTG TGAATTACC TGATAAGGGA GAGGGAATA CAAGGAGGGC	780
30	CTCTGGTGTT CTTGGCCTCA GCCAGCTGCC CACAAGCCAT AAACCAATAA AACAAGAATA	840
	CTGAGTCAGT TTTTATCTG GGTTCCTTTC ATTCCTACTG CACTTGGTGC TGCTTTGGCT	900
35	GACTGGGAAC ACCCCATAAC TACAGAGTCT GACAGGAAGA CTGGAGACTG TCCACTTCTA	960
	GCTCGGAAC TACTGTGTAA ATAACTTTT AGAACTGCTA CCATGAAGTG AAAATGCCAC	1020
	ATTTTGCTTT ATAATTTCTA CCCATGTTGG GAAAACTGG CTTTTTCCCA GCCCTTTCCA	1080
40	GGGCATAAAA CTCAACCCCT TCGATAGCAA GTCCCATCAG CCTATTATTT TTTTAAAGAA	1140
	AACTTGCACT TGTTTTTCTT TTTACAGTTA CTTCCTTCCT GCCCCAAAAT TATAAACTCT	1200
45	AAGTGTA AAAAGTCTTA ACAACAGCTT CTTGCTTGTA AAAATATGTA TTATACATCT	1260
	GTATTTTAA ATTCTGCTCC TGAAAAATGA CTGTCCCAT CTCCACTCAC TGCATTTGGG	1320
	GCCTTTCCCA TTGGTCTGCA TGTCTTTTAT CATTCAGGC CAGTGGACAG AGGGAGAAGG	1380
50	GAGAACAGGG GTCGCCAACA CTGTGTGTC TTTCTGACTG ATCCTGAACA AGAAAGAGTA	1440
	AACTGAGGC GCTCGCTCCC ATGCACAACT CTCCAAAACA CTTATCCTCC TGCAAGAGTG	1500
55	GGCTTTCCAG GGTCTTTACT GGAAGCAGT TAAGCCCCCT CCTCACCCTC TCCTTTTTC	1560
	TTTCTTTACT CCTTTGGCTT CAAAGGATTT TGGAAAAGAA ACAATATGCT TTCACTCAT	1620
60	TTTCAATTTT TAAATTTGCA GGGGATACTG AAAAAACGG CAGGTGGCCT AAGGCTGCTG	1680

TAAAGTTGAG GGGAGAGGAA ATCTTAAGAT TACAAGATAA AAAACGAATC CCCTAAACAA 1740
AAAGAACAAT AGAACTGGTC TTCCATTTTG CCACCTTTCC TGTTCATGAC AGCTACTAAC 1800
5 CTGGAGACAG TAACATTTCA TTAACCAAAG AAAGTGGGTC ACCTGACCTC TGAAGAGCTG 1860
AGTACTCAGG CCACTCCAAT CACCCCTACAA GATGCCAAGG AGGTCCCAGG AAGTCCAGCT 1920
CCTTAAACTG ACGCTAGNMA ATAAACCTGG GCAAGTGAGG CAAGAGAAAT GAGGAAGAAT 1980
10 CCATCTGTGA GGTGAYAGGC AAGGATGAAA GACAAAGAAG GAAAAGAGTA TCAAAGGCAG 2040
AAAGGAGATC ATTTAGTTGG GTCTGAAAGG AAAAGTCTTT GCTATCCGAC ATGTACTGCT 2100
15 AGTACCTGTA AGCATTTTAG GTCCCAGAAT GGAAAAAAA ATCAGCTATT GGTAATATAA 2160
TAATGTCCTT TCCCTGGAGT CAGTTTTTTT AAAAAGTTAA CTCCTAGTTT TTACTTGTTT 2220
AATTCATAAA GAGAAGGGAG CTGAGGCCAT TCCCTGTAGG AGTAAAGATA AAAGGATAGG 2280
20 AAAAGATTCA AAGCTCTAAT AGAGTCACAG CTTTCCCAGG TATAAACCT AAAATTAAGA 2340
AGTACAATAA GCAGAGGTGG AAAATGATCT AGTTCCTGAT AGCTACCCAC AGAGCAAGTG 2400
25 ATTTATAAAT TTGAAATCCA AACTACTTTC TTAATATCAC TTTGGTCTCC ATTTTTCCTA 2460
GGACAGGAAA TATGTCCCCC CCTAACTTTC TTGCTTCAAA AATTAAAATC CAGCATCCCA 2520
AGATCATCTT ACAAGTAATT TTGCACAGAC ATCTCCTCAC CCCAGTGCCT GTCTGGAGCT 2580
30 CACCCCAAGGT CANCCAACA ACTTGGTTGT GAACCCAACT GCCTTAACCT TCTGGGGGAG 2640
GGGGATTAGC TAGACTAGGA GACCCAGAAG TGAATGGGAA AGGGTGAGGA CTTCACAATG 2700
35 TTGGCCTGTG AGAGCTTGAT TAGAAGCCAA GACAGTGGCA GCAAAGGAAG ACTTGCCCCA 2760
GGAAAAACCT GTGGGTTGTG CTAATTTCTG TCCAGAAAAT AGGGTGAGCA GAAGCTTGTTG 2820
GGGTGCATGG AGGAATTGGG ACCTGGTTAT GTTGTATTTC TCGGACTGTG AATTTTGGTG 2880
40 ATGTAAACA GAATATTCTG TAAACCTAAT GTCTGTATAA ATAATGAGCG TTAACACAGT 2940
AAAATATTCA ATAAGAAGTC AAAAAAAAAA AAAAAAACT CGAGGGGGG CCCGGTACCC 3000
45 AATTTNCCAA ATAGAGATNG TATTAC 3026

50 (2) INFORMATION FOR SEQ ID NO: 311:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 712 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 311:

60 GCAGGCTTTG TGCTCACCTA CAAGCTGGGT GAGCAGGGTG CCAGCAGCCT GTTCTCTCTT 60

CTCTGCTGG ACCACGGCGT TTCTGCTCCC GAGTTGGGAC TGTGGAATGG TGTGGGTGCT 120
 GTGGTCTGCT CCATCGCTGG CTCTCCCTG GGTGGGACCT TGCTGGCCAA GCACTGGAAA 180
 5 CTGCTGCCCTC TGTGARGTC GGTGCTGCGC TTCCGCCTCG GGGGCCTAGC CTGTCAGACT 240
 GCCTTGGTCT TCCACCTGGA CACCCTGGGG GCCAGCATGG ACGCTGGCAC AATCTTGAGA 300
 10 GGGTCAGCCT TGCTGAGCCT ATGTCTGCAG CACTTCTTGG GAGGCCTGGT CACCACAGTC 360
 ACCTTCACTG GGATGATGCG CTGCAGCCAG CTGGCCCCA GGGCCTGCAG GCCACACACT 420
 ACAGCCTTCT GGGCACGCTG GAGCTGCTGG GGAAGCTGCT GCTGGGCACT CTGCGGAGGC 480
 15 CTGGCTGATG GGTGGGGCC ACATCCCTGC TTCTTGCTCC TGCTCATCCT CTCTGCCTTT 540
 CCCGTCTGT ACCTGGACCT AGCACCCAGC ACCTTCTCTT GAGCTGAGTG GCTGGAGTGG 600
 20 TCAATAAAGC CACATGTGCC TGTGGCCCAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA 660
 AACTGGAGGG GGGGCCCGT ACCCAAATCG CCGATATGA TCGTAAACAA TC 712

25

(2) INFORMATION FOR SEQ ID NO: 312:

30 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1289 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 312:

CAAAATTTC AACTTTTCAG GAGGGCAAGA GAATATCAAA CAAAGATTTC TGGAAGTATT 60
 TGCCCAACCT TCTGGTTGAG CTGCAAGAAA ATATTTATGG TGAGAACTTT TCTGTTTCCC 120
 40 GTTATGGGT TTTTGGTTGG TTTTGTGTTG TTTTCTACTA TGCTTTGGTC TGTA AAAATA 180
 TGCAACTGAA CTACATTCAG AAGGAAATAT TGCTACATA GAATATTATA TGAAGTTGGT 240
 45 ACATAATTCT GATGAGGAAA AAAATCTTT GCAATCTTT AAGCCATATT GTTGTTTTTC 300
 TGTGTGTTT TCCCTGGATG AAAATATCAG TATTAAGTAG ACAGCATATT ATTCAAGTGT 360
 TTAGACTTAT TAATATGTC TTGTCCTGTA TTTATACATA TGTGTATTTT GGAAAGTATT 420
 50 GCCTTTTITA AGGGAAGCTA TAATTCGATA CATAGTGAAA AAGGGAATGG TGACCCCTTT 480
 GTGCCTCTTC CACTGAGGAT AACAAACAGC ATTGTAATCC ATTCTCTTGC ACCTTCTTCT 540
 55 TCTTATCTTG TTATTACGGT TTTATTAATT TTGTAGAGGG ACAGGGAGTG GGCAAGGGGA 600
 AGAAGCAGCT TATTTGACTA ACCAGCCCT CTGTGGTCCA CCAGCGTCTT GGCTTGGTGG 660
 GAGGGCTCTC AATCAGCAGG GCCCCAGGAG GGAAGAAGAA GTGGGGCAA GCCTGGCCTC 720
 60

GCGGCTCGGG AGCTTTGCCA TCTGAGCCAC GCCTCCTCCA GGCCATGCTC CTTGAACTTG 780
 GAAATGTCAA CCGGAGCCCT TACACCAGCC CTCCAGCATC TAATAGACTT GAATCTACTC 840
 5 TAAACGAATA TTTAATCCAA CCTCACTACA TTGTAGCTCA GTCCAACGAC TAACCCTGAA 900
 ATGGGGGTGT TCCAGCCTTC AGCGAGATGG CCAAGCGGTC CCCTGGGGGC TGTGGCAGCG 960
 GGCTTATCCT TCTCTGTTGC CAACCTTGCC GTCGACCTC CTCCGCCCCC ATGCGGTGAC 1020
 10 CCGTCCGTG TCTGTGCTG TCCATACGTG TGAGTCCAGC TAAAAAGACA AAACAGAACC 1080
 CGTGGGCCCA GCTCGGAAGG TCGTGGAGA AGGCTCCGAC GTCTCCGAAG TGCAGCCCTT 1140
 15 GGGATGGCAT TCCGTGTGT GTCTTATTC TGGAGAATCT GTATACGGCT CGCCTATAGA 1200
 AATATAGCCT CTTCATGCTG TATTAAAAGG ACTTTTAAAA GCAAAAAAAA AAAAAAAAAA 1260
 CTTGAGGGGG GGNCCGGTAC CCAATTNTC 1289
 20

25 (2) INFORMATION FOR SEQ ID NO: 313:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 22 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 313:

Met Phe Leu Ile Phe Val Tyr Phe Leu Lys Ile Leu Phe Ser Ser Ser
 1 5 10 15

35 Leu Pro Phe Leu Trp Leu
 20

40 (2) INFORMATION FOR SEQ ID NO: 314:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 128 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 314:

Met Met Phe Leu Thr Gln Gly Gly Pro Leu Pro Ser Thr Arg Ala Arg
 1 5 10 15

50 Pro Thr Cys Gln Ala Gly Ala Leu Pro Lys Pro Ser Gly Leu Leu Gly
 20 25 30

55 Val Thr Cys Trp Asn Gly Leu Lys Gly Pro Leu Cys Gly Asn Arg Cys
 35 40 45

Ser Pro Asn Thr Leu Leu Leu Ala Ala Arg Gln Ala Leu Trp Lys Gly
 50 55 60

60 Arg Gly Arg Thr His Gln Asp Leu Pro Gly Pro Leu Gln Gly Arg Gln

	65		70		75		80
	Leu Gly Pro Glu	Pro Lys His Leu Ala	Leu Leu Pro Pro Arg Gly Gln				
		85	90			95	
5	Glu Ala Ser Trp	Ala Ser Ser Leu Pro Gly Gln Gly	Pro Leu Pro Leu				
		100	105			110	
	Pro His Ile Asn Cys Thr Val Phe Ser Leu Lys Ala Ser Phe Ile Lys						
10		115	120			125	

15

(2) INFORMATION FOR SEQ ID NO: 315:

20 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 28 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 315:

25 Met Gln Phe Leu Leu Thr Ala Phe Leu Leu Val Pro Leu Leu Ala Leu
1 5 10 15

Cys Asp Val Pro Ile Ser Leu Gly Phe Ser Pro Ser
20 25

30

(2) INFORMATION FOR SEQ ID NO: 316:

35 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 64 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 316:

40 Met Asp Gly Phe Ser Ser Arg Leu Phe Ser Ser Leu Pro Phe Val Ala
1 5 10 15

Leu Gln Trp Phe Ile Val Ile Ser His Leu Leu Ser Leu Ser Leu Ser
45 20 25 30

Ala Cys Cys Tyr Gln Thr His Cys Ser Leu Xaa Gln Leu Ser Ser Ala
35 40 45

50 Phe Ser Xaa Met Gly Glu Ser Cys Val Gly Glu Arg Glu Tyr Xaa Phe
50 55 60

55

(2) INFORMATION FOR SEQ ID NO: 317:

60 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 21 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 317:

5

Met Pro Leu Ile Asn Leu Leu Leu Tyr Tyr Val Pro Asn Gly Gly
1 5 10 15

10 Lys Gln Asp Lys Lys
20

(2) INFORMATION FOR SEQ ID NO: 318:

15

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 39 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 318:

Met Gly Arg His Leu Val Leu Val Met Phe Ile Thr Thr Ser Leu His
1 5 10 15

25 Ser Gly Thr Pro Val Pro Glu Asn Val Ile Cys Gly Val Thr Lys Gly
20 25 30

Pro Gln Gly Lys Lys Lys Lys
35

30

(2) INFORMATION FOR SEQ ID NO: 319:

35

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 33 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 319:

40

Met Leu Trp Trp Ser Arg Asp Tyr Thr Met Val Phe Leu Leu Phe Thr
1 5 10 15

45 Met Val Phe Thr Gly Asp Leu Val Ile Arg Gly Arg Thr Glu Leu Ser
20 25 30

Leu

50

(2) INFORMATION FOR SEQ ID NO: 320:

(i) SEQUENCE CHARACTERISTICS:

55

(A) LENGTH: 88 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 320:

60 Met Val Cys Ser Ser Leu Cys Asp Ile Gly Gly Ile Ile Thr Pro Phe

[illegible]

20 (2) INFORMATION FOR SEQ ID NO: 321:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 23 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 321:

30 Met Gln Pro Gly Ala Gly Val Leu Val Leu Gly Leu Leu Leu Pro Pro
1 5 10 15
Pro Gln Ser Pro Ser Leu Ser
20

35

(2) INFORMATION FOR SEQ ID NO: 322:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 27 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 322:

45 Met Thr Phe Thr Leu Gly Asp Ser Gln Val Leu Leu Ile Asn Leu Phe
1 5 10 15
Pro Ser Met Pro Ser Gly Ser Cys Ala Arg Pro
20 25

50

(2) INFORMATION FOR SEQ ID NO: 323:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 64 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 323:

60 Met Cys Leu Glu Cys Trp Ala Glu Asn Leu Gly Pro His His Thr Ser

549

1 5 10 15
 Ser Leu Leu Asn Pro Arg His Leu Pro Ser Ile Pro Ala Met Phe Pro
 20 25 30
 5 Val Ser Ser Gly Cys Phe Gln Glu Gln Gln Glu Met Asn Lys Ser Leu
 35 40 45
 10 Val Ser Cys Leu Phe Val Leu His Phe Val Leu His Cys Ile Phe Xaa
 50 55 60

 15
 (2) INFORMATION FOR SEQ ID NO: 324:

 20 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 196 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 324:
 25 Met Leu Ser Thr Ser Glu Tyr Ser Gln Ser Pro Lys Met Glu Ser Leu
 1 5 10 15

 Ser Ser His Arg Ile Asp Glu Asp Gly Glu Asn Thr Gln Ile Glu Asp
 20 25 30
 30 Thr Glu Pro Met Ser Pro Val Leu Asn Ser Lys Phe Val Pro Ala Glu
 35 40 45

 Asn Asp Ser Ile Leu Met Asn Pro Ala Gln Asp Gly Glu Val Gln Leu
 35 50 55 60

 Ser Gln Asn Asp Asp Lys Thr Lys Gly Asp Asp Thr Asp Thr Arg Asp
 65 70 75 80
 40 Asp Ile Ser Ile Leu Ala Thr Gly Cys Lys Gly Arg Glu Glu Thr Val
 85 90 95

 Ala Glu Glu Val Cys Ile Asp Leu Thr Cys Asp Ser Gly Ser Gln Ala
 100 105 110
 45 Val Pro Ser Pro Ala Thr Arg Ser Glu Ala Leu Ser Ser Val Leu Asp
 115 120 125

 Gln Glu Glu Ala Met Glu Ile Lys Glu His His Pro Glu Glu Gly Ser
 50 130 135 140

 Ser Gly Ser Glu Val Glu Glu Ile Pro Glu Thr Pro Cys Glu Ser Gln
 145 150 155 160
 55 Gly Glu Glu Leu Lys Glu Glu Asn Met Glu Ser Val Pro Leu His Leu
 165 170 175

 Ser Leu Thr Glu Thr Gln Ser Gln Gly Leu Cys Leu Arg Arg His Pro
 180 185 190
 60

Lys Lys Lys Lys
195

5

(2) INFORMATION FOR SEQ ID NO: 325:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 252 amino acids

10

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 325:

15 Met Gly Gly Asp Leu Val Leu Gly Leu Gly Ala Leu Arg Arg Arg Lys
1 5 10 15

Arg Leu Leu Glu Gln Glu Lys Ser Leu Ala Gly Trp Ala Leu Val Leu
20 20 25 30

20 Ala Xaa Xaa Gly Ile Gly Leu Met Val Leu His Ala Glu Met Leu Trp
35 40 45

Phe Gly Gly Cys Ser Ala Val Asn Ala Thr Gly His Leu Ser Asp Thr
50 55 60

25 Leu Trp Leu Ile Pro Ile Thr Phe Leu Thr Ile Gly Tyr Gly Asp Val
65 70 75 80

30 Val Pro Gly Thr Met Trp Gly Lys Ile Val Cys Leu Cys Thr Gly Val
85 90 95

Met Gly Val Cys Cys Thr Ala Leu Leu Val Ala Val Val Ala Arg Lys
100 105 110

35 Leu Glu Phe Asn Lys Ala Glu Lys His Val His Asn Phe Met Met Asp
115 120 125

Ile Gln Tyr Thr Lys Glu Met Lys Glu Ser Ala Ala Arg Val Leu Gln
130 135 140

40 Glu Ala Trp Met Phe Tyr Lys His Thr Arg Arg Lys Glu Ser His Ala
145 150 155 160

45 Ala Arg Xaa His Gln Arg Xaa Leu Leu Ala Ala Ile Asn Ala Phe Arg
165 170 175

Gln Val Arg Leu Lys His Arg Lys Leu Arg Glu Gln Val Asn Ser Met
180 185 190

50 Val Asp Ile Ser Lys Met His Met Ile Leu Tyr Asp Leu Gln Gln Asn
195 200 205

Leu Ser Ser Ser His Arg Ala Leu Glu Lys Gln Ile Asp Thr Leu Ala
210 215 220

55 Gly Lys Leu Asp Ala Leu Thr Glu Leu Leu Ser Thr Ala Leu Gly Pro
225 230 235 240

60 Arg Gln Leu Pro Glu Pro Ser Gln Gln Ser Lys Xaa
245 250

(2) INFORMATION FOR SEQ ID NO: 326:

5

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 68 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 326:

Met Trp Arg Cys Arg Gly Lys Leu Ser Phe Pro Leu Phe Ala Val Val
1 5 10 15

15 Ile Val Ser Cys Arg Lys Asp Gly Pro Asp Ala Ala Ala Ala Pro Ala
20 25 30

Val Ile Lys Asn Asn Ser His Tyr Gln Thr Ser Lys Ala Leu Glu Leu
35 40 45

20

Glu Lys Thr Thr Glu Asn Lys Glu Ser Asn Pro Phe Ile Leu Gln Val
50 55 60

Asn Lys Leu Xaa
65

25

(2) INFORMATION FOR SEQ ID NO: 327:

30

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 84 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 327:

Met Gly Glu Gly Lys Asn Gly Phe Gly Gly Phe Val His Thr Ala Asp
1 5 10 15

40 Ala Cys Trp Glu Gly Val His Ser Glu Pro Val Cys Arg Thr Val His
20 25 30

Thr Val His Thr Cys His His Gln Ala Phe Leu Val Leu Ile Gly Trp
35 40 45

45

Ser Lys Ser Gly Lys Glu Arg Lys Glu Ala Phe Leu Thr Ala Ile Ile
50 55 60

50 Leu Asn Ser Arg Ser Ile His Ile Ser Cys Ser Trp Pro Pro Ser Pro
65 70 75 80

Val Pro Gln Xaa

55

(2) INFORMATION FOR SEQ ID NO: 328:

(i) SEQUENCE CHARACTERISTICS:

60

(A) LENGTH: 36 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 328:

5 Met Leu Leu Ile Asn Leu Leu Trp Leu Val Thr Met Ile Lys Ser Val
 1 5 10 15
 Ile Asn Asn Asn Ile Ile Leu Phe Leu Lys Lys Lys Ser Leu Phe Phe
 20 25 30
 10 Ile Asp Ser Val
 35

15

(2) INFORMATION FOR SEQ ID NO: 329:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 63 amino acids

20

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 329:

25 Met Thr Phe Pro Phe Glu Lys Lys Ile Val Ala Phe Ser Ala Phe Tyr
 1 5 10 15
 Leu Ile Pro Gly Glu Ser Arg Leu Ala Pro Thr Phe Asn Pro Ser Ala
 20 25 30
 30 Asp Met Thr Val Ile Leu Arg Gly Arg Ala Gln His Lys Thr Ala Met
 35 40 45
 Leu Glu Ser Tyr Asn Trp Lys Val Ser Cys Gln Leu Arg Glu Xaa
 50 55 60
 35

(2) INFORMATION FOR SEQ ID NO: 330:

40

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 35 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 330:

45

Met His Ser Lys Gly Ser Ser Leu Leu Leu Phe Leu Pro Gln Leu Ile
 1 5 10 15

50

Leu Ile Leu Pro Val Cys Ala His Leu His Glu Glu Leu Asn Cys Cys
 20 25 30

Phe His Arg
 35

55

(2) INFORMATION FOR SEQ ID NO: 331:

(i) SEQUENCE CHARACTERISTICS:

60

(A) LENGTH: 23 amino acids

553

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 331:

5 Met Gly Ala Leu Val Leu Leu Leu Cys Leu Leu Val Gly Val Gln Gln
 1 5 10 15
 Ser Gly Ser Val Trp Asp Ser
 20

10

(2) INFORMATION FOR SEQ ID NO: 332:

15

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 40 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 332:

20

Met Gln Ser Ala Glu Ile Leu Ser Trp Thr Asp Val Leu His Asp Phe
 1 5 10 15

25

Leu Phe Ser Leu Phe Leu Trp Pro Ala Phe Glu Asp Arg Ala Leu Leu
 20 25 30

Ile Phe Thr Leu Asn Gln Ile Val
 35 40

30

(2) INFORMATION FOR SEQ ID NO: 333:

35

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 111 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 333:

40

Met Gln Ser Leu Val Gln Trp Gly Leu Asp Ser Tyr Asp Tyr Leu Gln
 1 5 10 15

Asn Ala Pro Pro Gly Phe Phe Pro Arg Leu Gly Val Ile Gly Phe Ala
 20 25 30

45

Gly Leu Ile Gly Leu Leu Leu Ala Arg Gly Ser Lys Ile Lys Lys Leu
 35 40 45

Val Tyr Pro Pro Gly Phe Met Gly Leu Ala Ala Ser Leu Tyr Tyr Pro
 50 55 60

50

Gln Gln Ala Ile Val Phe Ala Gln Val Ser Gly Glu Arg Leu Tyr Asp
 65 70 75 80

55

Trp Gly Leu Arg Gly Tyr Ile Val Ile Glu Asp Leu Trp Lys Glu Asn
 85 90 95

Phe Gln Lys Pro Gly Asn Val Lys Asn Ser Pro Gly Thr Lys Xaa
 100 105 110

60

(2) INFORMATION FOR SEQ ID NO: 334:

5

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 106 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 334:

10

Met Ala Pro Ser Leu Leu Leu Ala Pro Leu Cys Ser Leu Glu Ala
 1 5 10 15

15

Val Leu Ser Ser Pro Leu Glu Lys Gln Cys Gln Leu Pro Gly Ile Phe
 20 25 30

Cys Gln Leu Gln Leu Pro Cys Pro Leu Leu Leu Ser Ala Gln Leu Leu
 35 40 45

20

Lys Gly Ile Val Xaa Pro Arg Cys Pro Ala Ser Leu Pro Gln Pro Pro
 50 55 60

25

His Pro Ala Pro Ser Trp His Leu Pro Leu His Cys Thr Glu Arg Xaa
 65 70 75 80

Pro His His Leu Pro Leu Gln Gly Gly Ser Ser Asn Met Glu Glu Xaa
 85 90 95

30

Asn Tyr Arg Gly Tyr Xaa Asp Ala Gln Leu
 100 105

(2) INFORMATION FOR SEQ ID NO: 335:

35

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 50 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 335:

40

Met Thr Thr Cys Leu Phe Gly Leu Leu Ser Cys Glu Met Ser Ala Gln
 1 5 10 15

45

Val Ser Gln Lys Ser Cys Val Tyr Asp Glu Ser Glu Cys Phe Ser Ser
 20 25 30

Val Gly Gln Leu Leu Ala Leu Leu Ile Leu Val Tyr Val Leu Pro Ser
 35 40 45

50

Ile Xaa
 50

55

(2) INFORMATION FOR SEQ ID NO: 336:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 48 amino acids

(B) TYPE: amino acid

60

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 336:

5 Met Leu Trp Lys Cys Ser Gln Asn Ile Ala Arg Cys Leu Leu Leu Leu
 1 5 10 15

Leu Ala Leu Val Glu Ile Lys Leu Glu Asp Leu Gln Ser Gln Leu His
 20 25 30

10 Pro Thr Trp Lys Ser Ile Pro Gly Pro Ser Pro Arg Asn Gln His Arg
 35 40 45

15

(2) INFORMATION FOR SEQ ID NO: 337:

20

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 41 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 337:

25

Met Leu Ile Pro Leu Gln Cys Leu Phe Ser Ser Asp Arg Met Leu Thr
 1 5 10 15

Phe Leu Thr Pro Trp Gln Lys Gly Glu Lys Cys Val Leu Gly Trp Val
 20 25 30

Thr Lys Phe Leu Ser Glu Ile Ser Xaa
 35 40

35

(2) INFORMATION FOR SEQ ID NO: 338:

40

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 76 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 338:

45

Met Thr Phe Ser Ser Leu Lys Leu Phe Val Leu Thr Cys Ile Ile Lys
 1 5 10 15

Gly Leu Glu Arg Phe Ile Ile Leu Arg Glu Val Cys Asn Gln Glu Ile
 20 25 30

50 Gln Arg Ser Leu Ser Ser Asn Leu Val His Val Leu Leu Gln Pro Ala
 35 40 45

Thr Phe Lys Asp Val Leu Val Thr Glu Ile Ile Cys Leu Cys Met Cys
 50 55 60

Leu Tyr Ser Ile Lys Tyr Met Pro Pro Gln Lys Lys
 65 70 75

60

(2) INFORMATION FOR SEQ ID NO: 339:

- 5 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 31 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 339:

10 Lys Val Tyr Ile Phe Leu Ile Phe Met Val Leu Ile Leu Pro Ser Leu
1 5 10 15
Gly Leu Thr Arg Tyr Met Pro Pro Xaa Ser Xaa Leu Asn Ser Glu
20 25 30
15

(2) INFORMATION FOR SEQ ID NO: 340:

- 20 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 42 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 340:

25 Met Ala Lys Ile Ser Pro Phe Glu Val Val Lys Arg Thr Ser Val Pro
1 5 10 15
30 Val Leu Val Gly Leu Val Ile Val Ile Val Ala Thr Glu Leu Met Val
20 25 30
Pro Gly Thr Ala Ala Ala Val Thr Gly Lys
35 40
35

(2) INFORMATION FOR SEQ ID NO: 341:

- 40 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 26 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 341:

45 Met Arg Leu Phe Phe Ile Gly Phe Leu Leu Leu Phe Ser Phe Gly Leu
1 5 10 15
Leu Arg Gln Pro Ser Leu Ser Ala Glu His
20 25
50

(2) INFORMATION FOR SEQ ID NO: 342:

- 55 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 26 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 342:
- 60

Met Val Phe Ser Val Ser Ser Ala Leu Ala Leu Leu Leu Met Leu Leu
 1 5 10 15
 5 Arg Ser Ser Asp Leu Ala Lys Lys Thr Glu
 20 25

(2) INFORMATION FOR SEQ ID NO: 343:
 10

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 157 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 343:
 15

Met Ser Leu Glu Phe Tyr Gln Lys Lys Lys Ser Arg Trp Pro Phe Ser
 1 5 10 15
 20 Asp Glu Cys Ile Pro Trp Glu Val Trp Thr Val Lys Val His Val Val
 20 25 30
 Ala Leu Ala Thr Glu Gln Glu Arg Gln Ile Cys Arg Glu Lys Val Gly
 35 40 45
 25 Glu Lys Leu Cys Glu Lys Ile Ile Asn Ile Val Glu Val Met Asn Arg
 50 55 60
 His Glu Tyr Leu Pro Lys Met Pro Thr Gln Ser Glu Val Asp Asn Val
 30 65 70 75 80
 Phe Asp Thr Gly Leu Arg Asp Val Gln Pro Tyr Leu Tyr Lys Ile Ser
 85 90 95
 35 Phe Gln Ile Thr Asp Ala Leu Gly Thr Ser Val Thr Thr Thr Met Arg
 100 105 110
 Arg Leu Ile Lys Asp Thr Leu Pro Ser Glu Arg Arg Trp Ile Ser Gly
 115 120 125
 40 Ser Ser Leu Met Ala Pro Arg Pro Trp Leu Leu Gly Ile Ala Leu Leu
 130 135 140
 Gly Leu Trp Ala Leu Glu Pro Ala Leu Gly His Trp Xaa
 45 145 150 155

(2) INFORMATION FOR SEQ ID NO: 344:
 50

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 520 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 344:
 55

Met Phe Leu Leu Pro Leu Pro Ala Ala Gly Arg Val Val Val Arg Arg
 1 5 10 15
 60 Leu Ala Val Arg Arg Phe Gly Ser Arg Ser Leu Ser Thr Ala Asp Met

559

340 345 350
 Lys Asn Gly Lys Thr Ile Gln Val Asp Asn Thr Asp Ala Glu Gly Arg
 355 360 365
 5 Leu Ile Leu Ala Asp Ala Leu Cys Tyr Ala His Thr Phe Asn Pro Lys
 370 375 380
 Xaa Ile Leu Asn Ala Ala Thr Leu Thr Gly Ala Met Asp Val Ala Leu
 10 385 390 395 400
 Gly Ser Gly Ala Thr Gly Val Phe Thr Asn Ser Ser Trp Leu Trp Asn
 405 410 415
 15 Lys Leu Phe Glu Ala Ser Ile Glu Thr Gly Asp Arg Val Trp Arg Met
 420 425 430
 Pro Leu Phe Glu His Tyr Thr Arg Gln Val Val Asp Cys Gln Leu Ala
 435 440 445
 20 Asp Val Asn Asn Ile Gly Lys Tyr Arg Ser Ala Gly Ala Cys Thr Ala
 450 455 460
 Ala Ala Phe Leu Lys Glu Phe Val Thr His Pro Lys Trp Ala His Leu
 25 465 470 475 480
 Asp Ile Ala Gly Val Met Thr Asn Lys Asp Glu Val Pro Tyr Leu Arg
 485 490 495
 30 Lys Gly Met Thr Gly Arg Pro Thr Arg Thr Leu Ile Glu Phe Leu Leu
 500 505 510
 Arg Phe Ser Gln Asp Asn Ala Xaa
 515 520
 35

(2) INFORMATION FOR SEQ ID NO: 345:

40 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 39 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 345:
 45 Thr Ile Leu Phe Leu Phe Leu Gln Leu Ser Ala Leu Arg Leu Ile Val
 1 5 10 15
 Gly Lys Asp Ser Ile Asp Ile Asp Ile Ser Ser Arg Arg Arg Glu Asp
 50 20 25 30
 Gln Ser Leu Arg Leu Asn Ala
 35

55

(2) INFORMATION FOR SEQ ID NO: 346:

60 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 234 amino acids

560

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 346:

5 Met Thr Ser Glu Leu Asp Ile Phe Val Gly Asn Thr Thr Leu Ile Asp
 1 5 10 15
 Glu Asp Val Tyr Arg Leu Trp Leu Asp Gly Tyr Ser Val Thr Asp Ala
 20 25 30
 10 Val Ala Leu Arg Val Arg Ser Gly Ile Leu Glu Gln Thr Gly Ala Thr
 35 40 45
 Ala Ala Val Leu Gln Ser Asp Thr Met Asp His Tyr Arg Thr Phe His
 15 50 55 60
 Met Leu Glu Arg Leu Leu His Ala Pro Pro Lys Leu Leu His Gln Leu
 65 70 75 80
 20 Ile Phe Gln Ile Pro Ser Arg Gln Ala Leu Leu Ile Glu Arg Tyr
 85 90 95
 Tyr Ala Phe Asp Glu Ala Phe Val Arg Glu Val Leu Gly Lys Lys Leu
 100 105 110
 25 Ser Lys Gly Thr Lys Lys Asp Leu Asp Asp Ile Ser Thr Lys Thr Gly
 115 120 125
 Ile Thr Leu Lys Ser Cys Arg Arg Gln Phe Asp Asn Phe Lys Arg Val
 30 130 135 140
 Phe Lys Val Val Glu Glu Met Arg Gly Ser Leu Val Asp Asn Ile Gln
 145 150 155 160
 35 Gln His Phe Leu Leu Ser Asp Arg Leu Ala Arg Asp Tyr Ala Ala Ile
 165 170 175
 Val Phe Phe Ala Asn Asn Arg Phe Glu Thr Gly Lys Lys Lys Leu Gln
 180 185 190
 40 Tyr Leu Ser Phe Gly Asp Phe Ala Phe Cys Ala Glu Leu Met Ile Gln
 195 200 205
 Asn Trp Thr Leu Gly Pro Val Asp Ser Gln Met Asp Asp Met Asp Met
 45 210 215 220
 Asp Leu Asp Arg Asn Phe Ser Arg Thr Xaa
 225 230

50

(2) INFORMATION FOR SEQ ID NO: 347:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 169 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 347:

60 Met Ala Ala Ala Val Ala Gly Met Leu Arg Gly Gly Leu Leu Pro Gln

561

1 5 10 15
 Ala Gly Arg Leu Pro Thr Leu Gln Thr Val Arg Tyr Gly Ser Lys Ala
 20 25 30
 5 Val Thr Arg His Arg Arg Val Met His Phe Gln Arg Gln Lys Leu Met
 35 40 45
 10 Ala Val Thr Glu Tyr Ile Pro Pro Lys Pro Ala Ile His Pro Ser Cys
 50 55 60
 Leu Pro Ser Pro Pro Ser Pro Pro Gln Glu Glu Ile Gly Leu Ile Arg
 65 70 75 80
 15 Leu Leu Arg Arg Glu Ile Ala Ala Val Phe Gln Asp Asn Arg Met Ile
 85 90 95
 Ala Val Cys Gln Asn Val Ala Leu Ser Ala Glu Asp Lys Leu Leu Ile
 100 105 110
 20 Ala Thr Pro Ala Ala Glu Thr Gln Asp Pro Asp Glu Gly Leu Pro Gln
 115 120 125
 25 Pro Gly Pro Glu Ser Pro Ser Trp Arg Ile Pro Ser Thr Lys Ile Cys
 130 135 140
 Cys Pro Phe Leu Trp Gly Thr Thr Cys Cys Trp Ser Val Lys Ser Pro
 145 150 155 160
 30 Arg Ser Arg Arg Trp Tyr Gly Ser Xaa
 165

35 (2) INFORMATION FOR SEQ ID NO: 348:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 43 amino acids

(B) TYPE: amino acid

40 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 348:

Met Lys Arg Ser Phe Leu Leu Pro Leu Leu Leu Val Gly Phe Leu Asp
 1 5 10 15
 45 Thr Ala His Leu Ile Leu Leu Glu Thr Leu Ser Val Cys Leu Trp Leu
 20 25 30
 50 Pro Ser Leu Ile Asp Ser Arg Cys Val Met Ser
 35 40

55 (2) INFORMATION FOR SEQ ID NO: 349:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 78 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

60 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 349:

Met Lys Glu Gly Pro Pro Cys Lys Arg His His Tyr Tyr Gln Asn Cys
 1 5 10 15
 5 Gly Ala Lys Leu Leu Val Ser Leu Phe Gly Glu Thr Asn Gln Ile His
 20 25 30
 Leu Leu Glu Thr Gln Val Gly Thr Glu Lys Gly Gly Glu Arg Ile Trp
 35 40 45
 10 Glu Glu Lys Trp Arg Ile Ser Ser Thr Val Leu Phe Ile Ser Val Asn
 50 55 60
 Ser Tyr Val Glu Gly Ser Val Leu Glu Ile Lys Leu Phe Tyr
 15 65 70 75

(2) INFORMATION FOR SEQ ID NO: 350:

20

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 24 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 350:

Met Ser Glu Ile Leu Ser Leu Leu Phe Cys Leu Leu Gly Pro Ala Leu
 1 5 10 15

30

Asp Glu Arg Arg Glu Glu Lys Asp
 20

(2) INFORMATION FOR SEQ ID NO: 351:

35

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 274 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 351:

Met Ser Ser Ala Gly Thr Ala Thr Pro Leu Glu Met Asp His Lys Leu
 1 5 10 15

45

Thr Ser Gln Pro Gly Arg Pro Ser Phe Tyr Cys Asn Ser Arg His Ser
 20 25 30

Ile Val Gly Ser Ser His Gln Leu Gly Phe Trp Phe Ser His Leu Glu
 35 40 45

50

Ser Ser Gly Leu Lys Val Phe Gln Val Ser Leu Pro Cys Glu Cys Val
 50 55 60

Asn Leu Pro Thr Arg Ile Ala Ser Val Val Leu Ser Leu Met Ser Leu
 65 70 75 80

55

Leu Val Val Gly Gln Ala Pro Ala Trp Glu Gly Ser Leu Leu Arg Gly
 85 90 95

60

563

Arg Pro Ala Gly Gly Ala His Leu Cys Ala Met Xaa Val Ile Glu Gly
 100 105 110
 5 Leu Val Val Asp Val Gly Glu Arg Ile Leu His Gly Gln Arg Glu Val
 115 120 125
 Gly Gln Val Ser Gln Val Leu Pro Ala Leu Ser Leu Gly Leu Val Phe
 130 135 140
 10 Leu Cys Gln Gly Thr Val Glu Lys Val Ser Gly Ala Ala His Cys Ser
 145 150 155 160
 Ser Leu Leu Cys Cys Leu Pro Trp Gln Cys Ser Gly Gly Gly Phe Pro
 165 170 175
 15 Thr Xaa Arg Cys Ser Arg Pro Tyr Phe Ser Ser His Lys Gly Val Ala
 180 185 190
 20 Ala Thr Leu Ala Leu Thr Cys His Cys Asp Lys Val His Val Ala Gly
 195 200 205
 Leu Gly Lys Asp Trp Ala Ile Glu Gln Arg Arg Arg Thr Cys Glu Ser
 210 215 220
 25 Asp Xaa Glu Xaa Xaa Pro Phe Thr Leu Ala Gly Leu Val Leu Val Leu
 225 230 235 240
 Arg Phe Cys Gln Val Val Leu Val Trp Ile Pro Gln Leu Gly Asp Lys
 245 250 255
 30 His Trp Arg Gly Met Thr Arg Leu Gly Arg Val Ser Leu Thr Ser Ser
 260 265 270
 35 Ile Xaa

40 (2) INFORMATION FOR SEQ ID NO: 352:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 47 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 352:

Met Ile Phe Thr Ser Val Thr Lys Gly Ile Leu Leu Ile Ala Leu Trp
 1 5 10 15
 50 Val Pro Leu Phe His Phe Met Leu Ile Asp Ser Ile Leu Gly Pro Ser
 20 25 30
 Arg Leu Leu Thr Asp Gly Val Pro Phe Asn Pro Trp His Val Xaa
 35 40 45
 55

(2) INFORMATION FOR SEQ ID NO: 353:

60 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 3 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 353:

5

Met Lys Thr

1

10

(2) INFORMATION FOR SEQ ID NO: 354:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 52 amino acids

15

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 354:

20 Met Ser Ile Ser Gly Thr Asp Gly Leu Ile Leu Leu Leu Val Gly Leu
1 5 10 15

Glu Ala Xaa Val Arg Ser Ser Lys Lys Trp Ile Pro Lys Ala Leu Xaa
20 25 30

25 Val Thr Gln Ala Lys Trp Asn Ser Trp Pro Ser Arg Arg Asn Ala Gly
35 40 45

Phe Ala Leu His
50

30

(2) INFORMATION FOR SEQ ID NO: 355:

35

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 132 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 355:

40

Met Glu His Cys Leu Tyr His Ser Val His Gly Ile Asn Pro Tyr Ile
1 5 10 15

45 His Lys Asn Thr His Pro Ser Ile Asn Ile Tyr Met Val Trp Asp Glu
20 25 30

Gln Val Asn Ser Phe Glu Arg Glu Phe Val Pro Phe Phe Phe Leu Ile
35 40 45

50 Ile Leu Leu Asn Cys Cys Gln Leu Ser Asn Lys Gln Thr Glu Lys Leu
50 55 60

Phe Gly Lys Thr Leu His Thr Pro Phe Leu Ser Ser Ala Leu Lys Tyr
65 70 75 80

55

Arg Leu Asn Thr His Ile Leu Pro Val Phe Ser Tyr Ser Asp Ser Ile
85 90 95

60 Leu Thr Cys His Leu Ile Leu Ala Ser Tyr Phe Ser His Val Tyr Leu
100 105 110

Pro Val Thr Cys Ile Cys Tyr Leu Asn Arg Lys Lys Asn Ile Gln Lys
 115 120 125

5 Lys Lys Asn Xaa
 130

10 (2) INFORMATION FOR SEQ ID NO: 356:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 204 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 356:

Met Gly Ser Arg Asp His Leu Phe Lys Val Leu Val Val Gly Asp Ala
 1 5 10 15

20 Ala Val Gly Lys Thr Ser Leu Val Gln Asp Tyr Ser Gln Asp Ser Phe
 20 25 30

25 Ser Lys His Tyr Lys Ser Thr Val Gly Val Asp Phe Ala Leu Lys Val
 35 40 45

Leu Gln Trp Ser Asp Tyr Glu Ile Val Arg Leu Gln Leu Trp Asp Ile
 50 55 60

30 Ala Gly Gln Glu Arg Phe Thr Ser Met Thr Arg Leu Tyr Tyr Arg Asp
 65 70 75 80

Ala Ser Ala Cys Val Ile Met Phe Asp Val Thr Asn Ala Thr Thr Phe
 85 90 95

35 Ser Asn Ser Gln Arg Trp Lys Gln Asp Leu Asp Ser Lys Leu Thr Leu
 100 105 110

40 Pro Asn Gly Glu Pro Val Pro Cys Leu Leu Leu Ala Asn Lys Cys Asp
 115 120 125

Leu Ser Pro Trp Ala Val Ser Arg Asp Gln Ile Asp Arg Phe Ser Lys
 130 135 140

45 Glu Asn Gly Phe Thr Gly Trp Thr Glu Thr Ser Val Lys Glu Asn Lys
 145 150 155 160

Asn Ile Asn Glu Ala Met Arg Val Leu Ile Glu Lys Met Met Arg Asn
 165 170 175

50 Ser Thr Glu Asp Ile Met Ser Leu Ser Thr Gln Gly Asp Tyr Ile Asn
 180 185 190

55 Leu Gln Thr Lys Ser Ser Ser Trp Ser Cys Cys Xaa
 195 200

60 (2) INFORMATION FOR SEQ ID NO: 357:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 47 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 357:

Met Ile Ser Leu Ile Phe Gln Leu Glu Glu Glu Lys Leu Val Glu Lys
 1 5 10 15

10 Phe Phe Phe Phe Leu Phe Phe Phe Leu Lys Lys Gly Ser Gln Gly Ser
 20 25 30

Asn Leu Lys Ile Val Pro Arg His Met Arg Val Val Leu Arg Gly
 35 40 45

15

(2) INFORMATION FOR SEQ ID NO: 358:

20 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 73 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 358:

Met Thr Tyr Val Thr Cys Leu His Val Cys Leu Leu Val Glu Phe Leu
 1 5 10 15

30 Asn Ser Gln Leu Thr Asn His Arg Lys Tyr Tyr Phe Leu Ser Tyr Gly
 20 25 30

Phe Trp Phe Thr Gly Leu Arg Gly Phe Ser Glu Tyr Leu Trp Pro Gln
 35 40 45

35 Gln His Thr Ser Phe His Pro Asn Arg Asn Glu Ile Asn Phe Val Ser
 50 55 60

Thr Asp Asn Arg Ile Trp Val Thr Xaa
 65 70

40

(2) INFORMATION FOR SEQ ID NO: 359:

45 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 102 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 359:

Met Ser Asp Gln Glu Ala Lys Pro Ser Thr Glu Asp Leu Gly Asp Lys
 1 5 10 15

55 Lys Glu Gly Glu Tyr Ile Lys Leu Lys Val Ile Gly Gln Asp Ser Ser
 20 25 30

Glu Ile His Phe Lys Val Lys Met Thr Thr His Leu Lys Lys Leu Lys
 35 40 45

60 Glu Ser Tyr Cys Gln Arg Gln Gly Val Pro Met Asn Ser Leu Arg Phe

567

50 55 60

Leu Phe Glu Gly Gln Arg Ile Ala Asp Asn His Thr Pro Lys Glu Leu
 65 70 75 80

5 Gly Met Glu Glu Glu Asp Val Ile Glu Val Tyr Gln Glu Gln Thr Gly
 85 90 95

10 Gly His Ser Thr Val Xaa
 100

15 (2) INFORMATION FOR SEQ ID NO: 360:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 48 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 360:

Met Gly Phe Pro Gln Trp His Leu Gly Asn His Ala Val Glu Pro Val
 1 5 10 15

25 Thr Ser Ile Leu Leu Leu Phe Leu Leu Met Met Leu Gly Val Arg Gly
 20 25 30

Leu Leu Leu Val Gly Leu Val Tyr Leu Val Ser His Leu Ser Gln Arg
 35 40 45

30

35

(2) INFORMATION FOR SEQ ID NO: 361:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 179 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 361:

45 Met Ser Ala Glu Val Lys Val Thr Gly Gln Asn Gln Glu Gln Phe Leu
 1 5 10 15

Leu Leu Ala Lys Ser Ala Lys Gly Ala Ala Leu Ala Thr Leu Ile His
 20 25 30

50 Gln Val Leu Glu Ala Pro Gly Val Tyr Val Phe Gly Glu Leu Leu Asp
 35 40 45

Met Pro Asn Val Arg Glu Leu Ala Glu Ser Asp Phe Ala Ser Thr Phe
 50 55 60

55 Arg Leu Leu Thr Val Phe Ala Tyr Gly Thr Tyr Ala Asp Tyr Leu Ala
 65 70 75 80

60 Glu Ala Arg Asn Leu Pro Pro Leu Thr Glu Ala Gln Lys Asn Lys Leu
 85 90 95

Arg His Leu Ser Val Val Thr Leu Ala Ala Lys Val Lys Cys Ile Pro
 100 105 110

5 Tyr Ala Val Leu Leu Glu Ala Leu Ala Leu Arg Asn Val Arg Gln Leu
 115 120 125

Glu Asp Leu Val Ile Glu Ala Val Tyr Ala Asp Val Leu Arg Gly Ser
 130 135 140

10 Leu Asp Gln Arg Asn Gln Arg Leu Glu Val Asp Tyr Ser Ile Gly Arg
 145 150 155 160

Asp Ile Gln Arg Gln Asp Leu Ser Ala Ile Ala Arg Thr Leu Xaa Lys
 15 165 170 175

Asn His Xaa

20

(2) INFORMATION FOR SEQ ID NO: 362:

- 25 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 25 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 362:

30 Met Lys Ser Ser Ser Leu Phe Phe Phe Phe Leu Ala His Phe Ile His
 1 5 10 15

Ser His Asp Leu Pro Gly Leu Cys Arg
 20 25

35

(2) INFORMATION FOR SEQ ID NO: 363:

- 40 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 224 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 363:

45

Met Lys Phe Ala Ala Ser Gly Xaa Phe Leu His His Met Ala Gly Leu
 1 5 10 15

Ser Ser Ser Lys Leu Ser Met Ser Lys Ala Leu Pro Leu Thr Lys Val
 20 25 30

Val Gln Asn Asp Ala Tyr Thr Ala Pro Ala Leu Pro Ser Ser Ile Arg
 35 40 45

55 Thr Lys Ala Leu Thr Asn Met Ser Arg Thr Leu Val Asn Lys Glu Glu
 50 55 60

Pro Pro Lys Glu Leu Pro Ala Ala Glu Pro Val Leu Ser Pro Leu Glu
 65 70 75 80

60

	Gly	Thr	Lys	Met	Thr	Val	Asn	Asn	Leu	His	Pro	Arg	Val	Thr	Glu	Glu								
					85								90								95			
5	Asp	Ile	Val	Glu	Leu	Phe	Cys	Val	Cys	Gly	Ala	Leu	Lys	Arg	Ala	Arg								
	100								105								110							
	Leu	Val	His	Pro	Gly	Val	Ala	Glu	Val	Val	Phe	Val	Lys	Lys	Asp	Asp								
	115								120								125							
10	Ala	Ile	Thr	Ala	Tyr	Lys	Lys	Tyr	Asn	Asn	Arg	Cys	Leu	Asp	Gly	Gln								
	130								135								140							
	Pro	Met	Lys	Cys	Asn	Leu	His	Met	Asn	Gly	Asn	Val	Ile	Thr	Ser	Asp								
15	145				150								155				160							
	Gln	Pro	Ile	Leu	Leu	Arg	Leu	Ser	Asp	Ser	Pro	Ser	Met	Lys	Lys	Glu								
					165								170				175							
	Ser	Glu	Leu	Pro	Arg	Arg	Val	Asn	Ser	Ala	Ser	Ser	Ser	Asn	Pro	Pro								
20	180								185								190							
	Ala	Glu	Val	Asp	Pro	Asp	Thr	Ile	Leu	Lys	Ala	Leu	Phe	Lys	Ser	Ser								
	195								200								205							
25	Gly	Ala	Ser	Xaa	Thr	Thr	Gln	Pro	Thr	Glu	Phe	Lys	Ile	Lys	Leu	Xaa								
	210								215								220							

30

(2) INFORMATION FOR SEQ ID NO: 364:

35 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 349 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 364:

40 Met Ser Lys Asn Cys Ile Lys Leu Leu Cys Glu Asp Pro Val Phe Ala
1 5 10 15

45 Glu Tyr Ile Lys Cys Ile Leu Met Asp Glu Arg Thr Phe Leu Asn Asn
20 25 30

50 Asn Ile Val Tyr Thr Phe Met Thr His Phe Leu Leu Lys Val Gln Ser
35 40 45

55 Gln Val Phe Ser Glu Ala Asn Cys Ala Asn Leu Ile Ser Thr Leu Ile
50 55 60

60 Thr Asn Leu Ile Ser Gln Tyr Gln Asn Leu Gln Ser Asp Phe Ser Asn
65 70 75 80

65 Arg Val Glu Ile Ser Lys Ala Ser Ala Ser Leu Asn Gly Asp Leu Arg
85 90 95

70 Ala Leu Ala Leu Leu Leu Ser Val His Thr Pro Lys Gln Leu Asn Pro
100 105 110

Ala Leu Ile Pro Thr Leu Gln Glu Leu Leu Ser Lys Cys Arg Thr Cys
 115 120 125

5 Leu Gln Gln Arg Asn Ser Leu Gln Glu Gln Glu Ala Lys Glu Arg Lys
 130 135 140

Thr Lys Asp Asp Glu Gly Ala Thr Pro Ile Lys Arg Arg Arg Val Ser
 145 150 155 160

10 Ser Asp Glu Glu His Thr Val Asp Ser Cys Ile Ser Asp Met Lys Thr
 165 170 175

Glu Thr Arg Glu Val Leu Thr Pro Thr Ser Thr Ser Asp Asn Glu Thr
 180 185 190

15 Arg Asp Ser Ser Ile Ile Asp Pro Gly Thr Glu Gln Asp Leu Pro Ser
 195 200 205

20 Pro Glu Asn Ser Ser Val Lys Glu Tyr Arg Met Glu Val Pro Ser Ser
 210 215 220

Phe Ser Glu Asp Met Ser Asn Ile Arg Ser Gln His Ala Glu Glu Gln
 225 230 235 240

25 Ser Asn Asn Gly Arg Tyr Asp Asp Cys Lys Glu Phe Lys Asp Leu His
 245 250 255

Cys Ser Lys Asp Ser Thr Leu Ala Glu Glu Glu Ser Glu Phe Pro Ser
 260 265 270

30 Thr Ser Ile Ser Ala Val Leu Ser Asp Leu Ala Asp Leu Arg Ser Cys
 275 280 285

35 Asp Gly Gln Ala Leu Pro Ser Gln Asp Pro Glu Val Ala Leu Ser Leu
 290 295 300

Ser Cys Gly His Ser Arg Gly Leu Phe Ser His Met Gln Gln His Asp
 305 310 315 320

40 Ile Leu Asp Thr Leu Cys Arg Thr Ile Glu Ser Thr Ile His Val Val
 325 330 335

Thr Arg Ile Ser Gly Lys Gly Asn Gln Ala Ala Ser Xaa
 340 345

45

(2) INFORMATION FOR SEQ ID NO: 365:

50

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 467 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 365:

Met Leu His Gln Asp His Ile Thr Phe Ala Met Leu Leu Ala Arg Ile
 1 5 10 15

60

Lys Leu Lys Gly Thr Val Gly Glu Pro Thr Tyr Asp Ala Glu Phe Gln

	20	25	30
	His Phe Leu Arg Gly Asn Glu Ile Val Leu Ser Ala Gly Ser Thr Pro		
	35	40	45
5	Arg Ile Gln Gly Leu Thr Val Glu Gln Ala Glu Ala Val Val Arg Leu		
	50	55	60
10	Ser Cys Leu Pro Ala Phe Lys Asp Leu Ile Ala Lys Val Gln Ala Asp		
	65	70	75
	Glu Gln Phe Gly Ile Trp Leu Asp Ser Ser Ser Pro Glu Gln Thr Val		
	85	90	95
15	Pro Tyr Leu Trp Ser Glu Glu Thr Pro Ala Thr Pro Ile Gly Gln Ala		
	100	105	110
	Ile His Arg Leu Leu Leu Ile Gln Ala Phe Arg Pro Asp Arg Leu Leu		
	115	120	125
20	Ala Met Ala His Met Phe Val Ser Thr Asn Leu Gly Glu Ser Phe Met		
	130	135	140
	Ser Ile Met Glu Gln Pro Leu Asp Leu Thr His Ile Val Xaa Thr Glu		
	145	150	155
25	Val Lys Pro Asn Thr Pro Val Leu Met Cys Ser Val Pro Gly Tyr Asp		
	165	170	175
30	Ala Ser Gly His Val Glu Asp Leu Ala Ala Glu Gln Asn Thr Gln Ile		
	180	185	190
	Thr Ser Ile Ala Ile Gly Ser Ala Glu Gly Phe Asn Gln Ala Asp Lys		
	195	200	205
35	Ala Ile Asn Thr Ala Val Lys Ser Gly Arg Trp Val Met Leu Lys Asn		
	210	215	220
	Val His Leu Ala Pro Gly Trp Leu Met Gln Leu Glu Lys Lys Leu His		
	225	230	235
40	Ser Leu Gln Pro His Ala Cys Phe Arg Leu Phe Leu Thr Met Glu Ile		
	245	250	255
45	Asn Pro Lys Val Pro Val Asn Leu Leu Arg Ala Gly Arg Ile Phe Val		
	260	265	270
	Phe Glu Pro Pro Pro Gly Xaa Lys Ala Asn Met Leu Arg Thr Phe Ser		
	275	280	285
50	Ser Ile Pro Val Ser Arg Ile Cys Lys Ser Pro Asn Glu Arg Ala Arg		
	290	295	300
	Leu Tyr Phe Leu Leu Ala Trp Phe His Ala Ile Ile Gln Glu Arg Leu		
	305	310	315
55	Arg Tyr Ala Pro Leu Gly Trp Ser Lys Lys Tyr Glu Phe Gly Glu Ser		
	325	330	335
60	Asp Leu Arg Ser Xaa Cys Asp Thr Val Asp Thr Trp Leu Asp Asp Thr		

572

340 345 350

Ala Lys Gly Arg Gln Asn Ile Ser Pro Asp Lys Ile Pro Trp Ser Ala
355 360 365

5 Leu Lys Thr Leu Met Ala Gln Ser Ile Tyr Gly Gly Arg Val Asp Asn
370 375 380

Glu Phe Asp Gln Arg Leu Leu Asn Thr Phe Leu Glu Arg Leu Phe Thr
10 385 390 395 400

Thr Arg Ser Phe Asp Ser Glu Phe Lys Leu Ala Cys Lys Val Asp Gly
405 410 415

15 His Lys Asp Ile Gln Met Pro Asp Gly Met Gln Ala Arg Gly Val Cys
420 425 430

Ala Val Gly Gly Val Ala Pro Arg His Pro Asp Ala Leu Leu Ala Gly
435 440 445

20 Pro Ala Gln Gln Arg Arg Glu Ser Pro Pro Tyr His Thr Gly Cys Gly
450 455 460

His Asp Gln
25 465

(2) INFORMATION FOR SEQ ID NO: 366:

30

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 152 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 366:

Met Ala Asp Glu Ala Thr Arg Arg Val Val Ser Glu Ile Pro Val Leu
1 5 10 15

40 Lys Thr Asn Ala Gly Pro Arg Asp Arg Glu Leu Trp Val Gln Arg Leu
20 25 30

Lys Glu Glu Tyr Gln Ser Leu Ile Arg Tyr Val Glu Asn Asn Lys Asn
35 40 45

45 Ala Asp Asn Asp Trp Phe Arg Leu Glu Ser Asn Lys Glu Gly Thr Arg
50 55 60

Trp Phe Gly Lys Cys Trp Tyr Ile His Asp Leu Leu Lys Tyr Glu Phe
50 65 70 75 80

Asp Ile Glu Phe Asp Ile Pro Ile Thr Tyr Pro Thr Thr Ala Pro Glu
85 90 95

55 Ile Ala Val Pro Glu Leu Asp Gly Lys Thr Ala Lys Met Tyr Arg Gly
100 105 110

Gly Lys Ile Cys Leu Thr Asp His Phe Lys Pro Leu Trp Gly Gln Glu
115 120 125

60

Cys Ala Gln Ile Trp Thr Ser Ser Ser His Gly Ser Gly Ala Gly Ser
 130 135 140

5 Met Xaa Gly Ser Gly Asn Pro Xaa
 145 150

10 (2) INFORMATION FOR SEQ ID NO: 367:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 373 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 367:

Met Tyr Asp Gly Thr Lys Glu Val Pro Met Asn Pro Val Lys Ile Tyr
 1 5 10 15

20 Gln Val Cys Asp Ile Pro Gln Pro Gln Gly Ser Ile Ile Asn Pro Gly
 20 25 30

Ser Thr Gly Ser Ala Pro Trp Asp Glu Lys Asp Asn Asp Val Asp Glu
 35 40 45

25 Glu Asp Glu Glu Asp Glu Leu Asp Gln Ser Gln His His Val Pro Ile
 50 55 60

30 Gln Asp Thr Phe Pro Phe Leu Asn Ile Asn Gly Ser Pro Met Ala Pro
 65 70 75 80

Ala Ser Val Gly Asn Cys Ser Val Gly Asn Cys Ser Pro Glu Ala Val
 85 90 95

35 Trp Pro Lys Thr Glu Pro Leu Glu Met Glu Val Pro Gln Ala Pro Ile
 100 105 110

Gln Pro Phe Tyr Ser Ser Pro Glu Leu Trp Ile Ser Ser Leu Pro Met
 115 120 125

40 Thr Asp Leu Asp Ile Lys Phe Gln Tyr Arg Gly Lys Glu Tyr Gly Gln
 130 135 140

45 Thr Met Thr Val Ser Asn Pro Gln Gly Cys Arg Leu Phe Tyr Gly Asp
 145 150 155 160

Leu Gly Pro Met Pro Asp Gln Glu Glu Leu Phe Gly Pro Val Xaa Leu
 165 170 175

50 Glu Gln Val Lys Phe Pro Gly Pro Glu His Ile Thr Asn Glu Lys Gln
 180 185 190

Lys Leu Phe Thr Ser Lys Leu Leu Asp Val Met Asp Arg Gly Leu Ile
 195 200 205

55 Leu Glu Val Ser Gly His Ala Ile Tyr Ala Ile Arg Leu Cys Gln Cys
 210 215 220

60 Lys Val Tyr Trp Ser Gly Pro Cys Ala Pro Ser Leu Val Ala Pro Asn
 225 230 235 240

Leu Ile Glu Arg Gln Lys Lys Val Lys Leu Phe Cys Leu Glu Thr Phe
 245 250 255
 5 Leu Ser Asp Leu Ile Ala His Gln Lys Gly Gln Ile Glu Lys Gln Pro
 260 265 270
 Pro Phe Glu Ile Tyr Leu Cys Phe Gly Glu Glu Trp Pro Asp Gly Lys
 275 280 285
 10 Pro Leu Glu Arg Lys Leu Ile Leu Val Gln Val Ile Pro Val Val Ala
 290 295 300
 Arg Met Ile Tyr Glu Met Phe Ser Gly Asp Phe Thr Arg Ser Phe Asp
 15 305 310 315 320
 Ser Gly Ser Val Arg Leu Gln Ile Ser Thr Pro Asp Ile Lys Asp Asn
 325 330 335
 20 Ile Val Ala Gln Leu Lys Gln Leu Tyr Arg Ile Leu Gln Thr Gln Glu
 340 345 350
 Ser Trp Gln Pro Met Gln Pro Thr Pro Ser Met Gln Leu Pro Pro Ala
 355 360 365
 25 Leu Pro Pro Gln Xaa
 370

30

(2) INFORMATION FOR SEQ ID NO: 368:

(i) SEQUENCE CHARACTERISTICS:

35

(A) LENGTH: 83 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 368:

40 Met Gly Ser Ser Val Leu Pro Phe Cys Val Cys Val Thr Ser Pro Ser
 1 5 10 15
 Leu Gly Gly Arg Cys Ile Gln Gly Arg Phe Ala Ser His Ser Lys Phe
 20 25 30
 45 Trp Gly Phe Gly Arg Lys Thr Ala Ser Phe Gly Ala Val Gly Glu Thr
 35 40 45
 Pro Pro Asp Gln Glu Pro Gln Lys Glu Thr Glu Pro Ala Thr Ser Ser
 50 55 60
 50 His Ala Arg Pro Trp Ala Arg Val Ile Gly Leu Arg Ile Trp Pro Gln
 65 70 75 80
 Pro Asn Xaa

55

60

(2) INFORMATION FOR SEQ ID NO: 369:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 21 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 369:

Met Leu Leu Ser Val Ala Ile Phe Ile Leu Leu Thr Leu Val Tyr Ala
 1 5 10 15
 10 Tyr Trp Thr Met Xaa
 20

15 (2) INFORMATION FOR SEQ ID NO: 370:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 227 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 370:

Met Gly Ala Ser Ala Arg Leu Leu Arg Ala Val Ile Met Gly Ala Pro
 1 5 10 15
 25 Gly Ser Gly Lys Gly Thr Val Ser Ser Arg Ile Thr Thr His Phe Glu
 20 25 30
 30 Leu Lys His Leu Ser Ser Gly Asp Leu Leu Arg Asp Asn Met Leu Arg
 35 40 45
 Gly Thr Glu Ile Gly Val Leu Ala Lys Ala Phe Ile Asp Gln Gly Lys
 50 55 60
 35 Leu Ile Pro Asp Asp Val Met Thr Arg Leu Ala Leu His Glu Leu Lys
 65 70 75 80
 Asn Leu Thr Gln Tyr Ser Trp Leu Leu Asp Gly Phe Pro Arg Thr Leu
 85 90 95
 40 Pro Gln Ala Glu Ala Leu Asp Arg Ala Tyr Gln Ile Asp Thr Val Ile
 100 105 110
 Asn Leu Asn Val Pro Phe Glu Val Ile Lys Gln Arg Leu Thr Ala Arg
 115 120 125
 Trp Ile His Pro Ala Ser Gly Arg Val Tyr Asn Ile Glu Phe Asn Pro
 130 135 140
 50 Pro Lys Thr Val Gly Ile Asp Asp Leu Thr Gly Glu Pro Leu Ile Gln
 145 150 155 160
 Arg Glu Asp Asp Lys Pro Glu Thr Val Ile Lys Arg Leu Lys Ala Tyr
 165 170 175
 55 Glu Asp Gln Thr Lys Pro Val Leu Glu Tyr Tyr Gln Lys Lys Gly Val
 180 185 190
 Leu Glu Thr Phe Ser Gly Thr Glu Thr Asn Lys Ile Trp Pro Tyr Val
 195 200 205
 60

576

Tyr Ala Phe Leu Gln Thr Lys Val Pro Gln Arg Ser Gln Lys Ala Ser
 210 215 220

5 Val Thr Pro
 225

10 (2) INFORMATION FOR SEQ ID NO: 371:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 79 amino acids

(B) TYPE: amino acid

15 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 371:

Met Phe Leu Asn Cys Glu Ile Leu Glu Tyr Cys Tyr Tyr Leu Thr Gln
 1 5 10 15
 20 Leu Lys Ile Ser Met Gly Lys Tyr Leu Ser Ile Pro Thr Val Leu Leu
 20 25 30
 25 Lys Ile Ile Arg Cys Ser Ile Thr Ala Val Ser Asp Ser Ser Thr Ser
 35 40 45
 Trp Ala Ile Lys Ala Gln Leu Lys Ile Glu Asn Lys Asp Leu Asp Asn
 50 55 60
 30 Lys Thr Ala Lys Gly Gly Gly Gln Glu Ala Leu Thr Cys Thr Xaa
 65 70 75

35 (2) INFORMATION FOR SEQ ID NO: 372:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 51 amino acids

(B) TYPE: amino acid

40 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 372:

Met Arg Ala Val Phe Pro Cys Cys Pro Phe Leu Thr Leu Met Leu Pro
 1 5 10 15
 45 Leu Leu Glu Cys Leu Val Gly Met Ile Met Cys Tyr Leu Gly Ile Ser
 20 25 30
 50 Phe Thr Asp Thr Arg Lys Thr Ala Gly Leu Lys Lys Lys Lys Lys Lys
 35 40 45
 Lys Xaa Xaa
 50

55

(2) INFORMATION FOR SEQ ID NO: 373:

(i) SEQUENCE CHARACTERISTICS:

60 (A) LENGTH: 61 amino acids

577

(B) TYPE: amino acid
 (D) TOPOLOGY: linear
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 373:

5 Met Phe Leu Met Arg Met His Leu Cys Phe Cys Lys Tyr Cys Cys Ser
 1 5 10 15
 Phe Ile Val Thr Pro Thr Ser Thr Ser Asn Thr Ala Ser Tyr Leu Trp
 20 25 30
 10 Pro Trp Ile Ser Ala Ser Met Ala Gly Arg Gly Ser Ser Trp Ala Cys
 35 40 45
 Thr Leu Asn Ala Val Thr Arg Glu Gly Leu Pro Glu Xaa
 15 50 55 60

(2) INFORMATION FOR SEQ ID NO: 374:
 20

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 40 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 374:

Met Ser Leu Leu Asn Thr His Thr Leu Cys Phe Val Leu Phe Cys Phe
 1 5 10 15
 30 Thr Leu Ser Ile Asn Gln Glu Lys Leu Ala Asn His Leu Ala Phe Arg
 20 25 30
 Ile Leu Phe Phe Ile Val Phe Xaa
 35 40
 35

(2) INFORMATION FOR SEQ ID NO: 375:

40 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 44 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 375:

Met Cys Ser Gly Gln Ser Gln Val Trp Lys Met Ala Leu Gln Ala Leu
 1 5 10 15
 Asp Ser Glu Thr Val Val Ile Leu Pro Asp Met His Leu Ile Leu Ser
 20 25 30
 Leu Arg Leu Ile His Asn Ala Arg Pro Cys Leu Xaa
 35 40
 55

(2) INFORMATION FOR SEQ ID NO: 376:

60 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 203 amino acids

578

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 376:

5 Met Leu Ile Ser Glu Glu Glu Ile Pro Phe Lys Asp Asp Pro Arg Asp
1 5 10 15

Glu Thr Tyr Lys Pro His Leu Glu Arg Glu Thr Pro Lys Pro Arg Arg
20 25 30

10 Lys Ser Gly Lys Val Lys Glu Glu Lys Glu Lys Lys Glu Ile Lys Val
35 40 45

Glu Val Glu Val Glu Val Lys Glu Glu Glu Asn Glu Ile Arg Glu Asp
15 50 55 60

Glu Glu Pro Pro Arg Lys Arg Gly Arg Arg Arg Lys Asp Asp Lys Ser
65 70 75 80

20 Pro Arg Leu Pro Lys Arg Arg Lys Lys Pro Pro Ile Gln Tyr Val Arg
85 90 95

Cys Glu Met Glu Gly Cys Gly Thr Val Leu Ala His Pro Arg Tyr Leu
100 105 110

25 Gln His His Ile Lys Tyr Gln His Leu Leu Lys Lys Lys Tyr Val Cys
115 120 125

Pro His Pro Ser Cys Gly Arg Leu Phe Arg Leu Gln Lys Gln Leu Leu
130 135 140

Arg His Ala Lys His His Thr Asp Gln Arg Asp Tyr Ile Cys Glu Tyr
145 150 155 160

35 Cys Ala Arg Ala Phe Lys Ser Ser His Asn Leu Ala Val His Arg Met
165 170 175

Ile His Thr Gly Glu Lys His Tyr Asn Val Arg Ser Val Asp Leu Leu
180 185 190

40 Val Asp Lys Arg His Leu Leu Ile Gly Thr Xaa
195 200

45

(2) INFORMATION FOR SEQ ID NO: 377:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 29 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 377:

55 Met Leu Pro Arg Arg Thr Phe Tyr Phe Tyr Phe Ile Phe Ile Phe Phe
1 5 10 15

Leu Ala Ser Phe Trp Gly Phe Thr Leu Arg Ala Ser Phe
20 25

60

(2) INFORMATION FOR SEQ ID NO: 378:

- 5 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 136 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 378:

10 Met Phe Asp Ser Leu Ser Tyr Phe Lys Gly Ser Ser Leu Leu Leu Met
 1 5 10 15
 Leu Lys Thr Tyr Leu Ser Glu Asp Val Phe Gln His Ala Val Val Leu
 20 25 30
 15 Tyr Leu His Asn His Ser Tyr Ala Ser Ile Gln Ser Asp Asp Leu Trp
 35 40 45
 Asp Ser Phe Asn Glu Val Thr Asn Gln Thr Leu Asp Val Lys Arg Met
 20 50 55 60
 Met Lys Thr Trp Thr Leu Gln Lys Gly Phe Pro Leu Val Thr Val Gln
 65 70 75 80
 25 Lys Lys Gly Lys Glu Leu Phe Ile Gln Gln Glu Arg Phe Phe Leu Asn
 85 90 95
 Met Lys Pro Glu Ile Gln Pro Ser Asp Thr Arg Tyr Met Pro Ser Phe
 100 105 110
 30 Phe Ser Cys His Leu Phe Cys Thr Leu Arg Trp Lys Tyr Phe Glu Val
 115 120 125
 Phe Tyr Asn His Lys Phe Leu Xaa
 35 130 135

(2) INFORMATION FOR SEQ ID NO: 379:

- 40 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 41 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 379:

Met Ala Trp Arg Arg Arg Glu Pro Ala Ser Gly Leu Ala Ala Cys Trp
 1 5 10 15
 50 Leu Trp Arg Cys Ser Pro Trp Pro Cys Ala Cys Pro Gly Pro Gly Ala
 20 25 30
 Gly Leu Ser Ser Gly Ser Arg Pro Trp
 35 40
 55

(2) INFORMATION FOR SEQ ID NO: 380:

- 60 (i) SEQUENCE CHARACTERISTICS:

580

(A) LENGTH: 468 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 380:

5 Met Glu Phe Leu Lys Val Ala Arg Arg Asn Lys Arg Glu Gln Leu Glu
 1 5 10 15
 10 Gln Ile Gln Lys Glu Leu Ser Val Leu Glu Glu Asp Ile Lys Arg Val
 20 25 30
 Glu Glu Met Ser Gly Leu Tyr Ser Pro Val Ser Glu Asp Ser Thr Val
 35 40 45
 15 Pro Gln Phe Glu Ala Pro Ser Pro Ser His Ser Ser Ile Ile Asp Ser
 50 55 60
 Thr Glu Tyr Ser Gln Pro Pro Gly Phe Ser Gly Ser Ser Gln Thr Lys
 65 70 75 80
 20 Lys Gln Pro Trp Tyr Asn Ser Thr Leu Ala Ser Arg Arg Lys Arg Leu
 85 90 95
 Thr Ala His Phe Glu Asp Leu Glu Gln Cys Tyr Phe Ser Thr Arg Met
 25 100 105 110
 Ser Arg Ile Ser Asp Asp Ser Arg Thr Ala Ser Gln Leu Asp Glu Phe
 115 120 125
 30 Gln Glu Cys Leu Ser Lys Phe Thr Arg Tyr Asn Ser Val Arg Pro Leu
 130 135 140
 Ala Thr Leu Ser Tyr Ala Ser Asp Leu Tyr Asn Gly Ser Ser Ile Val
 145 150 155 160
 35 Ser Ser Ile Glu Phe Asp Arg Asp Cys Asp Tyr Phe Ala Ile Ala Gly
 165 170 175
 Val Thr Lys Lys Ile Lys Val Tyr Glu Tyr Asp Thr Val Ile Gln Asp
 40 180 185 190
 Ala Val Asp Ile His Tyr Pro Glu Asn Glu Met Thr Cys Asn Ser Lys
 195 200 205
 45 Ile Ser Cys Ile Ser Trp Ser Ser Tyr His Lys Asn Leu Leu Ala Ser
 210 215 220
 Ser Asp Tyr Glu Gly Thr Val Ile Leu Trp Asp Gly Phe Thr Gly Gln
 225 230 235 240
 50 Arg Ser Lys Val Tyr Gln Glu His Glu Lys Arg Cys Trp Ser Val Asp
 245 250 255
 Phe Asn Leu Met Asp Pro Lys Leu Leu Ala Ser Gly Ser Asp Asp Ala
 55 260 265 270
 Lys Val Lys Leu Trp Ser Thr Asn Leu Asp Asn Ser Val Ala Ser Ile
 275 280 285
 60 Glu Ala Lys Ala Asn Val Cys Cys Val Lys Phe Ser Pro Ser Ser Arg

581

290 295 300
 Tyr His Leu Ala Phe Gly Cys Ala Asp His Cys Val His Tyr Tyr Asp
 305 310 315 320
 5 Leu Arg Asn Thr Lys Gln Pro Ile Met Val Phe Lys Gly His Arg Lys
 325 330 335
 10 Ala Val Ser Tyr Ala Lys Phe Val Ser Gly Glu Glu Ile Val Ser Ala
 340 345 350
 Ser Thr Asp Ser Gln Leu Lys Leu Trp Asn Val Gly Lys Pro Tyr Cys
 355 360 365
 15 Leu Arg Ser Phe Lys Gly His Ile Asn Glu Lys Asn Phe Val Gly Leu
 370 375 380
 Ala Ser Asn Gly Asp Tyr Ile Ala Cys Gly Ser Glu Asn Asn Ser Leu
 20 385 390 395 400
 Tyr Leu Tyr Tyr Lys Gly Leu Ser Lys Thr Leu Leu Thr Phe Lys Phe
 405 410 415
 25 Asp Thr Val Lys Ser Val Leu Asp Lys Asp Arg Lys Glu Asp Asp Thr
 420 425 430
 Asn Glu Phe Val Ser Ala Val Cys Trp Arg Ala Leu Pro Asp Gly Glu
 435 440 445
 30 Ser Asn Val Leu Ile Ala Ala Asn Ser Gln Gly Thr Ile Lys Val Leu
 450 455 460
 Glu Leu Val Xaa
 35 465

(2) INFORMATION FOR SEQ ID NO: 381:

- 40 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 29 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 381:

50 Met Arg Lys Glu Asp Gly Phe Trp Phe Phe Phe Leu Phe Phe Phe
 1 5 10 15
 Val Val Gly Ser Lys Phe Val Asn Gly Asn Lys Leu Val
 50 20 25

(2) INFORMATION FOR SEQ ID NO: 382:

- 55 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 29 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 60 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 382:

Met Pro Leu Ala Pro Tyr Cys Asp Leu Leu Val Ala Leu Ser Phe Ala
 1 5 10 15

5 Leu Val Leu Glu Ser Pro Val Asp Ser Ser Asp Phe Thr
 20 25

10 (2) INFORMATION FOR SEQ ID NO: 383:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 138 amino acids

(B) TYPE: amino acid

15 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 383:

Met Asn Ser Leu Val Ser Trp Gln Leu Leu Leu Phe Leu Cys Ala Thr
 1 5 10 15

20 His Phe Gly Glu Pro Leu Glu Lys Val Ala Ser Val Gly Asn Ser Arg
 20 25 30

25 Pro Thr Gly Gln Gln Leu Glu Ser Leu Gly Leu Leu Ala Pro Gly Glu
 35 40 45

Gln Ser Leu Pro Cys Thr Glu Arg Lys Pro Ala Ala Thr Ala Arg Leu
 50 55 60

30 Ser Arg Arg Gly Thr Ser Leu Ser Pro Pro Pro Glu Ser Ser Gly Ser
 65 70 75 80

Pro Gln Gln Pro Gly Leu Ser Ala Pro His Ser Arg Gln Ile Pro Ala
 85 90 95

35 Pro Gln Gly Ala Val Leu Val Gln Arg Glu Lys Asp Leu Pro Asn Tyr
 100 105 110

40 Asn Trp Asn Ser Phe Gly Leu Arg Phe Gly Lys Arg Glu Ala Ala Pro
 115 120 125

Gly Asn His Gly Arg Ser Ala Gly Arg Gly
 130 135

45

(2) INFORMATION FOR SEQ ID NO: 384:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 74 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 384:

55 Met Ser Cys Phe Ile Asp Ser Xaa Asp Ser Lys Ile Leu His Leu Leu
 1 5 10 15

Val Val Ser Phe Ile Cys Xaa Leu Phe Leu Leu Ile Leu Thr His Gly
 20 25 30

60

Ile Leu Ile Leu Arg Xaa Phe Phe Ser Val Xaa Xaa His Ser Leu Lys
 35 40 45
 Asn Asn Leu Glu Glu Tyr Leu Ile Leu Met Asn Lys Ala Leu Leu Thr
 5 50 55 60
 Arg Glu Asp Phe Phe Val Leu Pro Xaa Ala
 65 70
 10
 (2) INFORMATION FOR SEQ ID NO: 385:
 (i) SEQUENCE CHARACTERISTICS:
 15 (A) LENGTH: 521 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 385:
 20 Met Ser Ala Gly Glu Val Glu Arg Leu Val Ser Glu Leu Ser Gly Gly
 1 5 10 15
 Thr Gly Gly Asp Glu Glu Glu Glu Trp Leu Tyr Gly Asp Glu Asn Glu
 20 25 30
 25 Val Glu Arg Pro Glu Glu Glu Asn Ala Ser Ala Asn Pro Pro Ser Gly
 35 40 45
 Ile Glu Asp Glu Thr Ala Glu Asn Gly Val Pro Lys Pro Lys Val Thr
 30 50 55 60
 Glu Thr Glu Asp Asp Ser Asp Ser Asp Ser Asp Asp Asp Glu Asp Asp
 65 70 75 80
 35 Val His Val Thr Ile Gly Asp Ile Lys Thr Gly Ala Pro Gln Tyr Gly
 85 90 95
 Ser Tyr Gly Thr Ala Pro Val Asn Leu Asn Ile Lys Thr Gly Gly Arg
 100 105 110
 40 Val Tyr Gly Thr Thr Gly Thr Lys Val Lys Gly Val Asp Leu Asp Ala
 115 120 125
 Pro Gly Ser Ile Asn Gly Val Pro Leu Leu Glu Val Asp Leu Asp Ser
 45 130 135 140
 Phe Glu Asp Lys Pro Trp Arg Lys Pro Gly Ala Asp Leu Ser Asp Tyr
 145 150 155 160
 50 Phe Asn Tyr Gly Phe Asn Glu Asp Thr Trp Lys Ala Tyr Cys Glu Lys
 165 170 175
 Gln Lys Arg Ile Arg Met Gly Leu Glu Val Ile Pro Val Thr Ser Thr
 180 185 190
 55 Thr Asn Lys Ile Thr Val Gln Gln Gly Arg Thr Gly Asn Ser Glu Lys
 195 200 205
 Glu Thr Ala Leu Pro Ser Thr Lys Ala Glu Phe Thr Ser Pro Pro Ser
 60 210 215 220

Leu Phe Lys Thr Gly Leu Pro Pro Ser Arg Arg Leu Pro Gly Ala Ile
 225 230 235 240
 5 Asp Val Ile Gly Gln Thr Ile Thr Ile Ser Arg Val Glu Gly Arg Arg
 245 250 255
 Arg Ala Asn Glu Asn Ser Asn Ile Gln Val Leu Ser Glu Arg Ser Ala
 260 265 270
 10 Thr Glu Val Asp Asn Asn Phe Ser Lys Pro Pro Pro Phe Phe Pro Pro
 275 280 285
 Gly Ala Pro Pro Thr His Leu Pro Pro Pro Pro Phe Leu Pro Pro Pro
 15 290 295 300
 Pro Thr Val Ser Thr Ala Pro Pro Leu Ile Pro Pro Pro Gly Phe Pro
 305 310 315 320
 20 Pro Pro Pro Gly Ala Pro Pro Pro Ser Leu Ile Pro Thr Ile Glu Ser
 325 330 335
 Gly His Ser Ser Gly Tyr Asp Ser Arg Ser Ala Arg Ala Phe Pro Tyr
 340 345 350
 25 Gly Asn Val Ala Phe Pro His Leu Pro Gly Ser Ala Pro Ser Trp Pro
 355 360 365
 Ser Leu Val Asp Thr Ser Lys Gln Trp Asp Tyr Tyr Ala Arg Arg Glu
 30 370 375 380
 Lys Asp Arg Asp Arg Glu Arg Asp Arg Asp Arg Glu Arg Asp Arg Asp
 385 390 395 400
 35 Arg Asp Arg Glu Arg Glu Arg Thr Arg Glu Arg Glu Arg Glu Arg Asp
 405 410 415
 His Ser Pro Thr Pro Ser Val Phe Asn Ser Asp Glu Glu Arg Tyr Arg
 420 425 430
 40 Tyr Arg Glu Tyr Ala Glu Arg Gly Tyr Glu Arg His Arg Ala Ser Arg
 435 440 445
 Glu Lys Glu Glu Arg His Arg Glu Arg Arg His Arg Glu Lys Glu Glu
 45 450 455 460
 Thr Arg His Lys Ser Ser Arg Ser Asn Ser Arg Arg Arg His Glu Ser
 465 470 475 480
 50 Glu Glu Gly Asp Ser His Arg Arg His Lys His Lys Lys Ser Lys Arg
 485 490 495
 Ser Lys Glu Gly Lys Glu Ala Gly Ser Glu Pro Ala Pro Glu Gln Glu
 500 505 510
 55 Ser Thr Glu Ala Thr Pro Ala Glu Xaa
 515 520
 60

(2) INFORMATION FOR SEQ ID NO: 386:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 137 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 386:

5 Met Asn Ser Arg Gly Ile Trp Leu Ala Tyr Ile Ile Leu Val Gly Leu
 10 1 5 10 15
 Leu His Met Val Leu Leu Ser Ile Pro Phe Phe Ser Ile Pro Val Val
 20 25 30
 15 Trp Thr Leu Thr Asn Val Ile His Asn Leu Ala Thr Tyr Val Phe Leu
 35 40 45
 His Thr Val Lys Gly Thr Pro Phe Glu Thr Pro Asp Gln Gly Lys Ala
 50 55 60
 20 Arg Leu Leu Thr His Trp Glu Gln Met Asp Tyr Gly Leu Gln Phe Thr
 65 70 75 80
 25 Ser Ser Arg Lys Phe Leu Ser Ile Ser Pro Ile Val Leu Tyr Leu Leu
 85 90 95
 Ala Ser Phe Tyr Thr Lys Tyr Asp Ala Ala His Phe Leu Ile Asn Thr
 100 105 110
 30 Ala Ser Leu Leu Ser Val Leu Leu Pro Lys Leu Pro Gln Phe His Gly
 115 120 125
 Val Arg Val Phe Gly Ile Asn Lys Tyr
 130 135
 35

(2) INFORMATION FOR SEQ ID NO: 387:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 186 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 387:

40
 45 Met Ala Ala Gln Lys Asp Gln Gln Lys Asp Ala Glu Ala Glu Gly Leu
 1 5 10 15
 50 Ser Gly Thr Thr Leu Leu Pro Lys Leu Ile Pro Ser Gly Ala Gly Arg
 20 25 30
 Glu Trp Leu Glu Arg Arg Arg Ala Thr Ile Arg Pro Trp Ser Thr Phe
 35 40 45
 55 Val Asp Gln Gln Arg Phe Ser Arg Pro Arg Asn Leu Gly Glu Leu Cys
 50 55 60
 60 Gln Arg Leu Val Arg Asn Val Glu Tyr Tyr Gln Ser Asn Tyr Val Phe
 65 70 75 80

586

Val Phe Leu Gly Leu Ile Leu Tyr Cys Val Val Thr Ser Pro Met Leu
85 90 95

5 Leu Val Ala Leu Ala Val Phe Phe Gly Ala Cys Tyr Ile Leu Tyr Leu
100 105 110

Arg Thr Leu Glu Ser Lys Leu Val Leu Phe Gly Arg Glu Val Ser Pro
115 120 125

10 Ala His Gln Tyr Ala Leu Ala Gly Gly Ile Ser Phe Pro Phe Phe Trp
130 135 140

Leu Ala Gly Ala Gly Ser Ala Val Phe Trp Val Leu Gly Ala Thr Leu
145 150 155 160

15 Val Val Ile Gly Ser His Ala Ala Phe His Gln Ile Glu Ala Val Asp
165 170 175

20 Gly Glu Glu Leu Gln Met Glu Pro Val Xaa
180 185

25 (2) INFORMATION FOR SEQ ID NO: 388:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 388:

Met
1

35

(2) INFORMATION FOR SEQ ID NO: 389:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 299 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 389:

45 Met Leu Ser Ile Phe Tyr Phe Ala Ile Pro Val Gly Ser Gly Leu Gly
1 5 10 15

Tyr Ile Ala Gly Ser Lys Val Lys Asp Met Ala Gly Asp Trp His Trp
20 25 30

50 Ala Leu Arg Val Thr Pro Gly Leu Gly Val Val Ala Val Leu Leu Leu
35 40 45

55 Phe Leu Val Val Arg Glu Pro Pro Arg Gly Ala Val Glu Arg His Ser
50 55 60

Asp Leu Pro Pro Leu Asn Pro Thr Ser Trp Trp Ala Asp Leu Arg Ala
65 70 75 80

60 Leu Ala Arg Asn Pro Ser Phe Val Leu Ser Ser Leu Gly Phe Thr Ala

587

85 90 95
 Val Ala Phe Val Thr Gly Ser Leu Ala Leu Trp Ala Pro Ala Phe Leu
 100 105 110
 5 Leu Arg Ser Arg Val Val Leu Gly Glu Thr Pro Pro Cys Leu Pro Gly
 115 120 125
 10 Asp Ser Cys Ser Ser Ser Asp Ser Leu Ile Phe Gly Leu Ile Thr Cys
 130 135 140
 Leu Thr Gly Val Leu Gly Val Gly Leu Gly Val Glu Ile Ser Arg Arg
 145 150 155 160
 15 Leu Arg His Ser Asn Pro Arg Ala Asp Pro Leu Val Cys Ala Thr Gly
 165 170 175
 Leu Leu Gly Ser Ala Pro Phe Leu Phe Leu Ser Leu Ala Cys Ala Arg
 180 185 190
 20 Gly Ser Ile Val Ala Thr Tyr Ile Phe Ile Phe Ile Gly Glu Thr Leu
 195 200 205
 Leu Ser Met Asn Trp Ala Ile Val Ala Asp Ile Leu Leu Tyr Val Val
 210 215 220
 Ile Pro Thr Arg Arg Ser Thr Ala Glu Ala Phe Gln Ile Val Leu Ser
 225 230 235 240
 30 His Leu Leu Gly Asp Ala Gly Ser Pro Tyr Leu Ile Gly Leu Ile Ser
 245 250 255
 Asp Arg Leu Arg Arg Asn Trp Pro Pro Ser Phe Leu Ser Glu Phe Arg
 260 265 270
 35 Ala Leu Gln Phe Ser Leu Met Leu Cys Ala Phe Val Gly Ala Leu Gly
 275 280 285
 Gly Ala Leu Pro Gly His Arg His Leu His Xaa
 290 295
 40

(2) INFORMATION FOR SEQ ID NO: 390:

45

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 49 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 390:

Met Gly Pro Gln Gly Trp Val Arg Pro Leu Lys Thr Ala Pro Lys Leu
 1 5 10 15
 55 Gly Glu Ala Ile Arg Leu Ile Leu Phe Leu Asn Phe Val Lys Gln Cys
 20 25 30
 Ile Ala Ser Val Asn Leu Cys Ile Leu Arg Leu Asn Ile Thr Pro Leu
 35 40 45
 60

Leu

5

(2) INFORMATION FOR SEQ ID NO: 391:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 61 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 391:

15 Met Tyr Val Asn Tyr Gly Thr Arg Asn Tyr Ser Thr Glu Gly Pro Ala
1 5 10 15

Ala Leu Leu Asp Gln Ala Lys Leu Ser Leu Leu Val Trp Val Leu Cys
20 25 30

20 Phe Val Leu Leu Phe Val Cys Phe Cys Gly Leu Ser Tyr Val Val Ile
35 40 45

Ala Gln Val Pro Val Gly Leu Leu Cys Ile Thr Glu Xaa
50 55 60

25

(2) INFORMATION FOR SEQ ID NO: 392:

30

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 79 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 392:

35

Met Leu Trp Phe Ala Asn Phe Phe Thr Tyr Leu Phe Leu Ser Gln Ser
1 5 10 15

40 Val Ala Phe Val His Ile Ser His Ile Gly Val Arg Gln Val Asn Thr
20 25 30

Asn Cys Tyr Phe Ser Arg Lys Ser Tyr Cys Tyr Gly Ile Leu Asn Pro
35 40 45

45 Ile Asn Cys Ile Lys Gly Lys Lys Lys Lys Lys Lys Lys Lys Lys
50 55 60

Lys Lys Lys Lys Ile Pro Ala Gly Arg Xaa Leu Phe Pro Phe Gly
65 70 75

50

(2) INFORMATION FOR SEQ ID NO: 393:

55

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 36 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 393:

60

Met Pro Gly Ala Phe Ser Glu Thr Val Ile Asn Asp Leu Leu Ser Leu
 1 5 10 15
 Phe Leu Val Leu Pro Ala Glu Leu Ser Tyr Ser Thr Leu Ser Gly Val
 5 20 25 30
 Tyr Arg Asn Ala
 35

10

(2) INFORMATION FOR SEQ ID NO: 394:

(i) SEQUENCE CHARACTERISTICS:
 15 (A) LENGTH: 180 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 394:

20 Met Ala Gln Ser Arg Asp Gly Gly Asn Pro Phe Ala Glu Pro Ser Glu
 1 5 10 15
 Leu Asp Asn Pro Phe Gln Asp Pro Ala Val Ile Gln His Arg Pro Ser
 20 25 30
 25 Arg Gln Tyr Ala Thr Leu Asp Val Tyr Asn Pro Phe Glu Thr Arg Glu
 35 40 45
 30 Pro Pro Pro Ala Tyr Glu Pro Pro Ala Pro Ala Pro Leu Pro Pro Pro
 50 55 60
 Ser Ala Pro Ser Leu Gln Pro Ser Arg Lys Leu Ser Pro Thr Glu Pro
 65 70 75 80
 35 Lys Asn Tyr Gly Ser Tyr Ser Thr Gln Ala Ser Ala Ala Ala Ala Thr
 85 90 95
 Ala Glu Leu Leu Lys Lys Gln Glu Glu Leu Asn Arg Lys Ala Glu Glu
 100 105 110
 40 Leu Asp Arg Arg Ser Glu Ser Cys Ser Met Leu Pro Trp Xaa Ala Gln
 115 120 125
 Leu Leu Asp Arg Thr Ile Gly Pro Leu Tyr Leu Leu Phe Val Gln Phe
 45 130 135 140
 Ser Pro Ala Phe Ser Arg Thr Ser Pro Trp Arg Ser Pro Lys Asn Phe
 145 150 155 160
 50 Arg Arg Leu Tyr Pro Pro Cys Thr Thr Ser Gly Cys Ala Ala Arg Trp
 165 170 175
 Xaa Phe Ser Xaa
 180
 55

(2) INFORMATION FOR SEQ ID NO: 395:

60 (i) SEQUENCE CHARACTERISTICS:

590

(A) LENGTH: 21 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 395:

5

Met Pro Thr Pro Cys Thr Ser Leu Pro Ser Cys Cys Gln His Arg Ser
 1 5 10 15

10

Ile Thr Met Thr Leu
 20

(2) INFORMATION FOR SEQ ID NO: 396:

15

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 60 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 396:

Met Pro Leu Phe Ile Pro Leu Ile Phe Phe Leu Ser Leu Leu His Cys
 1 5 10 15

25

Gln Ser Lys His Pro Ile Gln Met Ser Leu Cys Met Cys Val Asn Ile
 20 25 30

Ser Leu Val Trp Ser Pro Val Arg Trp Ile Phe Gly Ser Lys Gly Leu
 35 40 45

30

Phe Ser Val His Leu Gln Ser Ser Gln Arg Pro Ser
 50 55 60

35

(2) INFORMATION FOR SEQ ID NO: 397:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 152 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 397:

Met Ala Gly Pro Arg Pro Xaa Trp Arg Asp Gln Leu Leu Phe Met Ser
 1 5 10 15

45

Ile Ile Val Leu Val Ile Val Val Ile Cys Leu Met Leu Tyr Ala Leu
 20 25 30

50

Leu Trp Glu Ala Gly Asn Leu Thr Asp Leu Pro Asn Leu Arg Ile Gly
 35 40 45

Phe Tyr Asn Phe Cys Leu Trp Asn Glu Asp Thr Ser Thr Leu Gln Cys
 50 55 60

55

His Gln Phe Pro Glu Leu Glu Ala Leu Gly Val Pro Arg Val Gly Leu
 65 70 75 80

60

Gly Leu Ala Arg Leu Gly Val Tyr Gly Ser Leu Val Leu Thr Leu Phe
 85 90 95

Ala Pro Gln Pro Leu Leu Leu Ala Gln Cys Asn Xaa Asp Glu Arg Ala
100 105 110

5 Trp Arg Leu Ala Val Gly Phe Leu Ala Val Ser Ser Val Leu Leu Ala
115 120 125

Gly Gly Leu Gly Leu Phe Leu Ser Tyr Val Trp Asn Gly Ser Xaa Ser
130 135 140

10 Pro Ser Arg Gly Leu Gly Phe Xaa
145 150

15 (2) INFORMATION FOR SEQ ID NO: 398:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 480 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 398:

Met Ser Asp Gly Phe Asp Arg Ala Pro Gly Ala Gly Arg Gly Arg Xaa
25 1 5 10 15

Arg Gly Leu Gly Arg Gly Gly Gly Gly Pro Xaa Gly Gly Gly Phe Pro
20 25 30

30 Xaa Gly Xaa Xaa Pro Ala Glu Arg Xaa Arg His Gln Pro Pro Gln Pro
35 40 45

Lys Ala Pro Gly Phe Leu Gln Pro Xaa Pro Leu Arg Gln Pro Arg Thr
50 55 60

35 Thr Pro Pro Pro Gly Ala Gln Cys Glu Val Pro Ala Ser Pro Gln Arg
65 70 75 80

Pro Ser Arg Pro Gly Ala Leu Pro Glu Gln Thr Arg Pro Leu Arg Ala
40 85 90 95

Pro Pro Ser Ser Gln Asp Lys Ile Pro Gln Gln Asn Ser Glu Ser Ala
100 105 110

45 Met Ala Lys Pro Gln Val Val Val Ala Pro Val Leu Met Ser Lys Leu
115 120 125

Ser Val Asn Ala Pro Glu Phe Tyr Pro Ser Gly Tyr Ser Ser Ser Tyr
130 135 140

50 Thr Glu Ser Tyr Glu Asp Gly Cys Glu Asp Tyr Pro Thr Leu Ser Glu
145 150 155 160

Tyr Val Gln Asp Phe Leu Asn His Leu Thr Glu Gln Pro Gly Ser Phe
55 165 170 175

Glu Thr Glu Ile Glu Gln Phe Ala Glu Thr Leu Asn Gly Cys Val Thr
180 185 190

60 Thr Asp Asp Ala Leu Gln Glu Leu Val Glu Leu Ile Tyr Gln Gln Ala

592

	195	200	205
	Thr Ser Ile Pro Asn Phe Ser Tyr Met Gly Ala Arg Leu Cys Asn Tyr		
	210	215	220
5	Leu Ser His His Leu Thr Ile Ser Pro Gln Ser Gly Asn Phe Arg Gln		
	225	230	235 240
10	Leu Leu Leu Gln Arg Cys Arg Thr Glu Tyr Glu Val Lys Asp Gln Ala		
	245	250	255
	Ala Lys Gly Asp Glu Val Thr Arg Lys Arg Phe His Ala Phe Val Leu		
	260	265	270
15	Phe Leu Gly Glu Leu Tyr Leu Asn Leu Glu Ile Lys Gly Thr Asn Gly		
	275	280	285
	Gln Val Thr Arg Ala Asp Ile Leu Gln Val Gly Leu Arg Glu Leu Leu		
20	290	295	300
	Asn Ala Leu Phe Ser Asn Pro Met Asp Asp Asn Leu Ile Cys Ala Val		
	305	310	315 320
25	Lys Leu Leu Lys Leu Thr Gly Ser Val Leu Glu Asp Ala Trp Lys Glu		
	325	330	335
	Lys Gly Lys Met Asp Met Glu Glu Ile Ile Gln Arg Ile Glu Asn Val		
	340	345	350
30	Val Leu Asp Ala Asn Cys Ser Arg Asp Val Lys Gln Met Leu Leu Lys		
	355	360	365
	Leu Val Glu Leu Arg Ser Ser Asn Trp Gly Arg Val His Ala Thr Ser		
35	370	375	380
	Thr Tyr Arg Glu Ala Thr Pro Glu Asn Asp Pro Asn Tyr Phe Met Asn		
	385	390	395 400
40	Glu Pro Thr Phe Tyr Thr Ser Asp Gly Val Pro Phe Thr Ala Ala Asp		
	405	410	415
	Pro Asp Tyr Gln Glu Lys Tyr Gln Glu Leu Leu Glu Arg Glu Asp Phe		
	420	425	430
45	Phe Pro Asp Tyr Glu Glu Asn Gly Thr Asp Leu Ser Gly Ala Gly Asp		
	435	440	445
	Pro Tyr Leu Asp Asp Ile Asp Asp Glu Met Asp Pro Glu Ile Glu Glu		
50	450	455	460
	Ala Tyr Glu Lys Phe Cys Leu Glu Ser Glu Arg Lys Arg Lys Gln Xaa		
	465	470	475 480
55			

(2) INFORMATION FOR SEQ ID NO: 399:

60

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 423 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 399:

Met Glu Pro Lys Thr Ile Thr Asp Ala Leu Ala Ser Ser Ile Ile Lys
 1 5 10 15
 10 Ser Val Leu Pro Asn Phe Leu Pro Tyr Asn Val Met Leu Tyr Ser Asp
 20 25 30
 Ala Pro Val Ser Glu Leu Ser Leu Glu Leu Leu Leu Gln Val Val
 35 40 45
 15 Leu Pro Ala Leu Leu Glu Gln Gly His Thr Arg Gln Trp Leu Lys Gly
 50 55 60
 Leu Val Arg Ala Trp Thr Val Thr Ala Gly Tyr Leu Leu Asp Leu His
 20 65 70 75 80
 Ser Tyr Leu Leu Gly Asp Gln Glu Glu Asn Glu Asn Ser Ala Asn Gln
 85 90 95
 25 Gln Val Asn Asn Asn Gln His Ala Arg Asn Asn Asn Ala Ile Pro Val
 100 105 110
 Val Gly Glu Gly Leu His Ala Ala His Gln Ala Ile Leu Gln Gln Gly
 115 120 125
 30 Gly Pro Val Gly Phe Gln Xaa Tyr Arg Arg Pro Leu Asn Phe Pro Leu
 130 135 140
 Arg Ile Phe Leu Leu Ile Val Phe Met Cys Ile Thr Leu Leu Ile Ala
 35 145 150 155 160
 Ser Leu Ile Cys Leu Thr Leu Pro Val Phe Ala Gly Arg Trp Leu Met
 165 170 175
 40 Ser Phe Trp Thr Gly Thr Ala Lys Ile His Glu Leu Tyr Thr Ala Ala
 180 185 190
 Cys Gly Leu Tyr Val Cys Trp Leu Thr Ile Arg Ala Val Thr Val Met
 195 200 205
 45 Val Ala Trp Met Pro Gln Gly Arg Arg Val Ile Phe Gln Lys Val Lys
 210 215 220
 Glu Trp Ser Leu Met Ile Met Lys Thr Leu Ile Val Ala Val Leu Leu
 50 225 230 235 240
 Ala Gly Val Val Pro Leu Leu Leu Gly Leu Leu Phe Glu Leu Val Ile
 245 250 255
 55 Val Ala Pro Leu Arg Val Pro Leu Asp Gln Thr Pro Leu Phe Tyr Pro
 260 265 270
 Trp Gln Asp Trp Ala Leu Gly Val Leu His Ala Lys Ile Ile Ala Ala
 275 280 285
 60

594

Ile Thr Leu Met Gly Pro Gln Trp Trp Leu Lys Thr Val Ile Glu Gln
 290 295 300

5 Val Tyr Ala Asn Gly Ile Arg Asn Ile Asp Leu His Tyr Ile Val Arg
 305 310 315 320

Lys Leu Ala Ala Pro Val Ile Ser Val Leu Leu Leu Ser Leu Cys Val
 325 330 335

10 Pro Tyr Val Ile Ala Ser Gly Val Val Pro Leu Leu Gly Val Thr Ala
 340 345 350

Glu Met Gln Asn Leu Val His Arg Arg Ile Tyr Pro Phe Leu Leu Met
 355 360 365

15 Val Val Val Leu Met Ala Ile Leu Ser Phe Gln Val Arg Gln Phe Lys
 370 375 380

20 Arg Leu Tyr Glu His Ile Lys Asn Asp Lys Tyr Leu Val Gly Gln Arg
 385 390 395 400

Leu Val Asn Tyr Glu Arg Lys Ser Gly Lys Gln Gly Ser Ser Pro Pro
 405 410 415

25 Pro Pro Gln Ser Ser Gln Glu
 420

30 (2) INFORMATION FOR SEQ ID NO: 400:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 78 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 400:

Met Leu Arg Leu Asp Ile Ile Asn Ser Leu Val Thr Thr Val Phe Met
 1 5 10 15

40 Leu Ile Val Ser Val Leu Ala Leu Ile Pro Glu Thr Thr Thr Leu Thr
 20 25 30

Val Gly Gly Gly Val Phe Ala Leu Val Thr Ala Val Cys Cys Leu Ala
 35 40 45

45 Asp Gly Ala Leu Ile Tyr Arg Lys Leu Leu Phe Asn Pro Ser Gly Pro
 50 55 60

50 Tyr Gln Lys Lys Pro Val His Glu Lys Lys Glu Val Leu Xaa
 65 70 75

55 (2) INFORMATION FOR SEQ ID NO: 401:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 74 amino acids

(B) TYPE: amino acid

60 (D) TOPOLOGY: linear

595

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 401:

5 Met Leu Lys Gln Val Met Phe Val Phe Ser Gly Met Gly Pro Arg Ser
 1 5 10 15
 His Cys Trp Gly Leu Pro Leu His Val Ala Pro Leu Cys Arg Gly His
 20 25 30
 10 Gln Ala Asp Ser Ser His Leu Leu Pro Leu Lys His Gln Gly Ala Trp
 35 40 45
 Asn Arg Asn Leu Ala Asn Gln Arg His Phe Phe Cys Pro Ser Ile Phe
 50 55 60
 15 His Thr Cys Pro Thr Val Leu Phe Phe Xaa
 65 70

20 (2) INFORMATION FOR SEQ ID NO: 402:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 amino acids

(B) TYPE: amino acid

25 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 402:

30 Ala Arg Thr Ile Leu Val Leu Tyr Leu Ser Leu Gln Arg Leu Glu Asn
 1 5 10 15
 Leu Ala Tyr His
 20

35 (2) INFORMATION FOR SEQ ID NO: 403:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 87 amino acids

(B) TYPE: amino acid

40 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 403:

45 Met Pro Leu Pro Ser Val Pro Ile Leu Gly Ile Phe Ser Phe Leu Ile
 1 5 10 15
 Pro Ser Ser Gln Gly Val Ser Tyr Thr Lys Leu Pro Ile Ser Ser Pro
 20 25 30
 50 Gln Tyr Ser Pro Phe Val Asn Asp His Phe Ser Phe Leu Asn Pro Phe
 35 40 45
 Pro Val Gln Ile His Thr Gly Phe Ala Arg Val Gly Ser Tyr Met Gln
 50 55 60
 55 Met Pro Leu Val His Leu Cys Leu Leu Gln Thr Ser Leu Met Lys Asn
 65 70 75 80
 60 Ser Gly Val Gln Gln Gly Ser
 85

(2) INFORMATION FOR SEQ ID NO: 404:

5

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 92 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 404:

Met Asn Ala Ala Met Val His Ile Asn Arg Ala Leu Lys Leu Ile Ile
1 5 10 15

15

Arg Leu Phe Leu Val Glu Asp Leu Val Asp Ser Leu Lys Leu Ala Val
20 25 30

Phe Met Trp Leu Met Thr Tyr Val Gly Ala Val Phe Asn Gly Ile Thr
35 40 45

20

Leu Leu Ile Leu Ala Glu Leu Leu Ile Phe Ser Val Pro Ile Val Tyr
50 55 60

25

Glu Lys Tyr Lys Thr Gln Ile Asp His Tyr Val Gly Ile Ala Arg Asp
65 70 75 80

Gln Thr Lys Ser Ile Val Glu Lys Ile Pro Ser Lys
85 90

30

(2) INFORMATION FOR SEQ ID NO: 405:

35

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 21 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 405:

40

Met Ala Cys Ser Cys Leu Met Ile Gln Ser Phe Ser Thr Ser Ala Leu
1 5 10 15

Val Leu Phe Tyr Gly
20

45

(2) INFORMATION FOR SEQ ID NO: 406:

50

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 174 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 406:

55

Met Glu Glu Gly Gly Asn Leu Gly Gly Leu Ile Lys Met Val His Leu
1 5 10 15

60

Leu Val Leu Ser Gly Ala Trp Gly Met Gln Met Trp Val Thr Phe Val
20 25 30

Ser Gly Phe Pro Ala Phe Pro Lys Pro Ser Pro Thr Tyr Leu Arg Thr
 35 40 45
 5 Ser Ala Glu Gln Thr Leu Pro Leu Leu Leu Pro His Leu His Gly Leu
 50 55 60
 Cys Leu His Gln Pro Leu His Leu Gly Phe Thr Ala Cys Leu Gly Ser
 65 70 75 80
 10 Ala His Ile Leu Gly Gly Gln Pro Ala Leu Pro Ala Val Pro Glu Pro
 85 90 95
 Tyr Ala Gly His Cys Gln Arg Pro Leu Ala Gly Thr Pro His His Ser
 100 105 110
 15 Cys His Val Gly Pro Ala Asn Arg Gly Arg Arg Ser Glu Ala Trp Val
 115 120 125
 20 Gly Arg Tyr Gln Ala Ala Asn Arg Phe Pro Ile Leu Asn Ala Xaa Cys
 130 135 140
 Glu Arg Arg Thr Pro Ser Thr Val Leu Ser Ala Arg Ile Ser Ser Ala
 145 150 155 160
 25 Thr Met Gly Cys Pro Leu Phe Ala Ile Trp Ala Ala Ser Xaa
 165 170

30

(2) INFORMATION FOR SEQ ID NO: 407:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 64 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 407:

35 Met Ala Phe Ile Leu Leu Phe Tyr Cys Leu Met Thr Phe Leu Ser Leu
 1 5 10 15
 Glu Gln Asn Ser Ala Thr Val Glu Pro Ser Ser His Glu Ile Leu His
 20 25 30
 45 Leu Leu Gln Asn Cys Phe Glu Leu Leu Arg Thr Ser Thr Ser Gln Cys
 35 40 45
 Thr Glu Gly Ile Pro Cys Gln Arg Tyr Gln Asn Gly Leu His Ile Xaa
 50 55 60
 50

55

(2) INFORMATION FOR SEQ ID NO: 408:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 280 amino acids

(B) TYPE: amino acid

60

(D) TOPOLOGY: linear
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 408:

5	Met Glu Ala Val Val Asn Leu Tyr Gln Glu Val Met Lys His Ala Asp	1	5	10	15
	Pro Arg Ile Gln Gly Tyr Pro Leu Met Gly Ser Pro Leu Leu Met Thr	20	25	30	
10	Ser Ile Leu Leu Thr Tyr Val Tyr Phe Val Leu Ser Leu Gly Pro Arg	35	40	45	
	Ile Met Ala Asn Arg Lys Pro Phe Gln Leu Arg Gly Phe Met Ile Val	50	55	60	
15	Tyr Asn Phe Ser Leu Val Ala Leu Ser Leu Tyr Ile Val Tyr Glu Phe	65	70	75	80
	Leu Met Ser Gly Trp Leu Ser Thr Tyr Thr Trp Arg Cys Asp Pro Val	85	90	95	
20	Asp Tyr Ser Asn Ser Pro Glu Ala Leu Arg Met Val Arg Val Ala Trp	100	105	110	
	Leu Phe Leu Phe Ser Lys Phe Ile Glu Leu Met Asp Thr Val Ile Phe	115	120	125	
	Ile Leu Arg Lys Lys Asp Gly Gln Val Thr Phe Leu His Val Phe His	130	135	140	
30	His Ser Val Leu Pro Trp Ser Trp Trp Gly Val Lys Ile Ala Pro	145	150	155	160
	Gly Gly Met Gly Ser Phe His Ala Met Ile Asn Ser Ser Val His Val	165	170	175	
	Ile Met Tyr Leu Tyr Tyr Gly Leu Ser Ala Phe Gly Pro Val Ala Gln	180	185	190	
40	Pro Tyr Leu Trp Trp Lys Lys His Met Thr Ala Ile Gln Leu Ile Gln	195	200	205	
	Phe Val Leu Val Ser Leu His Ile Ser Gln Tyr Tyr Phe Met Ser Ser	210	215	220	
45	Cys Asn Tyr Gln Tyr Pro Val Ile Ile His Leu Ile Trp Met Tyr Gly	225	230	235	240
	Thr Ile Phe Phe Met Leu Phe Ser Asn Phe Trp Tyr His Ser Tyr Thr	245	250	255	
	Lys Gly Lys Arg Leu Pro Arg Ala Leu Gln Gln Asn Gly Ala Pro Gly	260	265	270	
55	Ile Ala Lys Val Lys Ala Asn Xaa	275	280		

60 (2) INFORMATION FOR SEQ ID NO: 409:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 284 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 409:

5 Met Xaa Leu Trp Pro Gln Thr Cys Ser Gly Lys Phe Asp Gly Thr Leu
 1 5 10 15
 10 Ala Phe Ser Ile His Xaa Leu Ala Val Ile Leu Gly Asp Gln Leu Thr
 20 25 30
 15 Ala Ala Asp Leu Val Pro Ile Phe Asn Gly Phe Leu Lys Asp Leu Asp
 35 40 45
 Glu Val Arg Ile Gly Val Leu Lys His Leu His Asp Phe Leu Lys Leu
 50 55 60
 20 Leu His Ile Asp Lys Arg Arg Glu Tyr Leu Tyr Gln Leu Gln Glu Phe
 65 70 75 80
 Leu Val Thr Asp Asn Ser Arg Asn Trp Arg Phe Arg Ala Glu Leu Ala
 85 90 95
 25 Glu Gln Leu Ile Leu Leu Leu Glu Leu Tyr Ser Pro Arg Asp Val Tyr
 100 105 110
 30 Asp Tyr Leu Arg Pro Ile Ala Leu Asn Leu Cys Ala Asp Lys Val Ser
 115 120 125
 Ser Val Arg Trp Ile Ser Tyr Lys Leu Val Ser Glu Met Val Lys Lys
 130 135 140
 35 Leu His Ala Ala Thr Pro Pro Thr Phe Gly Val Asp Leu Ile Asn Glu
 145 150 155 160
 Leu Val Glu Asn Phe Gly Arg Cys Pro Lys Trp Ser Gly Arg Gln Ala
 165 170 175
 40 Phe Val Phe Val Cys Gln Thr Val Ile Glu Asp Asp Cys Leu Pro Met
 180 185 190
 45 Asp Gln Phe Ala Val His Leu Met Pro His Leu Leu Thr Leu Ala Asn
 195 200 205
 Asp Arg Val Pro Asn Val Arg Val Leu Leu Ala Lys Thr Leu Arg Gln
 210 215 220
 50 Thr Leu Leu Glu Lys Asp Tyr Phe Leu Ala Ser Ala Ser Cys His Gln
 225 230 235 240
 Glu Ala Val Glu Gln Thr Ile Met Ala Leu Gln Met Asp Arg Asp Ser
 245 250 255
 55 Asp Val Lys Tyr Phe Ala Ser Ile His Pro Ala Ser Thr Lys Ile Ser
 260 265 270
 60 Glu Asp Ala Met Ser Thr Ala Ser Ser Thr Tyr Xaa
 275 280

(2) INFORMATION FOR SEQ ID NO: 410:

5

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 187 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 410:

Met Leu Phe Leu Phe Phe Val Ile Ile Phe Leu Phe Val Phe Leu Ile
1 5 10 15

15 Leu Ile Ile Gln Phe Ser Lys Pro Leu Thr Asn Pro His Pro Pro Ala
20 25 30

Gly Xaa Ser Asp Arg Arg Arg Arg Tyr Ser Ser Tyr Arg Ser His Asp
35 40 45

20

His Tyr Gln Arg Gln Arg Val Leu Gln Lys Glu Arg Ala Ile Glu Glu
50 55 60

25 Arg Arg Val Val Phe Ile Gly Lys Ile Pro Gly Arg Met Thr Arg Ser
65 70 75 80

Glu Leu Lys Gln Arg Phe Ser Val Phe Gly Glu Ile Glu Glu Cys Thr
85 90 95

30 Ile His Phe Arg Val Gln Gly Asp Asn Tyr Gly Phe Val Thr Tyr Arg
100 105 110

Tyr Ala Glu Glu Ala Phe Ala Ala Ile Glu Ser Gly His Lys Leu Arg
115 120 125

35

Gln Ala Asp Glu Gln Pro Phe Asp Leu Cys Phe Gly Gly Arg Arg Xaa
130 135 140

40 Xaa Cys Lys Arg Ser Tyr Ser Asp Leu Asp Ser Asn Arg Glu Asp Phe
145 150 155 160

Asp Pro Ala Pro Val Lys Ser Lys Phe Asp Ser Leu Asp Phe Asp Thr
165 170 175

45 Leu Leu Lys Gln Ala Gln Lys Asn Leu Arg Arg
180 185

(2) INFORMATION FOR SEQ ID NO: 411:

50

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 237 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 411:

Met Lys Leu Pro Gly Lys Phe Arg Arg Ala His Gln Gly Asn Leu Glu
1 5 10 15

60

601

Ser Gln Leu Thr Ser Glu Ser Tyr Tyr Lys Glu Thr Leu Ser Val Pro
 20 25 30
 5 Thr Val Glu His Ile Ile Gln Glu Lys Asp Ile Phe Ser Glu Gln
 35 40 45
 His Leu Lys Ala Leu Lys Cys Leu Ser Leu Val Pro Ser Val Met Gly
 50 55 60
 10 Gln Leu Lys Phe Asn Thr Ser Glu Glu His His Ala Asp Met Tyr Arg
 65 70 75 80
 Ser Asp Leu Pro Asn Pro Asp Thr Leu Ser Ala Glu Leu His Cys Trp
 85 90 95
 15 Arg Ile Lys Trp Lys His Arg Gly Lys Asp Ile Glu Leu Pro Ser Thr
 100 105 110
 Ile Tyr Glu Ala Leu His Leu Pro Asp Ile Lys Phe Phe Pro Asn Val
 115 120 125
 20 Tyr Ala Leu Leu Lys Val Leu Cys Ile Leu Pro Val Met Lys Val Glu
 130 135 140
 25 Asn Glu Arg Tyr Glu Asn Gly Arg Lys Arg Leu Lys Ala Tyr Leu Arg
 145 150 155 160
 Asn Thr Leu Thr Asp Gln Arg Ser Ser Asn Leu Ala Leu Leu Asn Ile
 165 170 175
 30 Asn Phe Asp Ile Lys His Asp Leu Asp Leu Met Val Asp Thr Tyr Ile
 180 185 190
 Lys Leu Tyr Thr Xaa Xaa Ser Xaa Leu Xaa Thr Xaa Xaa Ser Xaa Xaa
 195 200 205
 Val Glu Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Gly Xaa Xaa Xaa Xaa
 210 215 220
 40 Asp Xaa Xaa Xaa Arg Glu Lys Ala Val Arg Cys Met Xaa
 225 230 235

45 (2) INFORMATION FOR SEQ ID NO: 412:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 192 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 412:

Met Lys Pro Met Ala Val Val Ala Ser Thr Val Leu Gly Leu Val Gln
 1 5 10 15
 55 Asn Met Arg Ala Phe Gly Gly Ile Leu Val Val Val Tyr Tyr Val Phe
 20 25 30
 60 Ala Ile Ile Gly Ile Asn Leu Phe Arg Gly Val Ile Val Ala Leu Pro
 35 40 45

Gly Asn Ser Ser Leu Ala Pro Ala Asn Gly Ser Ala Pro Cys Gly Ser
 50 55 60
 5 Phe Glu Gln Leu Glu Tyr Trp Ala Asn Asn Phe Asp Asp Phe Ala Ala
 65 70 75 80
 Ala Leu Val Thr Leu Trp Asn Leu Met Val Val Asn Asn Trp Gln Val
 85 90 95
 10 Phe Leu Asp Ala Tyr Arg Arg Tyr Ser Gly Pro Trp Ser Lys Ile Tyr
 100 105 110
 Phe Val Leu Trp Trp Leu Val Ser Ser Val Ile Trp Val Asn Leu Phe
 115 120 125
 Leu Ala Leu Ile Leu Glu Asn Phe Leu His Lys Trp Asp Pro Arg Ser
 130 135 140
 20 His Leu Gln Pro Leu Ala Gly Thr Pro Glu Ala Thr Tyr Gln Met Thr
 145 150 155 160
 Val Glu Leu Leu Phe Arg Asp Ile Leu Glu Glu Pro Gly Glu Asp Glu
 165 170 175
 25 Leu Thr Glu Arg Leu Ser Gln His Pro His Leu Trp Leu Cys Arg Xaa
 180 185 190

30

35 (2) INFORMATION FOR SEQ ID NO: 413:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 21 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 413:

Asn Val Val Val Val Ala Phe Gly Leu Ile Leu Ile Ile Glu Ser Leu
 1 5 10 15

45 Gly Glu Gln Cys Pro
 20

50 (2) INFORMATION FOR SEQ ID NO: 414:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 51 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 414:

Met Asn Trp Gly Leu Ser Ile Trp Leu His Tyr Tyr Glu Lys Lys Lys
 1 5 10 15

60

Glu Gln Val Phe Leu Val Ile Leu Ala His Val Val Arg Arg Cys Ala
 20 25 30
 5 Ser Asp Gly Ile Leu Gln Phe Glu Ser Ser Leu Leu Lys Met Arg Arg
 35 40 45
 Ala Pro Xaa
 50

10

(2) INFORMATION FOR SEQ ID NO: 415:

15 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 32 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 415:

20 Met Leu Ile Ile Ser Leu Arg Pro Gln Phe Pro Ser Leu Ile Val Gln
 1 5 10 15
 Leu Glu Cys Ser Val Leu Phe Leu Pro Ile Ser Leu Asn Leu Leu Leu
 20 25 30
 25

30

(2) INFORMATION FOR SEQ ID NO: 416:

35 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 163 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 416:

40 Met Val Lys Val Cys Asn Asp Ser Asp Arg Trp Ser Leu Ile Ser Leu
 1 5 10 15
 Ser Asn Asn Ser Gly Lys Asn Val Glu Leu Lys Phe Val Asp Ser Leu
 20 25 30
 45 Arg Arg Gln Phe Glu Phe Ser Val Asp Ser Phe Gln Ile Lys Leu Asp
 35 40 45
 Ser Leu Leu Leu Phe Tyr Glu Cys Ser Glu Asn Pro Met Thr Glu Thr
 50 55 60
 50 Phe His Pro Thr Ile Ile Gly Glu Ser Val Tyr Gly Asp Phe Gln Glu
 65 70 75 80
 Ala Phe Asp His Leu Cys Asn Lys Ile Ile Ala Thr Arg Asn Pro Glu
 85 90 95
 55 Glu Ile Arg Gly Gly Gly Leu Leu Lys Tyr Cys Asn Leu Leu Val Arg
 100 105 110
 60 Gly Phe Arg Pro Ala Ser Asp Glu Ile Lys Thr Leu Gln Arg Tyr Met

115 120 125

Cys Ser Arg Phe Phe Ile Asp Phe Ser Asp Ile Gly Glu Gln Gln Arg
 130 135 140

5 Lys Leu Glu Ser Tyr Leu Gln Asn His Phe Val Gly Ile Gly Arg Pro
 145 150 155 160

10 Gln Val Xaa

15 (2) INFORMATION FOR SEQ ID NO: 417:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 174 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 417:

Met Ala Pro Lys Gly Lys Val Gly Thr Arg Gly Lys Lys Gln Ile Phe
 1 5 10 15

25 Glu Glu Asn Arg Glu Thr Leu Lys Phe Tyr Leu Arg Ile Ile Leu Gly
 20 25 30

Ala Asn Ala Ile Tyr Cys Leu Val Thr Leu Val Phe Phe Tyr Ser Ser
 35 40 45

30 Ala Ser Phe Trp Ala Trp Leu Ala Leu Gly Phe Ser Leu Ala Val Tyr
 50 55 60

35 Gly Ala Ser Tyr His Ser Met Ser Ser Met Ala Arg Ala Ala Phe Ser
 65 70 75 80

Glu Asp Gly Ala Leu Met Asp Gly Gly Met Asp Leu Asn Met Glu Gln
 85 90 95

40 Gly Met Ala Glu His Leu Lys Asp Val Ile Leu Leu Thr Ala Ile Val
 100 105 110

Gln Val Leu Ser Cys Phe Ser Leu Tyr Val Trp Ser Phe Trp Leu Leu
 115 120 125

45 Ala Pro Gly Arg Ala Leu Tyr Leu Leu Trp Val Asn Val Leu Gly Pro
 130 135 140

50 Trp Phe Thr Ala Asp Ser Gly Thr Pro Ala Pro Glu His Asn Glu Lys
 145 150 155 160

Arg Gln Arg Arg Gln Glu Arg Arg Gln Met Lys Arg Leu Xaa
 165 170

55

(2) INFORMATION FOR SEQ ID NO: 418:

(i) SEQUENCE CHARACTERISTICS:

60 (A) LENGTH: 50 amino acids

605

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 418:

5 Met Glu Leu Pro Lys Gly Leu Gln Gly Val Gly Pro Val Ala Met Met
 1 5 10 15
 Arg Pro Phe Tyr Leu Leu Leu Pro Val Leu Cys Thr Gln Ala Leu Arg
 20 25 30
 10 Gln Ser Gln Gly Lys Ser Pro Leu Leu Trp Lys Arg Thr Cys Cys Leu
 35 40 45
 Ala Xaa
 15 50

(2) INFORMATION FOR SEQ ID NO: 419:

20

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 120 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 419:

Met Leu Gly Lys Gly Gly Gly Arg Ala Gly Leu Leu Arg Tyr Arg Leu
 1 5 10 15
 30 Leu Tyr Phe Thr Leu Val Val Gly Glu Gly Glu Pro Gly Glu Asn Lys
 20 25 30
 Val Thr Ile Pro Phe Phe Glu Thr Gly Lys Lys Ile Ile Phe Cys Ser
 35 40 45
 35 Val Lys Met Val Glu Asn Ser Asn Val Pro Ser His Lys Gly Pro Val
 50 55 60
 40 Pro Leu Arg Ser Glu Gln Trp Glu Leu Lys Ile Ser Glu Thr Leu Gly
 65 70 75 80
 Glu Gly Lys Ile Gly Phe Leu Leu Ile Gly Arg Cys Ser Ser Gly Xaa
 85 90 95
 45 Gly Gly Leu Cys Phe Cys Trp Asp Val Leu Cys Cys Met Tyr Ala Tyr
 100 105 110
 Met Asp Arg Ser Leu Leu Ser Leu
 115 120
 50

(2) INFORMATION FOR SEQ ID NO: 420:

55

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 159 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

60

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 420:

606

Met Thr His Leu Leu Leu Thr Ala Thr Val Thr Pro Ser Glu Gln Asn
 1 5 10 15

5 Ser Ser Arg Glu Pro Gly Trp Glu Thr Ala Met Ala Lys Asp Ile Leu
 20 25 30

Gly Glu Ala Gly Leu His Phe Asp Glu Leu Asn Lys Leu Arg Val Leu
 35 40 45

10 Asp Pro Glu Val Thr Gln Gln Thr Ile Glu Leu Lys Glu Glu Cys Lys
 50 55 60

Asp Phe Val Asp Lys Ile Gly Gln Phe Gln Lys Ile Val Gly Gly Leu
 65 70 75 80

15 Ile Glu Leu Val Asp Gln Leu Ala Lys Glu Ala Glu Asn Glu Lys Met
 85 90 95

Lys Ala Ile Gly Ala Arg Asn Leu Leu Lys Ser Ile Ala Lys Gln Arg
 100 105 110

Glu Ala Gln Gln Gln Gln Leu Gln Ala Leu Ile Ala Glu Lys Lys Met
 115 120 125

25 Gln Leu Glu Arg Tyr Arg Val Glu Tyr Glu Ala Leu Cys Lys Val Glu
 130 135 140

Ala Glu Gln Asn Glu Phe Ile Asp Gln Phe Ile Phe Gln Lys Xaa
 145 150 155

30

(2) INFORMATION FOR SEQ ID NO: 421:

- 35 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 154 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 421:

40 Met Asn Val Gly Val Ala His Ser Glu Val Asn Pro Asn Thr Arg Val
 1 5 10 15

45 Met Asn Ser Arg Gly Met Trp Leu Thr Tyr Ala Leu Gly Val Gly Leu
 20 25 30

Leu His Ile Val Leu Leu Ser Ile Pro Phe Phe Ser Val Pro Val Ala
 35 40 45

50 Trp Thr Leu Thr Asn Ile Ile His Asn Leu Gly Met Tyr Val Phe Leu
 50 55 60

His Ala Val Lys Gly Thr Pro Phe Glu Thr Pro Asp Gln Gly Lys Ala
 65 70 75 80

55 Arg Leu Leu Thr His Trp Glu Gln Leu Asp Tyr Gly Val Gln Phe Thr
 85 90 95

Ser Ser Arg Lys Phe Phe Thr Ile Ser Pro Ile Ile Leu Tyr Phe Leu
 100 105 110

60

Ala Ser Phe Tyr Thr Lys Tyr Asp Pro Thr His Phe Ile Leu Asn Thr
 115 120 125

5 Ala Ser Leu Leu Ser Val Leu Ile Pro Lys Met Pro Gln Leu His Gly
 130 135 140

Val Arg Ile Phe Gly Ile Asn Lys Tyr Xaa
 145 150

10

(2) INFORMATION FOR SEQ ID NO: 422:

15 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 204 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 422:

Met Val Cys Gly Gly Phe Ala Cys Ser Lys Asn Cys Leu Cys Ala Leu
 1 5 10 15

25 Asn Leu Leu Tyr Thr Leu Val Ser Leu Leu Leu Ile Gly Ile Ala Ala
 20 25 30

Trp Gly Ile Gly Phe Gly Leu Ile Ser Ser Leu Arg Val Val Gly Val
 35 40 45

30 Val Ile Ala Val Gly Ile Phe Leu Phe Leu Ile Ala Leu Val Gly Leu
 50 55 60

Ile Gly Ala Val Lys His His Gln Val Leu Leu Phe Phe Tyr Met Ile
 65 70 75 80

35 Ile Leu Leu Leu Val Phe Ile Val Gln Phe Ser Val Ser Cys Ala Cys
 85 90 95

Leu Ala Leu Asn Gln Glu Gln Gln Gly Gln Leu Leu Glu Val Gly Trp
 100 105 110

40 Asn Asn Thr Ala Ser Ala Arg Asn Asp Ile Gln Arg Asn Leu Asn Cys
 115 120 125

45 Cys Gly Phe Arg Ser Val Asn Pro Asn Asp Thr Cys Leu Ala Ser Cys
 130 135 140

Val Lys Ser Asp His Ser Cys Ser Pro Cys Ala Pro Ile Ile Gly Glu
 145 150 155 160

50 Tyr Ala Gly Glu Val Leu Arg Phe Val Gly Gly Ile Gly Leu Phe Phe
 165 170 175

Ser Phe Thr Glu Ile Leu Gly Val Trp Leu Thr Tyr Arg Tyr Arg Asn
 180 185 190

Gln Lys Asp Pro Arg Ala Asn Pro Ser Ala Phe Leu
 195 200

60

(2) INFORMATION FOR SEQ ID NO: 423:

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 67 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 423:

10 Met Leu Gln Ser Ile Ile Lys Asn Ile Trp Ile Pro Met Lys Pro Tyr
1 5 10 15
Tyr Thr Lys Val Tyr Gln Glu Ile Trp Ile Gly Met Gly Leu Met Gly
20 25 30
15 Phe Ile Val Tyr Lys Ile Arg Ala Ala Asp Lys Arg Ser Lys Ala Leu
35 40 45
Lys Ala Ser Ala Pro Ala Pro Gly His His Asn Gln Ile Tyr Leu Glu
20 50 55 60
Tyr Met Xaa
65

25

(2) INFORMATION FOR SEQ ID NO: 424:

(i) SEQUENCE CHARACTERISTICS:

- 30 (A) LENGTH: 25 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 424:

35 Met Leu Gly Val Ser Leu Phe Leu Leu Val Val Leu Tyr His Tyr Val
1 5 10 15
Ala Val Asn Asn Pro Lys Lys Gln Glu
20 25
40

(2) INFORMATION FOR SEQ ID NO: 425:

(i) SEQUENCE CHARACTERISTICS:

- 45 (A) LENGTH: 299 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 425:

50 Met Ala Ala Xaa Glu Pro Ala Val Leu Ala Leu Pro Asn Ser Gly Ala
1 5 10 15
Gly Gly Ala Gly Ala Pro Ser Gly Thr Val Pro Val Leu Phe Cys Phe
55 20 25 30
Ser Val Phe Ala Arg Pro Ser Ser Val Pro His Gly Ala Gly Tyr Glu
35 40 45
60 Leu Leu Ile Gln Lys Phe Leu Ser Leu Tyr Gly Asp Gln Ile Asp Met

609

50 55 60
 His Arg Lys Phe Val Val Gln Leu Phe Ala Glu Glu Trp Gly Gln Tyr
 65 70 75 80
 5 Val Asp Leu Pro Lys Gly Phe Ala Val Ser Glu Arg Cys Lys Val Arg
 85 90 95
 10 Leu Val Pro Leu Gln Ile Gln Leu Thr Thr Leu Gly Asn Leu Thr Pro
 100 105 110
 Ser Ser Thr Val Phe Phe Cys Cys Asp Met Gln Glu Arg Phe Arg Pro
 115 120 125
 15 Ala Ile Lys Tyr Phe Gly Asp Ile Ile Ser Val Gly Gln Arg Leu Leu
 130 135 140
 Gln Gly Ala Arg Ile Leu Gly Ile Pro Val Ile Val Thr Glu Gln Tyr
 20 145 150 155 160
 Pro Lys Gly Leu Gly Ser Thr Val Gln Glu Ile Asp Leu Thr Gly Val
 165 170 175
 25 Lys Leu Val Leu Pro Lys Thr Lys Phe Ser Met Val Leu Pro Glu Val
 180 185 190
 Glu Ala Ala Leu Ala Glu Ile Pro Gly Val Arg Ser Val Val Leu Phe
 195 200 205
 30 Gly Val Glu Thr His Val Cys Ile Gln Gln Thr Ala Leu Glu Leu Val
 210 215 220
 Gly Arg Gly Val Glu Val His Ile Val Ala Asp Ala Thr Ser Ser Arg
 35 225 230 235 240
 Ser Met Met Asp Arg Met Phe Ala Leu Glu Arg Leu Ala Xaa Xaa Gly
 245 250 255
 40 Ile Ile Val Thr Thr Ser Glu Ala Val Leu Leu Gln Leu Val Ala Asp
 260 265 270
 Lys Asp His Pro Lys Phe Lys Glu Ile Gln Asn Leu Ile Lys Ala Ser
 275 280 285
 45 Ala Pro Glu Ser Gly Leu Leu Ser Lys Val Xaa
 290 295

50 (2) INFORMATION FOR SEQ ID NO: 426:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 13 amino acids

(B) TYPE: amino acid

55 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 426:

Met Arg Asp Leu Gly Thr Leu Leu Ser Pro Val Cys Ser
 1 5 10
 60

(2) INFORMATION FOR SEQ ID NO: 427:

5

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 198 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 427:

10

Met Phe Gly Cys Leu Val Ala Gly Arg Leu Val Gln Thr Ala Ala Gln
 1 5 10 15

15

Gln Val Ala Glu Asp Lys Phe Val Phe Asp Leu Pro Asp Tyr Glu Ser
 20 25 30

Ile Asn His Val Val Val Phe Met Leu Gly Thr Ile Pro Phe Pro Glu
 35 40 45

20

Gly Met Gly Gly Ser Val Tyr Phe Ser Tyr Pro Asp Ser Asn Gly Met
 50 55 60

25

Pro Val Trp Gln Leu Leu Gly Phe Val Thr Asn Gly Lys Pro Ser Ala
 65 70 75 80

Ile Phe Lys Ile Ser Gly Leu Lys Ser Gly Glu Gly Ser Gln His Pro
 85 90 95

30

Phe Gly Ala Met Asn Ile Val Arg Thr Pro Ser Val Ala Gln Ile Gly
 100 105 110

Ile Ser Val Glu Leu Leu Asp Ser Met Ala Gln Gln Thr Pro Val Gly
 115 120 125

35

Asn Ala Ala Val Ser Ser Val Asp Ser Phe Thr Gln Phe Thr Gln Lys
 130 135 140

40

Met Leu Asp Asn Phe Tyr Asn Phe Ala Ser Ser Phe Ala Val Ser Gln
 145 150 155 160

Ala Gln Met Thr Pro Ser Pro Ser Glu Met Phe Ile Pro Ala Asn Val
 165 170 175

45

Val Leu Lys Trp Tyr Glu Asn Phe Gln Arg Arg Leu Ala Gln Asn Pro
 180 185 190

Xaa Phe Trp Xaa Thr Xaa
 195

50

(2) INFORMATION FOR SEQ ID NO: 428:

55

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 47 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 428:

60

Met Gly Leu Pro Leu Met Ala Leu Met Trp Ser Thr Leu Pro Ala Ser

611

1 5 10 15
 Ala Gly Val Asn Phe Ile Leu Ala Leu Pro Leu Leu Leu Trp Lys
 20 25 30
 5 Asn Arg Gly Gly Val Gly Arg Ser Val Met Ser Ala Val Glu Xaa
 35 40 45
 10
 (2) INFORMATION FOR SEQ ID NO: 429:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 370 amino acids
 15 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 429:
 20 Met Lys Lys Val Glu Glu Lys Arg Val Asp Val Asn Ser Ala Val Ala
 1 5 10 15
 Met Gly Glu Val Ile Leu Ala Val Cys His Pro Asp Cys Ile Thr Thr
 20 25 30
 25 Ile Lys His Trp Ile Thr Ile Ile Arg Ala Arg Phe Glu Glu Val Leu
 35 40 45
 Thr Trp Ala Lys Gln His Gln Gln Arg Leu Glu Thr Ala Leu Ser Glu
 50 55 60
 30 Leu Val Ala Asn Ala Glu Leu Leu Glu Glu Leu Leu Ala Trp Ile Gln
 65 70 75 80
 Trp Ala Glu Thr Thr Leu Ile Gln Arg Asp Gln Glu Pro Ile Pro Gln
 35 85 90 95
 Asn Ile Asp Arg Val Lys Ala Leu Ile Ala Glu His Gln Thr Phe Met
 100 105 110
 40 Glu Glu Met Thr Arg Lys Gln Pro Asp Val Asp Arg Val Thr Lys Thr
 115 120 125
 Tyr Lys Arg Lys Asn Ile Glu Pro Thr His Ala Pro Phe Ile Glu Lys
 130 135 140
 45 Ser Arg Ser Gly Gly Arg Lys Ser Leu Ser Gln Pro Thr Pro Pro Pro
 145 150 155 160
 Met Pro Ile Leu Ser Gln Ser Glu Ala Lys Asn Pro Arg Ile Asn Gln
 50 165 170 175
 Leu Ser Ala Arg Trp Gln Gln Val Trp Leu Leu Ala Leu Glu Arg Gln
 180 185 190
 55 Arg Lys Leu Asn Asp Ala Leu Asp Arg Leu Glu Glu Leu Lys Glu Phe
 195 200 205
 Ala Asn Phe Asp Phe Asp Val Trp Arg Lys Lys Tyr Met Arg Trp Met
 210 215 220
 60

612

Asn His Lys Lys Ser Arg Val Met Asp Phe Phe Arg Arg Ile Asp Lys
 225 230 235 240
 5 Asp Gln Asp Gly Lys Ile Thr Arg Gln Glu Phe Ile Asp Gly Ile Leu
 245 250 255
 Ala Ser Lys Phe Pro Thr Thr Lys Leu Glu Met Thr Ala Val Ala Asp
 260 265 270
 10 Ile Phe Asp Arg Asp Gly Asp Gly Tyr Ile Asp Tyr Tyr Glu Phe Val
 275 280 285
 Ala Ala Leu His Pro Asn Lys Asp Ala Tyr Arg Pro Thr Thr Asp Ala
 290 295 300
 15 Asp Lys Ile Glu Asp Glu Val Thr Arg Gln Val Ala Gln Cys Lys Cys
 305 310 315 320
 Ala Lys Arg Phe Gln Val Glu Gln Ile Gly Glu Asn Lys Tyr Arg Phe
 325 330 335
 Phe Leu Gly Asn Gln Phe Gly Asp Ser Gln Gln Leu Arg Leu Val Arg
 340 345 350
 25 Ile Leu Arg Asn Arg Asp Gly Ser Arg Trp Trp Arg Met Asp Gly Leu
 355 360 365
 Gly Xaa
 370
 30

(2) INFORMATION FOR SEQ ID NO: 430:

35 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 30 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 430:

40 Met Asn Val Lys Thr Phe Ser Xaa Asp His Met His Phe Leu Cys Cys
 1 5 10 15
 45 Leu Tyr Leu Arg Tyr Val Thr Phe Val Tyr Leu Asn Leu Phe
 20 25 30

(2) INFORMATION FOR SEQ ID NO: 431:

50 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 24 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 431:

Met Glu Pro His Leu Arg Cys Arg Val Thr Arg Val Arg Gly Ser Leu
 1 5 10 15
 60 Gly Asn Thr Gly Arg Trp Leu Leu

5 (2) INFORMATION FOR SEQ ID NO: 432:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 53 amino acids

(B) TYPE: amino acid

10 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 432:

Met His Tyr Leu Val Leu Gly Gly Leu Gly Val Phe Leu Phe Phe Ser
 1 5 10 15
 Cys Phe Val Phe Leu Phe Phe Xaa Phe Ser Phe Ala Phe Phe Pro Phe
 20 25 30
 Tyr Leu Glu Gly Met Gly Gly Ser Gly Asn Arg Glu Val Gly Gly Gly
 35 40 45
 Phe Cys Leu Phe Phe
 50

25

(2) INFORMATION FOR SEQ ID NO: 433:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 176 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 433:

35 Met Val Ser Lys Ala Leu Leu Arg Leu Val Ser Ala Val Asn Arg Arg
 1 5 10 15
 Arg Met Lys Leu Leu Leu Gly Ile Ala Leu Leu Ala Tyr Val Ala Ser
 20 25 30
 Val Trp Gly Asn Phe Val Asn Met Arg Ser Ile Gln Glu Asn Gly Glu
 35 40 45
 Leu Lys Ile Glu Ser Lys Ile Glu Glu Met Val Glu Pro Leu Arg Glu
 50 55 60
 Lys Ile Arg Asp Leu Glu Lys Ser Phe Thr Gln Lys Tyr Pro Pro Val
 65 70 75 80
 Lys Phe Leu Ser Glu Lys Asp Arg Lys Arg Ile Leu Ile Thr Gly Gly
 85 90 95
 Ala Gly Phe Val Gly Ser His Leu Thr Asp Lys Leu Met Met Asp Gly
 100 105 110
 His Glu Val Thr Val Val Asp Asn Phe Phe Thr Gly Arg Lys Arg Asn
 115 120 125
 Val Glu His Trp Ile Gly His Glu Asn Phe Glu Leu Ile Asn His Asp
 130 135 140

60

Val Trp Ser Pro Ser Thr Ser Arg Leu Thr Arg Tyr Thr Ile Trp His
 145 150 155 160

5 Leu Gln Pro Pro Leu Gln Thr Thr Cys Ile Ile Leu Ser Arg His Xaa
 165 170 175

10

(2) INFORMATION FOR SEQ ID NO: 434:

15

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 77 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 434:

20

Met Leu Arg Cys Trp Pro Leu Phe Trp Leu Pro Leu Val Ser Pro Phe
 1 5 10 15

25

Cys Ser Leu Phe Trp Leu Leu Val Glu Trp Phe Gly Thr Asn Ile Asp
 20 25 30

Arg Glu Ser Tyr Asp Ala Ile Gly Gly Pro Ser Trp Met Thr Ala Ser
 35 40 45

30

Ser Phe Cys Leu Ser Asn Ser Asn Ile Trp Ser Leu Glu Ile Ser Ser
 50 55 60

Gly Ser Thr Ser Val Val His Ser Gln Gln Ala Met Asp
 65 70 75

35

(2) INFORMATION FOR SEQ ID NO: 435:

40

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 32 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 435:

45

Met Arg Ser Cys Glu Ile Gln Leu Cys Val Trp Leu Leu Val Ser Ser
 1 5 10 15

50

His Val Asp Met Val Leu Gly Gly Ser Pro Ser Thr Leu Tyr Met Met
 20 25 30

55

(2) INFORMATION FOR SEQ ID NO: 436:

60

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 30 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 436:

5 Met Val Val Asn Ser Leu Cys Phe Leu Ser Leu Leu Val Ile Leu
 1 5 10 15

Glu Leu Ser Thr Asp Ser Ser Ala Arg Leu Leu Tyr His Glu
 20 25 30

10

(2) INFORMATION FOR SEQ ID NO: 437:

15 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 69 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 437:

20

Met Asp Lys Gln Lys His Leu Glu Val Arg Arg Ser Val Phe Lys Ile
 1 5 10 15

25

Gln Gly Lys Ile Ala Phe Ser Leu Met Phe Val Leu Lys Asp Leu Ser
 20 25 30

Pro Thr Ile Phe Ser His Ser Ile Leu Leu Leu Leu Pro His His Val
 35 40 45

30

Leu Pro Cys Thr Pro Gln Met Val Arg Gly Val Thr Gln Val Leu Arg
 50 55 60

Glu Phe Gly Asp Gln
 65

35

(2) INFORMATION FOR SEQ ID NO: 438:

40 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 19 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 438:

45

Met Pro Leu Cys Phe Phe Ser Phe Leu Cys Cys Trp Val Leu Val Phe
 1 5 10 15

Lys Leu Ile

50

(2) INFORMATION FOR SEQ ID NO: 439:

55

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 43 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

60

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 439:

Met Lys Phe Ser Leu Val Leu Leu Ile Lys Ile Ile Ser Phe Glu Arg
 1 5 10 15
 5 Leu Leu Ile Phe Leu Phe Pro Leu Ser Phe Leu Pro Asn Ile Trp Arg
 20 25 30
 Arg Val Met Val Asn Leu Asn Ile Leu Phe Xaa
 35 40
 10

(2) INFORMATION FOR SEQ ID NO: 440:

15 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 33 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 440:

Met Leu Leu Phe Pro Ser Leu Leu Phe Ala Ala Thr Tyr Asn Val Ala
 1 5 10 15
 25 Asn Pro Ser Arg Leu Ile Leu Tyr Met Ile Ser Ala Gly Ala Asp Ser
 20 25 30
 Gln

30

(2) INFORMATION FOR SEQ ID NO: 441:

35 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 53 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 441:

40 Met Trp Gln Val Arg Gly Leu Pro Pro Val Pro Leu Leu Leu Thr Met
 1 5 10 15
 Ser Pro Pro Pro Cys Leu Ser Ser Pro Phe Pro Phe Ile Ser Val Pro
 20 25 30
 45 Leu Phe Glu Ala Val Pro Ile Ser Val Ser Asp Gln Pro Ser Pro Xaa
 35 40 45
 Leu Thr Thr Leu Leu
 50 50

(2) INFORMATION FOR SEQ ID NO: 442:

55 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 64 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 60 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 442:

Met Ile Thr Ser Val Leu Val Phe Leu Ile Phe Phe Phe Pro Tyr Leu
 1 5 10 15
 5 Ser Leu Val Thr Leu Leu Gln Ala Arg Asn Leu Trp Val Ile His Arg
 20 25 30
 Ala Ala Leu Cys Glu Ser Gly Leu Phe His Trp Arg Lys Gly Ile Glu
 35 40 45
 10 Asn Gln Leu Glu Pro Met Tyr Phe Leu Pro His Gly Thr Leu Phe Leu
 50 55 60

15

(2) INFORMATION FOR SEQ ID NO: 443:
 20 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 34 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 443:

Met Leu Tyr Ser Cys Glu Pro Tyr Leu Ile Ile Leu Asn Ile Tyr Ser
 1 5 10 15
 30 Gln Lys Ala Phe Tyr Phe Tyr Phe Phe Glu Gly Ser Phe Ser Val Cys
 20 25 30
 Thr Leu

35

(2) INFORMATION FOR SEQ ID NO: 444:
 40 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 89 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 444:

Met Arg Gln Arg Gln Ala Ala Cys Gln Pro Pro Pro Ser Arg Asn Gly
 1 5 10 15
 50 Leu Ala Gln Glu Cys Pro Pro His Ile Pro Ser Ser Phe Phe Leu Val
 20 25 30
 Lys Leu Leu Phe Ile Pro Trp Leu Ala Ser Leu Leu Ser Ser Pro Leu
 35 40 45
 55 Asn Leu Leu Leu Leu Val Ser Ile Ser Trp Asp Leu Gly Leu Lys Leu
 50 55 60
 Asn Leu Gln Gln Cys Arg Gln His Gln Val Leu Gln Glu Lys Asn Thr
 65 70 75 80
 60

Lys Lys Phe Asn Lys Lys Lys Lys Lys
85

5

(2) INFORMATION FOR SEQ ID NO: 445:

(i) SEQUENCE CHARACTERISTICS:

10

(A) LENGTH: 350 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 445:

15

Met Asp Phe Ile Thr Ser Thr Ala Ile Leu Pro Leu Leu Phe Gly Cys
1 5 10 15

Leu Gly Val Phe Gly Leu Phe Arg Leu Leu Gln Trp Val Arg Gly Lys
20 25 30

20

Ala Tyr Leu Arg Asn Ala Val Val Val Ile Thr Gly Ala Thr Ser Gly
35 40 45

Leu Gly Lys Glu Cys Ala Lys Val Phe Tyr Ala Ala Gly Ala Lys Leu
50 55 60

25

Val Leu Cys Gly Arg Asn Gly Gly Ala Leu Glu Glu Leu Ile Arg Glu
65 70 75 80

30

Leu Thr Ala Ser His Ala Thr Lys Val Gln Thr His Lys Pro Tyr Leu
85 90 95

Val Thr Phe Asp Leu Thr Asp Ser Gly Ala Ile Val Ala Ala Ala Ala
100 105 110

35

Glu Ile Leu Gln Cys Phe Gly Tyr Val Asp Ile Leu Val Asn Asn Ala
115 120 125

Gly Ile Ser Tyr Arg Gly Thr Ile Met Asp Thr Thr Val Asp Val Asp
130 135 140

40

Lys Arg Val Met Glu Thr Asn Tyr Phe Gly Pro Val Ala Leu Thr Lys
145 150 155 160

45

Ala Leu Leu Pro Ser Met Ile Lys Arg Arg Gln Gly His Ile Val Ala
165 170 175

Ile Ser Ser Ile Gln Gly Lys Met Ser Ile Pro Phe Arg Ser Ala Tyr
180 185 190

50

Ala Ala Ser Lys His Ala Thr Gln Ala Phe Phe Asp Cys Leu Arg Ala
195 200 205

Glu Met Glu Gln Tyr Glu Ile Glu Val Thr Val Ile Ser Pro Gly Tyr
210 215 220

55

Ile His Thr Asn Leu Ser Val Asn Ala Ile Thr Ala Asp Gly Ser Arg
225 230 235 240

60

Tyr Gly Val Met Asp Thr Thr Thr Ala Gln Gly Arg Ser Pro Val Glu
245 250 255

Val Ala Gln Asp Val Leu Ala Ala Val Gly Lys Lys Lys Lys Asp Val
 260 265 270

5 Ile Leu Ala Asp Leu Leu Pro Ser Leu Ala Val Tyr Leu Arg Thr Leu
 275 280 285

Ala Pro Gly Leu Phe Phe Ser Leu Met Pro Pro Gly Pro Glu Lys Ser
 290 295 300

10 Gly Asn Pro Arg Thr Pro Ser Thr Leu Thr Ser Gln Gly Gln Gly Arg
 305 310 315 320

15 Glu Ala Ala Leu Leu Gly Leu Leu Thr Leu Gln Gly Thr Val Ala Phe
 325 330 335

Val Glu Thr Leu Met Glu Ile Cys Leu Thr Ser Gly Lys Asp
 340 345 350

20

(2) INFORMATION FOR SEQ ID NO: 446:

- 25 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 49 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 446:

30 Met Val Phe Leu Pro Arg Gly Val Val Val Ser Gly Gly Ala Ala Cys
 1 5 10 15

Leu Trp Leu Thr Phe Ile Leu Glu Thr Glu Val Tyr Leu Asp Leu Ala
 20 25 30

35 Thr Glu Ala Arg Ala His Ser Arg Met Gly Leu Gly Leu Trp Pro Pro
 35 40 45

40 Asn

45 (2) INFORMATION FOR SEQ ID NO: 447:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 278 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 447:

Met Ala Ser Ala Glu Leu Asp Tyr Thr Ile Glu Ile Pro Asp Gln Pro
 1 5 10 15

55 Cys Trp Ser Gln Lys Asn Ser Pro Ser Pro Gly Gly Lys Glu Ala Glu
 20 25 30

Thr Arg Gln Pro Val Val Ile Leu Leu Gly Trp Gly Gly Cys Lys Asp
 35 40 45

60

620

Lys Asn Leu Ala Lys Tyr Ser Ala Ile Tyr His Lys Arg Gly Cys Ile
 50 55 60
 Val Ile Arg Tyr Thr Ala Pro Trp His Met Val Phe Phe Ser Glu Ser
 5 65 70 75 80
 Leu Gly Ile Pro Ser Leu Arg Val Leu Ala Gln Lys Leu Leu Glu Leu
 85 90 95
 10 Leu Phe Asp Tyr Glu Ile Glu Lys Glu Pro Leu Leu Phe His Val Phe
 100 105 110
 Ser Asn Gly Gly Val Met Leu Tyr Arg Tyr Val Leu Glu Leu Leu Gln
 115 120 125
 15 Thr Arg Arg Phe Cys Arg Leu Arg Val Val Gly Thr Ile Phe Asp Ser
 130 135 140
 Ala Pro Gly Asp Ser Asn Leu Val Gly Ala Leu Arg Ala Leu Ala Ala
 20 145 150 155 160
 Ile Leu Glu Arg Arg Ala Ala Met Leu Arg Leu Leu Leu Val Ala
 165 170 175
 25 Phe Ala Leu Val Val Val Leu Phe His Val Leu Leu Ala Pro Ile Thr
 180 185 190
 Ala Xaa Phe His Thr His Phe Tyr Asp Arg Leu Gln Asp Ala Gly Ser
 195 200 205
 30 Arg Trp Pro Glu Leu Tyr Leu Tyr Ser Arg Ala Asp Glu Val Val Leu
 210 215 220
 Ala Arg Asp Ile Glu Arg Met Val Glu Ala Arg Leu Ala Arg Arg Val
 225 230 235 240
 Leu Ala Arg Ser Val Asp Phe Val Ser Ser Ala His Val Ser His Leu
 245 250 255
 40 Arg Asp Tyr Pro Thr Tyr Tyr Thr Ser Leu Cys Val Asp Phe Met Arg
 260 265 270
 Asn Cys Val Arg Cys Xaa
 275
 45

(2) INFORMATION FOR SEQ ID NO: 448:

50

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 199 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 448:

60

Met Ser Phe Ile Phe Asp Trp Ile Tyr Ser Gly Phe Ser Ser Val Leu
 1 5 10 15
 Gln Phe Leu Gly Leu Tyr Lys Lys Thr Gly Lys Leu Val Phe Leu Gly
 20 25 30

Leu Asp Asn Ala Gly Lys Thr Thr Leu Leu His Met Leu Lys Asp Asp
 35 40 45
 5 Arg Leu Gly Gln His Val Pro Thr Leu His Pro Thr Ser Glu Glu Leu
 50 55 60
 Thr Ile Ala Gly Met Thr Phe Thr Thr Phe Asp Leu Gly Gly His Val
 65 70 75 80
 10 Gln Ala Arg Arg Val Trp Lys Asn Tyr Leu Pro Ala Ile Asn Gly Ile
 85 90 95
 15 Val Phe Leu Val Asp Cys Ala Asp His Glu Arg Leu Leu Glu Ser Lys
 100 105 110
 Glu Glu Leu Asp Ser Leu Met Thr Asp Glu Thr Ile Ala Asn Val Pro
 115 120 125
 20 Ile Leu Ile Leu Gly Asn Lys Ile Asp Arg Pro Glu Ala Ile Ser Glu
 130 135 140
 Glu Arg Leu Arg Glu Met Phe Gly Leu Tyr Gly Gln Thr Thr Gly Lys
 145 150 155 160
 25 Gly Ser Ile Ser Leu Lys Glu Leu Asn Ala Arg Pro Leu Glu Val Phe
 165 170 175
 30 Met Cys Ser Val Leu Lys Arg Gln Gly Tyr Gly Glu Gly Phe Arg Trp
 180 185 190
 Met Ala Gln Tyr Ile Asp Xaa
 195

35

(2) INFORMATION FOR SEQ ID NO: 449:

- 40 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 258 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 449:

45 Met Thr Leu Ser Arg Phe Ala Tyr Asn Gly Lys Arg Cys Pro Ser Ser
 1 5 10 15
 Tyr Asn Ile Leu Asp Asn Ser Lys Ile Ile Ser Glu Glu Cys Arg Lys
 20 25 30
 50 Glu Leu Thr Ala Leu Leu His His Tyr Tyr Pro Ile Glu Ile Asp Pro
 35 40 45
 55 His Arg Thr Val Lys Glu Lys Leu Pro His Met Val Glu Trp Trp Thr
 50 55 60
 Lys Ala His Asn Leu Leu Cys Gln Gln Lys Ile Gln Lys Phe Gln Ile
 65 70 75 80
 60 Ala Gln Val Val Arg Glu Ser Asn Ala Met Leu Arg Glu Gly Tyr Lys

622

85 90 95

Thr Phe Phe Asn Thr Leu Tyr His Asn Asn Ile Pro Leu Phe Ile Phe
100 105 110

5 Ser Ala Gly Ile Gly Asp Ile Leu Glu Glu Ile Ile Arg Gln Met Lys
115 120 125

10 Val Phe His Pro Asn Ile His Ile Val Ser Asn Tyr Met Asp Phe Asn
130 135 140

Glu Asp Gly Phe Leu Gln Gly Phe Lys Gly Gln Leu Ile His Thr Tyr
145 150 155 160

15 Asn Lys Asn Ser Ser Val Cys Glu Asn Xaa Gly Tyr Phe Gln Gln Leu
165 170 175

Glu Gly Lys Thr Asn Val Ile Leu Leu Gly Asp Ser Ile Gly Asp Leu
180 185 190

20 Thr Met Ala Asp Gly Val Pro Gly Val Gln Asn Ile Leu Lys Ile Gly
195 200 205

25 Phe Leu Asn Asp Lys Val Glu Glu Arg Arg Xaa Arg Tyr Met Asp Ser
210 215 220

Tyr Asp Ile Val Leu Glu Lys Asp Glu Thr Leu Asp Val Val Asn Gly
225 230 235 240

30 Leu Leu Gln His Ile Leu Cys Gln Gly Val Gln Leu Glu Met Gln Gly
245 250 255

Pro Xaa

35

(2) INFORMATION FOR SEQ ID NO: 450:

40 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 87 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 450:

Met Ser His Val Leu Leu Cys Pro Ser Leu Ser Cys Ser Asn Leu Leu
1 5 10 15

50 Pro Pro Ser His Ser Leu Gly Thr Met Gly Ser Leu Ser Pro His Leu
20 25 30

Cys Gly His Thr Met Cys Pro Val Asn Pro Glu Leu Pro Leu Ser Ser
35 40 45

55 Arg Leu Thr Thr Asp Gln Pro Gln Pro Asp Ala Cys Ser Pro Thr Leu
50 55 60

60 Leu Thr Leu Pro Leu Pro Ser Ser Phe Leu Pro His Ser Lys Pro Thr
65 70 75 80

Phe Xaa His Pro Cys Ser Pro
85

5

(2) INFORMATION FOR SEQ ID NO: 451:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 315 amino acids

10

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 451:

15 Met Phe Ser Ile Asn Pro Leu Glu Asn Leu Lys Val Tyr Ile Ser Ser
1 5 10 15

Arg Pro Pro Leu Val Val Phe Met Ile Ser Val Xaa Pro Met Ala Ile
20 25 30

20 Ala Phe Leu Thr Leu Gly Tyr Phe Phe Lys Ile Lys Glu Ile Lys Ser
35 40 45

Pro Glu Met Ala Glu Asp Trp Asn Thr Phe Leu Leu Arg Phe Asn Asp
25 50 55 60

25 Leu Asp Leu Cys Val Ser Glu Asn Glu Thr Leu Lys His Leu Thr Asn
65 70 75 80

30 Asp Thr Thr Thr Pro Glu Ser Thr Met Thr Ser Gly Gln Ala Arg Ala
85 90 95

Ser Thr Gln Ser Pro Gln Ala Leu Glu Asp Ser Gly Pro Val Asn Ile
100 105 110

35 Ser Val Ser Ile Thr Leu Thr Leu Asp Pro Leu Lys Pro Phe Gly Gly
115 120 125

Tyr Ser Arg Asn Val Thr His Leu Tyr Ser Thr Ile Leu Gly His Gln
40 130 135 140

Ile Gly Leu Ser Gly Arg Glu Ala His Glu Glu Ile Asn Ile Thr Phe
145 150 155 160

45 Thr Leu Pro Thr Ala Trp Ser Ser Asp Asp Cys Ala Leu His Gly His
165 170 175

Cys Glu Gln Val Val Phe Thr Ala Cys Met Thr Leu Thr Ala Ser Pro
180 185 190

50 Gly Val Phe Pro Val Thr Val Gln Pro Pro His Cys Val Pro Asp Thr
195 200 205

Tyr Ser Asn Ala Thr Leu Trp Tyr Lys Ile Phe Thr Thr Ala Arg Asp
55 210 215 220

Ala Asn Thr Lys Tyr Ala Gln Asp Tyr Asn Pro Phe Trp Cys Tyr Lys
225 230 235 240

60 Gly Ala Ile Gly Lys Val Tyr His Ala Leu Asn Pro Lys Leu Thr Val
245 250 255

Ile Val Pro Asp Asp Asp Arg Ser Leu Ile Asn Leu His Leu Met His
 260 265 270

5 Thr Ser Tyr Phe Leu Phe Val Met Val Ile Thr Met Phe Cys Tyr Ala
 275 280 285

Val Ile Lys Gly Arg Pro Ser Lys Leu Arg Gln Ser Asn Pro Glu Phe
 290 295 300

10 Cys Pro Glu Lys Val Ala Leu Ala Glu Ala Xaa
 305 310 315

15

(2) INFORMATION FOR SEQ ID NO: 452:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 52 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 452:

25 Met Pro Gly Leu Ser Leu Ala Leu Leu Pro Phe Gly Pro Gly Cys Thr
 1 5 10 15

Glu Ala Leu His Ala Gly Cys Phe Pro Ala Phe Ala Ser Ala Thr Arg
 20 25 30

30 Val Asn Gly Glu Ala Ala Leu Ser Pro Gly Leu Cys Asp Pro Ile Ser
 35 40 45

Val Pro Tyr Val
 50

35

(2) INFORMATION FOR SEQ ID NO: 453:

40 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 383 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 453:

Met Ala Val Gly Gln Ile Met Thr Phe Gly Ser Pro Val Ile Gly Cys
 1 5 10 15

50 Gly Phe Ile Ser Gly Trp Asn Leu Val Ser Met Cys Val Glu Tyr Val
 20 25 30

Leu Leu Trp Lys Val Tyr Gln Lys Thr Pro Ala Leu Ala Val Lys Ala
 35 40 45

55 Gly Leu Lys Glu Glu Glu Thr Glu Leu Lys Gln Leu Asn Leu His Lys
 50 55 60

Asp Thr Glu Pro Lys Pro Leu Glu Gly Thr His Leu Met Gly Val Lys
 65 70 75 80

60

625

Asp Ser Asn Ile His Glu Leu Glu His Glu Gln Glu Pro Thr Cys Ala
 85 90 95
 5 Ser Gln Met Ala Glu Pro Phe Arg Thr Phe Arg Asp Gly Trp Val Ser
 100 105 110
 Tyr Tyr Asn Gln Pro Val Phe Leu Ala Gly Met Gly Leu Ala Phe Leu
 115 120 125
 10 Tyr Met Thr Val Leu Gly Phe Asp Cys Ile Thr Thr Gly Tyr Ala Tyr
 130 135 140
 Thr Gln Gly Leu Ser Gly Phe His Pro Gln Tyr Phe Asp Gly Ser Ile
 145 150 155 160
 15 Ser Tyr Asn Trp Asn Asn Gly Asn Cys Ser Phe Tyr Leu Ala Thr Ser
 165 170 175
 Lys Met Trp Phe Gly Ser Ala Gly Leu Ile Ser Gly Leu Ala Gln Leu
 180 185 190
 Ser Cys Leu Ile Leu Cys Val Ile Ser Val Phe Met Pro Gly Ser Pro
 195 200 205
 25 Leu Asp Leu Ser Val Ser Pro Phe Glu Asp Ile Arg Ser Arg Phe Ile
 210 215 220
 Gln Gly Glu Ser Ile Thr Pro Thr Lys Ile Pro Glu Ile Thr Thr Glu
 225 230 235 240
 30 Ile Tyr Met Ser Asn Gly Ser Asn Ser Ala Asn Ile Val Pro Glu Thr
 245 250 255
 Ser Pro Glu Ser Val Pro Ile Ile Ser Val Ser Leu Leu Phe Ala Gly
 260 265 270
 Val Ile Ala Ala Arg Ile Gly Leu Trp Ser Phe Asp Leu Thr Val Thr
 275 280 285
 40 Gln Leu Leu Gln Glu Asn Val Ile Glu Ser Glu Arg Gly Ile Ile Asn
 290 295 300
 Gly Val Gln Asn Ser Met Asn Tyr Leu Leu Asp Leu Leu His Phe Ile
 305 310 315 320
 45 Met Val Ile Leu Ala Pro Asn Pro Glu Ala Phe Gly Leu Leu Val Leu
 325 330 335
 Ile Ser Val Ser Phe Val Ala Met Gly His Ile Met Tyr Phe Arg Phe
 340 345 350
 Ala Gln Asn Thr Leu Gly Asn Lys Leu Phe Ala Cys Gly Pro Asp Ala
 355 360 365
 55 Lys Glu Val Arg Lys Glu Asn Gln Ala Asn Thr Ser Val Val Xaa
 370 375 380

60 (2) INFORMATION FOR SEQ ID NO: 454:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 186 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 454:

5 Met Arg Ser Ile Gly Asn Lys Asn Thr Ile Leu Leu Gly Leu Gly Phe
 1 5 10 15
 10 Gln Ile Leu Gln Leu Ala Trp Tyr Gly Phe Gly Ser Glu Pro Trp Met
 20 25 30
 15 Met Trp Ala Ala Gly Ala Val Ala Ala Met Ser Ser Ile Thr Phe Pro
 35 40 45
 Ala Val Ser Ala Leu Val Ser Arg Thr Ala Asp Ala Asp Gln Gln Gly
 50 55 60
 20 Val Val Gln Gly Met Ile Thr Gly Ile Arg Gly Leu Cys Asn Gly Leu
 65 70 75 80
 Gly Pro Ala Leu Tyr Gly Phe Ile Phe Tyr Ile Phe His Val Glu Leu
 85 90 95
 25 Lys Glu Leu Pro Ile Thr Gly Thr Asp Leu Gly Thr Asn Thr Ser Pro
 100 105 110
 30 Gln His His Phe Glu Gln Asn Ser Ile Ile Pro Gly Pro Pro Phe Leu
 115 120 125
 Phe Gly Ala Cys Ser Val Leu Leu Ala Leu Leu Val Ala Leu Phe Ile
 130 135 140
 35 Pro Glu His Thr Asn Leu Ser Leu Arg Ser Ser Ser Trp Arg Lys His
 145 150 155 160
 Cys Gly Ser His Ser His Pro His Asn Thr Gln Ala Pro Gly Glu Ala
 165 170 175
 40 Lys Glu Pro Leu Leu Gln Asp Thr Asn Val
 180 185

45

(2) INFORMATION FOR SEQ ID NO: 455:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 163 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 455:

50 Met Leu Gln Thr Ser Asn Tyr Ser Leu Val Leu Ser Leu Gln Phe Leu
 1 5 10 15
 Leu Leu Ser Tyr Asp Leu Phe Val Asn Ser Phe Ser Glu Leu Leu Gln
 20 25 30
 60 Lys Thr Pro Val Ile Gln Leu Val Leu Phe Ile Ile Gln Asp Ile Ala

627

35 40 45

Val Leu Phe Asn Ile Ile Ile Ile Phe Leu Met Phe Phe Asn Thr Phe
50 55 60

5 Val Phe Gln Ala Gly Leu Val Asn Leu Leu Phe His Lys Phe Lys Gly
65 70 75 80

10 Thr Ile Ile Leu Thr Ala Val Tyr Phe Ala Leu Ser Ile Ser Leu His
85 90 95

Val Trp Val Met Asn Leu Arg Trp Lys Asn Ser Asn Ser Phe Ile Trp
100 105 110

15 Thr Asp Gly Leu Gln Met Leu Phe Val Phe Gln Arg Leu Ala Ala Val
115 120 125

Leu Tyr Cys Tyr Phe Tyr Lys Arg Thr Ala Val Arg Leu Gly Asp Pro
130 135 140

20 His Phe Tyr Gln Asp Ser Leu Trp Leu Arg Lys Glu Phe Met Gln Val
145 150 155 160

25 Arg Arg Xaa

30 (2) INFORMATION FOR SEQ ID NO: 456:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 46 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 456:

Met Arg Ile Gln Val Phe Ile Leu Leu Leu Gly Ala Gly Gly Thr Ser
1 5 10 15

40 Gln Phe Thr Lys Pro Pro Ser Leu Pro Leu Glu Pro Glu Pro Ala Val
20 25 30

Glu Ser Ser Pro Thr Glu Thr Ser Glu Gln Ile Arg Glu Lys
35 40 45

45

(2) INFORMATION FOR SEQ ID NO: 457:

50 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 105 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 457:

Met Ser Tyr Leu Ala Phe Leu Tyr Met Thr Phe Asp Phe Cys Cys Leu
1 5 10 15

60 Tyr Phe Ser Thr Val Tyr Ala Pro Ser Phe Lys Tyr Ile Cys Val His
20 25 30

Thr Asp Thr His Ile Cys Val Cys Val Cys Ile Tyr Leu Ser Ser Val
 35 40 45
 5 Val Ser Lys Ser Ser Ala Glu Ala Asp Gly Val Leu Gln Pro Arg Arg
 50 55 60
 His Pro Ala Ser Leu Leu Ile Val Phe Ala Thr Ser Ile Ser Glu Ser
 65 70 75 80
 10 Ser Leu Leu Ile Phe Ser Phe Gln Lys Thr Glu Ala Lys Leu Ile Val
 85 90 95
 15 Phe Ala Val Ser Leu Ala Ala Lys Xaa
 100 105

20 (2) INFORMATION FOR SEQ ID NO: 458:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 70 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 458:

Met Leu Pro Pro Phe Ser Leu Val Tyr Thr His Phe Leu Val Ala Ser
 1 5 10 15
 30 Leu Leu Pro Val Ile Leu Ala Val Phe Pro Asp Ser Ala Gln Ile Val
 20 25 30
 Pro Leu Leu Lys Pro Ile Pro Arg Pro Gln Pro Glu Val Ile Phe Pro
 35 40 45
 35 Ser Ser Glu Leu Leu Glu Gln Leu Leu Ser Val Gln Phe Val Trp Gln
 50 55 60
 40 Ala His Thr Val Ala Xaa
 65 70

45 (2) INFORMATION FOR SEQ ID NO: 459:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 155 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 459:

Met Ala Leu Leu Leu Ser Val Leu Arg Val Leu Leu Gly Gly Phe Phe
 1 5 10 15
 55 Ala Leu Val Gly Leu Ala Lys Leu Ser Glu Glu Ile Ser Ala Pro Val
 20 25 30
 Ser Glu Arg Met Asn Ala Leu Phe Val Gln Phe Ala Glu Val Phe Pro
 35 40 45
 60

Leu Lys Val Phe Gly Tyr Gln Pro Asp Pro Leu Asn Tyr Gln Ile Ala
 50 55 60
 5 Val Gly Phe Leu Glu Leu Leu Ala Gly Leu Leu Leu Val Met Gly Pro
 65 70 75 80
 Pro Met Leu Gln Glu Ile Ser Asn Leu Phe Leu Ile Leu Leu Met Met
 85 90 95
 10 Gly Ala Ile Phe Thr Leu Ala Ala Leu Lys Glu Ser Leu Ser Thr Cys
 100 105 110
 Ile Pro Ala Ile Val Cys Leu Gly Phe Leu Leu Leu Leu Asn Val Gly
 115 120 125
 15 Gln Leu Leu Ala Gln Thr Lys Lys Val Val Arg Pro Thr Arg Lys Lys
 130 135 140
 20 Thr Leu Ser Thr Phe Lys Glu Ser Trp Lys Xaa
 145 150 155

25 (2) INFORMATION FOR SEQ ID NO: 460:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 332 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 460:

Met Lys Leu Gly Arg Ala Val Leu Gly Leu Leu Leu Ala Pro Ser
 1 5 10 15
 35 Val Val Gln Ala Val Glu Pro Ile Ser Leu Gly Leu Ala Leu Ala Gly
 20 25 30
 Val Leu Thr Gly Tyr Ile Tyr Pro Arg Leu Tyr Cys Leu Phe Ala Glu
 35 40 45
 40 Cys Cys Gly Gln Lys Arg Ser Leu Ser Arg Glu Ala Leu Gln Lys Asp
 50 55 60
 Leu Asp Asp Asn Leu Phe Gly Gln His Leu Ala Lys Lys Ile Ile Leu
 65 70 75 80
 Asn Ala Val Phe Gly Phe Ile Asn Asn Pro Lys Pro Lys Lys Pro Leu
 85 90 95
 50 Thr Leu Ser Leu His Gly Trp Thr Gly Thr Gly Lys Asn Phe Val Ser
 100 105 110
 Lys Ile Ile Ala Glu Asn Ile Tyr Glu Gly Gly Leu Asn Ser Asp Tyr
 115 120 125
 55 Val His Leu Phe Val Ala Thr Leu His Phe Pro His Ala Ser Asn Ile
 130 135 140
 60 Thr Leu Tyr Lys Asp Gln Leu Gln Leu Trp Ile Arg Gly Asn Val Ser
 145 150 155 160

630

Ala Cys Ala Arg Ser Ile Phe Ile Phe Asp Glu Met Asp Lys Met His
165 170 175

5 Ala Gly Leu Ile Asp Ala Ile Lys Pro Phe Leu Asp Tyr Tyr Asp Leu
180 185 190

Val Asp Gly Val Ser Tyr Gln Lys Ala Met Phe Ile Phe Leu Ser Asn
195 200 205

10 Ala Gly Ala Glu Arg Ile Thr Asp Val Ala Leu Asp Phe Trp Arg Ser
210 215 220

Gly Lys Gln Arg Glu Asp Ile Lys Leu Lys Asp Ile Glu His Ala Leu
15 225 230 235 240

Ser Val Ser Val Phe Asn Asn Lys Asn Ser Gly Phe Trp His Ser Ser
245 250 255

20 Leu Ile Asp Arg Asn Leu Ile Asp Tyr Phe Val Pro Phe Leu Pro Leu
260 265 270

Glu Tyr Lys His Leu Lys Met Cys Ile Arg Val Glu Met Gln Ser Arg
275 280 285

25 Gly Tyr Glu Ile Asp Glu Asp Ile Val Ser Arg Val Ala Glu Glu Met
290 295 300

Thr Phe Phe Pro Lys Glu Glu Arg Val Phe Ser Asp Lys Gly Cys Lys
30 305 310 315 320

Thr Val Phe Thr Lys Leu Asp Tyr Tyr Tyr Asp Asp
325 330

35

(2) INFORMATION FOR SEQ ID NO: 461:

- (i) SEQUENCE CHARACTERISTICS:
- 40 (A) LENGTH: 5 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 461:

45 Met Leu Lys Cys Ile
1 5

50

(2) INFORMATION FOR SEQ ID NO: 462:

- (i) SEQUENCE CHARACTERISTICS:
- 55 (A) LENGTH: 14 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 462:

Met Ile Leu Thr Leu Leu Ser Val Val Ser Thr Met Ala Ser
1 5 10

60

(2) INFORMATION FOR SEQ ID NO: 463:

5

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 285 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 463:

Met Lys Leu His Pro Pro Pro Pro Ser Pro Val Thr Gln Asp His Arg
 1 5 10 15
 Ser Lys Ser Ser His Ser Asn Trp Met Pro Arg Met Gly Ala Cys Ser
 20 25 30
 Met Ser Arg Thr Ser Ser Ser Gly Pro Pro Ser Leu Cys Lys Ser Thr
 35 40 45
 Ser Gly Arg Ser Cys Thr Arg Pro His Cys Trp Pro Ser Leu Pro Ala
 50 55 60
 Trp Val Ser Val Phe Thr Arg Thr Asn Thr Gly Ser Trp Cys Tyr Pro
 65 70 75 80
 Ala Trp Gly Gly Ala Phe Ser Arg Pro Trp Met Ser Ala Gln Ser Met
 85 90 95
 Cys Cys Ala Glu Arg Ser Val Leu Gln Val Ala Cys Arg Leu Leu Asp
 100 105 110
 Ala Leu Glu Phe Leu His Glu Asn Glu Tyr Val His Gly Asn Val Thr
 115 120 125
 Ala Glu Asn Ile Phe Val Asp Pro Glu Asp Gln Ser Gln Val Thr Leu
 130 135 140
 Ala Gly Tyr Gly Phe Ala Phe Arg Tyr Cys Pro Ser Gly Lys His Val
 145 150 155 160
 Ala Tyr Val Glu Gly Ser Arg Ser Pro His Glu Gly Asp Leu Glu Phe
 165 170 175
 Ile Ser Met Asp Leu His Lys Gly Cys Gly Pro Ser Arg Arg Xaa Asp
 180 185 190
 Leu Gln Ser Leu Gly Tyr Cys Met Leu Lys Trp Leu Tyr Gly Phe Leu
 195 200 205
 Pro Trp Thr Asn Cys Leu Pro Xaa Xaa Glu Asp Ile Met Lys Gln Lys
 210 215 220
 Gln Lys Phe Val Asp Lys Pro Gly Pro Phe Val Gly Pro Cys Gly His
 225 230 235 240
 Trp Ile Arg Pro Ser Glu Thr Leu Gln Lys Tyr Leu Lys Val Val Met
 245 250 255
 Ala Leu Thr Tyr Glu Glu Lys Pro Pro Tyr Ala Met Leu Arg Asn Asn
 260 265 270

Leu Glu Ala Leu Leu Gln Asp Leu Arg Val Ser Pro Tyr
 275 280 285

5

(2) INFORMATION FOR SEQ ID NO: 464:

10

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 80 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 464:

15

Met Thr Ser Pro Pro His Gln Gly Trp Glu Gln Arg Gly Cys Gly
 1 5 10 15

20

Glu Ser Gln Val Pro Leu Ala Leu Ser Arg Val Phe Ser Thr Ser His
 20 25 30

Tyr Cys Leu Leu Leu Val Ala Asn Gln Ser Ile Phe Phe Pro Cys Leu
 35 40 45

25

Trp Ala Val Glu Arg Leu Leu Gly Val Arg Cys Thr Cys Pro Leu Ser
 50 55 60

Trp Gly Lys Arg Ile Ile Ser Glu His Cys Ser Ala Gln Ser Ser Xaa
 65 70 75 80

30

35

(2) INFORMATION FOR SEQ ID NO: 465:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 47 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 465:

45

Met His Thr Trp Tyr Asn Asp Arg Arg Gln Asn Cys His Cys Leu Leu
 1 5 10 15

Phe Phe Leu Ile Tyr Leu Arg Lys Ile Tyr Gln Val Val Pro His Val
 20 25 30

50

Pro Leu Leu Val Lys Cys Arg Gly Arg Leu Lys Gly Val Asn Ile
 35 40 45

55

(2) INFORMATION FOR SEQ ID NO: 466:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 96 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

60

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 466:

Met Glu Leu Val Leu Val Phe Leu Cys Ser Leu Leu Ala Pro Met Val
 1 5 10 15
 5 Leu Ala Ser Ala Ala Glu Lys Glu Lys Glu Met Asp Pro Phe His Tyr
 20 25 30
 Asp Tyr Gln Thr Leu Arg Ile Gly Gly Leu Val Phe Ala Val Val Leu
 35 40 45
 10 Phe Ser Val Gly Ile Leu Leu Ile Leu Ser Arg Arg Cys Lys Cys Ser
 50 55 60
 Phe Asn Gln Lys Pro Arg Ala Pro Gly Asp Glu Glu Ala Gln Val Glu
 15 65 70 75 80
 Asn Leu Ile Thr Ala Asn Ala Thr Glu Pro Gln Lys Ala Glu Asn Xaa
 85 90 95

20

25 (2) INFORMATION FOR SEQ ID NO: 467:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 399 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 467:

Met Ala Ser Gly Ala Asp Ser Lys Gly Asp Asp Leu Ser Thr Ala Ile
 1 5 10 15
 35 Leu Lys Gln Lys Asn Arg Pro Asn Arg Leu Ile Val Asp Glu Ala Ile
 20 25 30
 40 Asn Glu Asp Asn Ser Val Val Ser Leu Ser Gln Pro Lys Met Asp Glu
 35 40 45
 Leu Gln Leu Phe Arg Gly Asp Thr Val Leu Leu Lys Gly Lys Lys Arg
 50 55 60
 45 Arg Glu Ala Val Cys Ile Val Leu Ser Asp Asp Thr Cys Ser Asp Glu
 65 70 75 80
 Lys Ile Arg Met Asn Arg Val Val Arg Asn Asn Leu Arg Val Arg Leu
 85 90 95
 50 Gly Asp Val Ile Ser Ile Gln Pro Cys Pro Asp Val Lys Tyr Gly Lys
 100 105 110
 55 Arg Ile His Val Leu Pro Ile Asp Asp Thr Val Glu Gly Ile Thr Gly
 115 120 125
 Asn Leu Phe Glu Val Tyr Leu Lys Pro Tyr Phe Leu Glu Ala Tyr Arg
 130 135 140
 60 Pro Ile Arg Lys Gly Asp Ile Phe Leu Val Arg Gly Gly Met Arg Ala

634

	145					150						155					160
	Val	Glu	Phe	Lys	Val	Val	Glu	Thr	Asp	Pro	Ser	Pro	Tyr	Cys	Ile	Val	
					165					170					175		
5	Ala	Pro	Asp	Thr	Val	Ile	His	Cys	Glu	Gly	Glu	Pro	Ile	Lys	Arg	Glu	
				180					185					190			
10	Asp	Glu	Glu	Glu	Ser	Leu	Asn	Glu	Val	Gly	Tyr	Asp	Asp	Ile	Gly	Gly	
			195					200					205				
	Cys	Arg	Lys	Gln	Leu	Ala	Gln	Ile	Lys	Glu	Met	Val	Glu	Leu	Pro	Leu	
		210					215					220					
15	Arg	His	Pro	Ala	Leu	Phe	Lys	Ala	Ile	Gly	Val	Lys	Pro	Pro	Arg	Gly	
	225					230					235					240	
	Ile	Leu	Leu	Tyr	Gly	Pro	Pro	Gly	Thr	Gly	Lys	Thr	Leu	Ile	Ala	Arg	
				245						250					255		
20	Ala	Val	Ala	Asn	Glu	Thr	Gly	Ala	Phe	Phe	Phe	Leu	Ile	Asn	Gly	Pro	
			260					265						270			
25	Glu	Ile	Met	Ser	Lys	Leu	Ala	Gly	Glu	Ser	Glu	Ser	Asn	Leu	Arg	Lys	
		275						280					285				
	Ala	Phe	Glu	Glu	Ala	Glu	Lys	Asn	Ala	Pro	Ala	Ile	Ile	Phe	Ile	Asp	
		290					295					300					
30	Glu	Leu	Asp	Ala	Ile	Ala	Pro	Lys	Arg	Glu	Lys	Thr	His	Gly	Glu	Val	
	305					310					315					320	
	Glu	Arg	Arg	Ile	Val	Ser	Gln	Leu	Leu	Thr	Leu	Met	Asp	Gly	Leu	Lys	
				325						330					335		
35	Gln	Arg	Ala	His	Val	Ile	Val	Met	Ala	Ala	Thr	Asn	Arg	Pro	Asn	Ser	
			340						345					350			
	Ile	Asp	Pro	Ala	Leu	Arg	Arg	Phe	Gly	Arg	Phe	Asp	Arg	Glu	Val	Asp	
		355						360					365				
40	Ile	Gly	Ile	Pro	Asp	Ala	Thr	Gly	Arg	Leu	Glu	Ile	Leu	Gln	Ile	His	
		370					375					380					
45	Thr	Lys	Asn	Met	Lys	Leu	Ala	Asp	Asp	Val	Asp	Leu	Glu	Gln	Xaa		
	385					390					395						

50 (2) INFORMATION FOR SEQ ID NO: 468:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 468:

Leu

1

60

(2) INFORMATION FOR SEQ ID NO: 469:

5

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 273 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 469:

10

Met Ala Ala Pro Lys Gly Ser Leu Trp Val Arg Thr Gln Leu Gly Leu
1 5 10 15

15

Pro Pro Leu Leu Leu Leu Thr Met Ala Leu Ala Gly Gly Ser Gly Thr
20 25 30

Ala Ser Ala Glu Ala Phe Asp Ser Val Leu Gly Asp Thr Ala Ser Cys
35 40 45

20

His Arg Ala Cys Gln Leu Thr Tyr Pro Leu His Thr Tyr Pro Lys Glu
50 55 60

Glu Glu Leu Tyr Ala Cys Gln Arg Gly Cys Arg Leu Phe Ser Ile Cys
65 70 75 80

25

Gln Phe Val Asp Asp Gly Ile Asp Leu Asn Arg Thr Lys Leu Glu Cys
85 90 95

30

Glu Ser Ala Cys Thr Glu Ala Tyr Ser Gln Ser Asp Glu Gln Tyr Ala
100 105 110

Cys His Leu Gly Cys Gln Asn Gln Leu Pro Phe Ala Glu Leu Arg Gln
115 120 125

35

Glu Gln Leu Met Ser Leu Met Pro Lys Met His Leu Leu Phe Pro Leu
130 135 140

Thr Leu Val Arg Ser Phe Trp Ser Asp Met Met Asp Ser Ala Gln Ser
145 150 155 160

40

Phe Ile Thr Ser Ser Trp Thr Phe Tyr Leu Gln Ala Asp Asp Gly Lys
165 170 175

45

Ile Val Ile Phe Xaa Ser Lys Pro Arg Asn Pro Arg Tyr Ala Pro His
180 185 190

Leu Glu Pro Gly Ala Leu Pro Asn Leu Xaa Xaa Xaa Ser Leu Ser Lys
195 200 205

50

Met Ser Xaa Xaa Ser Xaa Met Arg Asn Ser Gln Ala His Arg Asn Phe
210 215 220

Leu Glu Asp Gly Glu Ser Asp Gly Phe Leu Arg Cys Leu Ser Leu Asn
225 230 235 240

55

Ser Gly Trp Ile Leu Thr Thr Thr Leu Val Leu Ser Val Met Val Leu
245 250 255

60

Leu Trp Ile Cys Cys Ala Thr Cys Cys Tyr Thr Leu Leu Asp Ala Val
260 265 270

Xaa

5

(2) INFORMATION FOR SEQ ID NO: 470:

10

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 192 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 470:

15

Met Met Val Leu Ser Leu Gly Ile Ile Leu Ala Ser Ala Ser Phe Ser
 1 5 10 15

20

Pro Asn Phe Thr Gln Val Thr Ser Thr Leu Leu Asn Ser Ala Tyr Pro
 20 25 30

Phe Ile Gly Pro Phe Phe Phe Ile Ile Ser Gly Ser Leu Ser Ile Ala
 35 40 45

25

Thr Glu Lys Arg Leu Thr Lys Leu Leu Val His Ser Ser Leu Val Gly
 50 55 60

Ser Ile Leu Ser Ala Leu Ser Ala Leu Val Gly Phe Ile Ile Leu Ser
 65 70 75 80

30

Val Lys Gln Ala Thr Leu Asn Pro Ala Ser Leu Gln Cys Glu Leu Asp
 85 90 95

35

Lys Asn Asn Ile Pro Thr Arg Ser Tyr Val Ser Tyr Phe Tyr His Asp
 100 105 110

Ser Leu Tyr Thr Thr Asp Cys Tyr Thr Ala Lys Ala Ser Leu Ala Gly
 115 120 125

40

Xaa Leu Ser Leu Met Leu Ile Cys Thr Leu Leu Glu Phe Cys Leu Ala
 130 135 140

Val Leu Thr Ala Val Leu Arg Trp Lys Gln Ala Tyr Ser Asp Phe Pro
 145 150 155 160

45

Gly Ser Val Leu Phe Leu Pro His Ser Tyr Ile Gly Asn Ser Gly Met
 165 170 175

50

Ser Ser Lys Met Thr His Asp Cys Gly Tyr Glu Glu Leu Leu Thr Ser
 180 185 190

55

(2) INFORMATION FOR SEQ ID NO: 471:

60

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 234 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 471:

5 Met Arg Lys Thr Arg Leu Trp Gly Leu Leu Trp Met Leu Phe Val Ser
 1 5 10 15
 Glu Leu Arg Ala Ala Thr Lys Leu Thr Glu Glu Lys Tyr Glu Leu Lys
 20 25 30
 10 Glu Gly Gln Thr Leu Asp Val Lys Cys Asp Tyr Thr Leu Glu Lys Phe
 35 40 45
 Ala Ser Ser Gln Lys Ala Trp Gln Ile Ile Arg Asp Gly Glu Met Pro
 50 55 60
 15 Lys Thr Leu Ala Cys Thr Glu Arg Pro Ser Lys Asn Ser His Pro Val
 65 70 75 80
 Gln Val Gly Arg Ile Ile Leu Glu Asp Tyr His Asp His Gly Leu Leu
 85 90 95
 Arg Val Arg Met Val Asn Leu Gln Val Glu Asp Ser Gly Leu Tyr Gln
 100 105 110
 25 Cys Val Ile Tyr Gln Pro Pro Lys Glu Pro His Met Leu Phe Asp Arg
 115 120 125
 Ile Arg Leu Val Val Thr Lys Gly Phe Ser Gly Thr Pro Gly Ser Asn
 130 135 140
 30 Glu Asn Ser Thr Gln Asn Val Tyr Lys Ile Pro Pro Thr Thr Thr Lys
 145 150 155 160
 Ala Leu Cys Pro Leu Tyr Thr Ser Pro Arg Thr Val Thr Gln Ala Pro
 165 170 175
 35 Pro Lys Ser Thr Ala Asp Val Ser Thr Pro Asp Ser Glu Ile Asn Leu
 180 185 190
 40 Thr Asn Val Thr Asp Ile Ile Arg Val Pro Val Phe Asn Ile Val Ile
 195 200 205
 Leu Leu Ala Gly Gly Phe Leu Ser Lys Ser Leu Val Phe Ser Val Leu
 210 215 220
 45 Phe Ala Val Thr Leu Arg Ser Phe Val Pro
 225 230

50

(2) INFORMATION FOR SEQ ID NO: 472:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 105 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 472:

60 Met Leu His Ile Leu Pro Leu Lys Ser Tyr Asp Phe Pro His Phe Ser
 1 5 10 15

	Leu	Met	Gly	Arg	Tyr	Arg	Cys	Ala	Ser	Leu	Leu	Phe	Cys	Phe	Leu	Leu	
				20					25						30		
5	Leu	Phe	Phe	Phe	Phe	Cys	Ser	Val	Leu	Trp	Thr	Phe	Ser	Asp	Met	His	
			35					40					45				
	Arg	Ser	Gly	Glu	Asp	Gly	Pro	Trp	Thr	Pro	Cys	Val	His	His	Leu	Ala	
10		50					55					60					
	Ala	Ser	Leu	Ile	Ser	Tyr	Gly	Gln	Pro	Gly	Phe	Ile	Cys	Ile	Ser	Leu	
	65					70					75					80	
15	Phe	Ser	Pro	Val	Leu	Phe	Ile	Glu	Asn	Pro	Arg	His	Tyr	Ala	Asn	Ala	
					85					90					95		
	Thr	Val	Thr	Thr	Leu	Gly	Asp	Trp	Xaa								
			100						105								

20

(2) INFORMATION FOR SEQ ID NO: 473:

25 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 32 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 473:

30 Met Val Phe Leu Lys Tyr Arg Phe Leu Phe Phe Leu Val Phe Leu Ala
1 5 10 15
Asn Cys Ile Tyr Ser Leu His Tyr Lys Pro Ser Leu Met Tyr Pro Lys
20 25 30

40

(2) INFORMATION FOR SEQ ID NO: 474:

45 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 571 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 474:

50 Met Ala Leu Ser Arg Gly Leu Pro Arg Glu Leu Ala Glu Ala Val Ala
1 5 10 15
Gly Gly Arg Val Leu Val Val Gly Ala Gly Gly Ile Gly Cys Glu Leu
20 25 30

55 Leu Lys Asn Leu Val Leu Thr Gly Phe Ser His Ile Asp Leu Ile Asp
 35 40 45

Leu Asp Thr Ile Asp Val Ser Asn Leu Asn Arg Gln Phe Leu Phe Gln
 50 55 60

60

Lys Lys His Val Gly Arg Ser Lys Ala Gln Val Ala Lys Glu Ser Val
 65 70 75 80
 5 Leu Gln Phe Tyr Pro Lys Ala Asn Ile Val Ala Tyr His Asp Ser Ile
 85 90 95
 Met Asn Pro Asp Tyr Asn Val Glu Phe Phe Arg Gln Phe Ile Leu Val
 100 105 110
 10 Met Asn Ala Leu Asp Asn Arg Ala Ala Arg Asn His Val Asn Arg Met
 115 120 125
 Cys Leu Ala Ala Asp Val Pro Leu Ile Glu Ser Gly Thr Ala Gly Tyr
 130 135 140
 15 Leu Gly Gln Val Thr Thr Ile Lys Lys Gly Val Thr Glu Cys Tyr Glu
 145 150 155 160
 Cys His Pro Lys Pro Thr Gln Arg Thr Phe Pro Gly Cys Thr Ile Arg
 165 170 175
 20 Asn Thr Pro Ser Glu Pro Ile His Cys Ile Val Trp Ala Lys Tyr Leu
 180 185 190
 25 Phe Asn Gln Leu Phe Gly Glu Glu Asp Ala Asp Gln Glu Val Ser Pro
 195 200 205
 Asp Arg Ala Asp Pro Glu Ala Ala Trp Glu Pro Thr Glu Ala Glu Ala
 210 215 220
 30 Arg Ala Arg Ala Ser Asn Glu Asp Gly Asp Ile Lys Arg Ile Ser Thr
 225 230 235 240
 Lys Glu Trp Ala Lys Ser Thr Gly Tyr Asp Pro Val Lys Leu Phe Thr
 245 250 255
 35 Lys Leu Phe Lys Asp Asp Ile Arg Tyr Leu Leu Thr Met Asp Lys Leu
 260 265 270
 40 Trp Arg Lys Arg Lys Pro Pro Val Pro Leu Asp Trp Ala Glu Val Gln
 275 280 285
 Ser Gln Gly Glu Glu Thr Asn Ala Ser Asp Gln Gln Asn Glu Pro Gln
 290 295 300
 45 Leu Gly Leu Lys Asp Gln Gln Val Leu Asp Val Lys Ser Tyr Ala Arg
 305 310 315 320
 Leu Phe Ser Lys Ser Ile Glu Thr Leu Arg Val His Leu Ala Glu Lys
 325 330 335
 50 Gly Asp Gly Ala Glu Leu Ile Trp Asp Lys Asp Asp Pro Ser Ala Met
 340 345 350
 55 Asp Phe Val Thr Ser Ala Ala Asn Leu Arg Met His Ile Phe Ser Met
 355 360 365
 Asn Met Lys Ser Arg Phe Asp Ile Lys Ser Met Ala Gly Asn Ile Ile
 370 375 380
 60

640

Pro Ala Ile Ala Thr Thr Asn Ala Val Ile Ala Gly Leu Ile Val Leu
 385 390 395 400
 5 Glu Gly Leu Lys Ile Leu Ser Gly Lys Ile Asp Gln Cys Arg Thr Ile
 405 410 415
 Phe Leu Asn Lys Gln Pro Asn Pro Arg Lys Lys Leu Leu Val Pro Cys
 420 425 430
 10 Ala Leu Asp Pro Pro Asn Pro Asn Cys Tyr Val Cys Ala Ser Lys Pro
 435 440 445
 Glu Val Thr Val Arg Leu Asn Val His Lys Val Thr Val Leu Thr Leu
 450 455 460
 15 Gln Asp Lys Ile Val Lys Glu Lys Phe Ala Met Val Ala Pro Asp Val
 465 470 475 480
 Gln Ile Glu Asp Gly Lys Gly Thr Ile Leu Ile Ser Ser Glu Glu Gly
 485 490 495
 20 Glu Thr Glu Ala Asn Asn His Lys Lys Leu Ser Glu Phe Gly Ile Arg
 500 505 510
 25 Asn Gly Ser Arg Leu Gln Ala Asp Asp Phe Leu Gln Asp Tyr Thr Leu
 515 520 525
 Leu Ile Asn Ile Leu His Ser Glu Asp Leu Gly Lys Asp Val Glu Phe
 530 535 540
 30 Glu Val Val Gly Asp Ala Pro Glu Lys Val Gly Xaa Lys Gln Ala Glu
 545 550 555 560
 35 Asp Ala Ala Lys Ser Ile Thr Asn Gly Gln Xaa
 565 570

40 (2) INFORMATION FOR SEQ ID NO: 475:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 312 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 475:

Met Gln Val Val Thr Cys Leu Thr Arg Asp Ser Tyr Leu Thr His Cys
 1 5 10 15
 50 Phe Leu Gln His Leu Met Val Val Leu Ser Ser Leu Glu Arg Thr Pro
 20 25 30
 Ser Pro Glu Pro Val Asp Lys Asp Phe Tyr Ser Glu Phe Gly Asn Lys
 35 40 45
 55 Thr Thr Gly Lys Met Glu Asn Tyr Glu Leu Ile His Ser Ser Arg Val
 50 55 60
 60 Lys Phe Thr Tyr Pro Ser Glu Glu Glu Ile Gly Asp Leu Thr Phe Thr
 65 70 75 80

Val Ala Gln Lys Met Ala Glu Pro Glu Lys Ala Pro Ala Leu Ser Ile
 85 90 95
 5 Leu Leu Tyr Val Gln Ala Phe Gln Val Gly Met Pro Pro Pro Gly Cys
 100 105 110
 Cys Arg Gly Pro Leu Arg Pro Lys Thr Leu Leu Leu Thr Ser Ser Glu
 115 120 125
 10 Ile Phe Leu Leu Asp Glu Asp Cys Val His Tyr Pro Leu Pro Glu Phe
 130 135 140
 Ala Lys Glu Pro Pro Gln Arg Asp Arg Tyr Arg Leu Asp Asp Gly Arg
 15 145 150 155 160
 Arg Val Arg Asp Leu Asp Arg Val Leu Met Gly Tyr Gln Thr Tyr Pro
 165 170 175
 20 Gln Pro Ser Pro Ser Ser Ser Met Thr Cys Lys Val Met Thr Ser Trp
 180 185 190
 Ala Val Ser Pro Trp Thr Thr Leu Gly Arg Cys Gln Val Ala Arg Leu
 195 200 205
 25 Glu Pro Ala Arg Ala Val Lys Ser Ser Gly Arg Cys Leu Ser Pro Val
 210 215 220
 Leu Arg Ala Glu Arg Ser Ser Ser Arg Cys Trp Leu Ala Ser Gly Arg
 30 225 230 235 240
 Pro Cys Val Ala Val Ser Cys Leu Ser Ser Ser Pro Ala Ser Pro Gly
 245 250 255
 35 His Ser Gln Pro Val Val Ser Ser Leu Thr Pro Thr Gly Ala Gly Gln
 260 265 270
 Gln Ala Phe Val Phe Ser Lys Asn Val Leu Ser Ser Leu Trp Tyr Leu
 275 280 285
 40 Asn Leu Thr Val Leu Ala Glu Asn Val Asn Met Cys Val Cys Cys Val
 290 295 300
 Asn Ser Phe Ser Cys Trp Glu Xaa
 45 305 310

50 (2) INFORMATION FOR SEQ ID NO: 476:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 329 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 476:

Met Ala Gln His His Leu Trp Ile Leu Leu Leu Cys Leu Gln Thr Trp
 1 5 10 15
 60 Pro Glu Ala Ala Gly Lys Asp Ser Glu Ile Phe Thr Val Asn Gly Ile

642

	20	25	30
	Leu Gly Glu Ser Val Thr Phe Pro Val Asn Ile Gln Glu Pro Arg Gln		
	35	40	45
5	Val Lys Ile Ile Ala Trp Thr Ser Lys Thr Ser Val Ala Tyr Val Thr		
	50	55	60
10	Pro Gly Asp Ser Glu Thr Ala Pro Val Val Thr Val Thr His Arg Asn		
	65	70	75
	Tyr Tyr Glu Arg Ile His Ala Leu Gly Pro Asn Tyr Asn Leu Val Ile		
	85	90	95
15	Ser Asp Leu Arg Met Glu Asp Ala Gly Asp Tyr Lys Ala Asp Ile Asn		
	100	105	110
	Thr Gln Ala Asp Pro Tyr Thr Thr Thr Lys Arg Tyr Asn Leu Gln Ile		
	115	120	125
20	Tyr Arg Arg Leu Gly Lys Pro Lys Ile Thr Gln Ser Leu Met Ala Ser		
	130	135	140
	Val Asn Ser Thr Cys Asn Val Thr Leu Thr Cys Ser Val Glu Lys Glu		
25	145	150	155
	Glu Lys Asn Val Thr Tyr Asn Trp Ser Pro Leu Gly Glu Glu Gly Asn		
	165	170	175
30	Val Leu Gln Ile Phe Gln Thr Pro Glu Asp Gln Glu Leu Thr Tyr Thr		
	180	185	190
	Cys Thr Ala Gln Asn Pro Val Ser Asn Asn Ser Asp Ser Ile Ser Ala		
	195	200	205
35	Arg Gln Leu Cys Ala Asp Ile Ala Met Gly Phe Arg Thr His His Thr		
	210	215	220
	Gly Leu Leu Ser Val Leu Ala Met Phe Phe Leu Leu Val Leu Ile Leu		
40	225	230	235
	Ser Ser Val Phe Leu Phe Arg Leu Phe Lys Arg Arg Gln Asp Ala Ala		
	245	250	255
45	Ser Lys Lys Thr Ile Tyr Thr Tyr Ile Met Ala Ser Arg Asn Thr Gln		
	260	265	270
	Pro Ala Glu Ser Arg Ile Tyr Asp Glu Ile Leu Gln Ser Lys Val Leu		
	275	280	285
50	Pro Ser Lys Glu Glu Pro Val Asn Thr Val Tyr Ser Glu Val Gln Phe		
	290	295	300
	Ala Asp Lys Met Gly Lys Ala Ser Thr Gln Asp Ser Lys Pro Pro Gly		
55	305	310	315
	Thr Ser Ser Tyr Glu Ile Val Ile Xaa		
	325		

60

(2) INFORMATION FOR SEQ ID NO: 477:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 178 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 477:

5
 10 Met Lys Leu Gln Cys Val Ser Leu Trp Leu Leu Gly Thr Ile Leu Ile
 1 5 10 15
 Leu Cys Ser Val Asp Asn His Gly Leu Arg Arg Cys Leu Ile Ser Thr
 20 25 30
 15 Asp Met His His Ile Glu Glu Ser Phe Gln Glu Ile Lys Arg Ala Ile
 35 40 45
 Gln Ala Lys Asp Thr Phe Pro Asn Val Thr Ile Leu Ser Thr Leu Glu
 20 50 55 60
 Thr Leu Gln Ile Ile Lys Pro Leu Asp Val Cys Cys Val Thr Lys Asn
 65 70 75 80
 25 Leu Leu Ala Phe Tyr Val Asp Arg Val Phe Lys Asp His Gln Glu Pro
 85 90 95
 Asn Pro Lys Ile Leu Arg Lys Ile Ser Ser Ile Ala Asn Ser Phe Leu
 100 105 110
 30 Tyr Met Gln Lys Thr Leu Arg Gln Cys Gln Glu Gln Arg Gln Cys His
 115 120 125
 Cys Arg Gln Glu Ala Thr Asn Ala Thr Arg Val Ile His Asp Asn Tyr
 35 130 135 140
 Asp Gln Leu Glu Val His Ala Ala Ala Ile Lys Ser Leu Gly Glu Leu
 145 150 155 160
 40 Asp Val Phe Leu Ala Trp Ile Asn Lys Asn His Glu Val Met Ser Ser
 165 170 175
 Ala Xaa

45

(2) INFORMATION FOR SEQ ID NO: 478:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 52 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 478:

50
 55 Asp Thr Ala Ile Arg Val Ala Leu Ala Val Ala Val Leu Lys Thr Val
 1 5 10 15
 Ile Leu Gly Leu Leu Cys Leu Leu Cys Gly Gly Gly Glu Gly Lys
 60 20 25 30

Val Ala Gly Arg Gln Ala Val Thr Ser Asp Gln Gln Ser Val Gly Arg
 35 40 45

5 Arg Asp Val Tyr
 50

10 (2) INFORMATION FOR SEQ ID NO: 479:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 62 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 479:

Met Gln Lys Lys Asn Ser Leu Phe Phe Phe Phe Ala Phe Tyr Tyr Glu
 1 5 10 15
 20 Asn Lys Thr Asn Ala Pro Gly Glu Gly Ser Met Ile Thr Arg Asn Ile
 20 25 30
 25 Lys Glu Tyr Phe Leu Pro Phe Leu Phe Cys Cys Val Glu Ala Ser Ile
 25 35 40 45
 Ala Ile Asn Lys Leu Asn Tyr Leu His Trp Thr His Phe Gln
 50 55 60

30

(2) INFORMATION FOR SEQ ID NO: 480:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 27 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 480:

40 Met Pro Gly Leu Ser Leu Ile Leu Thr Val Thr Leu Leu Ala Val Ser
 1 5 10 15
 Asp Ser Ala Ala Thr Cys Ile Val Ala Lys Gly
 20 25

45

(2) INFORMATION FOR SEQ ID NO: 481:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 339 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 481:

55 Met Ser Gly Pro Asp Val Glu Thr Pro Ser Ala Ile Gln Ile Cys Arg
 1 5 10 15
 60 Ile Met Arg Pro Asp Asp Ala Asn Val Ala Gly Asn Val His Gly Gly
 20 25 30

645

Thr Ile Leu Lys Met Ile Glu Glu Ala Gly Ala Ile Ile Ser Thr Arg
 35 40 45
 5 His Cys Asn Ser Gln Asn Gly Glu Arg Cys Val Ala Ala Leu Ala Arg
 50 55 60
 Val Glu Arg Thr Asp Phe Leu Ser Pro Met Cys Ile Gly Glu Val Ala
 65 70 75 80
 10 His Val Ser Ala Glu Ile Thr Tyr Thr Ser Lys His Ser Val Glu Val
 85 90 95
 Gln Val Asn Val Met Ser Glu Asn Ile Leu Thr Gly Ala Lys Lys Leu
 100 105 110
 15 Thr Asn Lys Ala Thr Leu Trp Tyr Val Pro Leu Ser Leu Lys Asn Val
 115 120 125
 Asp Lys Val Leu Glu Val Pro Pro Val Val Tyr Ser Arg Xaa Glu Gln
 130 135 140
 Glu Glu Glu Gly Arg Lys Arg Tyr Glu Ala Gln Lys Leu Glu Arg Met
 145 150 155 160
 25 Glu Thr Lys Trp Arg Asn Gly Asp Ile Val Gln Pro Val Leu Asn Pro
 165 170 175
 Glu Pro Asn Thr Val Ser Tyr Ser Gln Ser Ser Leu Ile His Leu Val
 180 185 190
 Gly Pro Ser Asp Cys Thr Leu His Gly Phe Val His Gly Gly Val Thr
 195 200 205
 35 Met Lys Leu Met Asp Glu Val Ala Gly Ile Val Ala Ala Arg His Cys
 210 215 220
 Lys Thr Asn Ile Val Thr Ala Ser Val Asp Ala Ile Asn Phe His Asp
 225 230 235 240
 40 Lys Ile Arg Lys Gly Cys Val Ile Thr Ile Ser Gly Arg Met Thr Phe
 245 250 255
 Thr Ser Asn Lys Ser Met Glu Ile Glu Val Leu Val Asp Ala Asp Pro
 260 265 270
 Val Val Asp Ser Ser Gln Lys Arg Tyr Arg Ala Ala Ser Ala Phe Phe
 275 280 285
 50 Thr Tyr Val Ser Leu Ser Gln Glu Gly Arg Ser Leu Pro Val Pro Gln
 290 295 300
 Leu Val Pro Glu Thr Glu Asp Glu Lys Lys Arg Phe Glu Glu Gly Lys
 305 310 315 320
 55 Gly Arg Tyr Leu Gln Met Lys Ala Lys Xaa Gln Gly His Ala Xaa Xaa
 325 330 335
 Gln Pro Xaa
 60

5 (2) INFORMATION FOR SEQ ID NO: 482:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 32 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 482:

Met Leu Asn Ser Asn Ile Asn Asp Leu Leu Met Val Thr Tyr Leu Ala
1 5 10 15

15 Asn Leu Thr Gln Ser Gln Ile Ala Leu Asn Glu Lys Leu Val Asn Leu
20 25 30

20

(2) INFORMATION FOR SEQ ID NO: 483:

25 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 48 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 483:

Met Arg Glu Thr Ser Ile Arg Val Leu Leu Met Leu Pro Ala Leu Glu
1 5 10 15

35 Ser Thr Ser Gly Leu Ser Ala Phe Met Gly Leu Gly Thr Arg Ile Gly
20 25 30

Cys Phe Lys Thr Ile Thr Cys Trp Pro Thr Ser Leu Thr Gln Arg Xaa
35 40 45

40

45 (2) INFORMATION FOR SEQ ID NO: 484:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 38 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 484:

Met Tyr Met Tyr Ser Leu Asn Val Phe Leu Ser Phe Ile Phe Leu Ala
1 5 10 15

55 Leu Val Phe Lys Cys Val His Val Cys Gln Gly Ala Asn Ala Phe Leu
20 25 30

60 Phe Leu Lys Leu Val Phe
35

(2) INFORMATION FOR SEQ ID NO: 485:

5

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 61 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 485:

Met Gly Leu Arg Leu Ile Cys Leu Glu Leu Thr Met Val Lys Ala Leu
1 5 10 15

15 Val Cys Glu Met Phe Leu Phe Phe Leu Met Thr Gln Lys Leu Ile Trp
20 25 30

Gln Glu Cys Thr Glu Lys Phe Ala Lys Leu Leu Val Gln Leu Ile Ser
35 40 45

20

Leu Val Phe Ala Trp Glu Phe Phe Ser Glu Asp Thr Pro
50 55 60

25

(2) INFORMATION FOR SEQ ID NO: 486:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 346 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 486:

35 Met Leu Ala Ala Arg Leu Val Cys Leu Arg Thr Leu Pro Ser Arg Val
1 5 10 15

Phe His Pro Ala Phe Thr Lys Ala Ser Pro Val Val Lys Asn Ser Ile
20 25 30

40 Thr Lys Asn Gln Trp Leu Leu Thr Pro Ser Arg Glu Tyr Ala Thr Lys
35 40 45

Thr Arg Ile Gly Ile Arg Arg Gly Arg Thr Gly Gln Glu Leu Lys Glu
50 55 60

45

Ala Ala Leu Glu Pro Ser Met Glu Lys Ile Phe Lys Ile Asp Gln Met
65 70 75 80

50 Gly Arg Trp Phe Val Ala Gly Gly Ala Ala Val Gly Leu Gly Ala Leu
85 90 95

Cys Tyr Tyr Gly Leu Gly Leu Ser Asn Glu Ile Gly Ala Ile Glu Lys
100 105 110

55 Ala Val Ile Trp Pro Gln Tyr Val Lys Asp Arg Ile His Ser Thr Tyr
115 120 125

Met Tyr Leu Ala Gly Ser Ile Gly Leu Thr Ala Leu Ser Ala Ile Ala
130 135 140

60

648

Ile Ser Arg Thr Pro Val Leu Met Asn Phe Met Met Arg Gly Ser Trp
 145 150 155 160
 Val Thr Ile Gly Val Thr Phe Ala Ala Met Val Gly Ala Gly Met Leu
 5 165 170 175
 Val Arg Ser Ile Pro Tyr Asp Gln Ser Pro Gly Pro Lys His Leu Ala
 180 185 190
 10 Trp Leu Leu His Ser Gly Val Met Gly Ala Val Val Ala Pro Leu Thr
 195 200 205
 Ile Leu Gly Gly Pro Leu Leu Ile Arg Ala Ala Trp Tyr Thr Ala Gly
 210 215 220
 15 Ile Val Gly Gly Leu Ser Thr Val Ala Met Cys Ala Pro Ser Glu Lys
 225 230 235 240
 Phe Leu Asn Met Gly Ala Pro Leu Gly Val Gly Leu Gly Leu Val Phe
 20 245 250 255
 Val Ser Ser Leu Gly Ser Met Phe Leu Pro Pro Thr Thr Val Ala Gly
 260 265 270
 25 Ala Thr Leu Tyr Ser Val Ala Met Tyr Gly Gly Leu Val Leu Phe Ser
 275 280 285
 Met Phe Leu Leu Tyr Asp Thr Gln Lys Val Ile Lys Arg Ala Glu Val
 290 295 300
 30 Ser Pro Met Tyr Gly Val Gln Lys Tyr Asp Pro Ile Asn Ser Met Leu
 305 310 315 320
 Ser Ile Tyr Met Asp Thr Leu Asn Ile Phe Met Arg Val Ala Thr Met
 35 325 330 335
 Leu Ala Thr Gly Gly Asn Arg Lys Lys Xaa
 340 345

40

(2) INFORMATION FOR SEQ ID NO: 487:

45 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 237 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 487:

50 Met Glu Glu Val Leu Leu Leu Gly Leu Lys Asp Arg Glu Gly Tyr Thr
 1 5 10 15
 Ser Phe Trp Asn Asp Cys Ile Ser Ser Gly Leu Arg Gly Cys Met Leu
 20 25 30
 55 Ile Glu Leu Ala Leu Arg Gly Arg Leu Gln Leu Glu Ala Cys Gly Met
 35 40 45
 60 Arg Arg Lys Ser Leu Leu Thr Arg Lys Val Ile Cys Lys Ser Asp Ala
 50 55 60

Pro Thr Gly Asp Val Leu Leu Asp Glu Ala Leu Lys His Val Lys Glu
 65 70 75 80
 5 Thr Gln Pro Pro Glu Thr Val Gln Asn Trp Ile Glu Leu Leu Ser Gly
 85 90 95
 Glu Thr Trp Asn Pro Leu Lys Leu His Tyr Gln Leu Arg Asn Val Arg
 100 105 110
 10 Glu Arg Leu Ala Lys Asn Leu Val Glu Lys Gly Val Leu Thr Thr Glu
 115 120 125
 Lys Gln Asn Phe Leu Leu Phe Asp Met Thr Thr His Pro Leu Thr Asn
 130 135 140
 15 Asn Asn Ile Lys Gln Arg Leu Ile Lys Lys Val Gln Glu Ala Val Leu
 145 150 155 160
 20 Asp Lys Trp Val Asn Asp Pro His Arg Met Asp Arg Arg Leu Leu Ala
 165 170 175
 Leu Ile Tyr Leu Ala His Ala Ser Asp Val Leu Glu Asn Ala Phe Ala
 180 185 190
 25 Pro Leu Leu Asp Glu Gln Tyr Asp Leu Ala Thr Lys Arg Val Arg Gln
 195 200 205
 30 Leu Leu Asp Leu Asp Pro Glu Val Glu Cys Leu Lys Ala Asn Thr Asn
 210 215 220
 Glu Val Leu Trp Ala Val Val Ala Ala Phe Thr Lys Xaa
 225 230 235
 35
 (2) INFORMATION FOR SEQ ID NO: 488:
 (i) SEQUENCE CHARACTERISTICS:
 40 (A) LENGTH: 200 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 488:
 45 Met Ala Gln Arg Met Val Trp Val Asp Leu Glu Met Thr Gly Leu Asp
 1 5 10 15
 Ile Glu Lys Asp Gln Ile Ile Glu Met Ala Cys Leu Ile Thr Asp Ser
 20 25 30
 50 Asp Leu Asn Ile Leu Ala Glu Gly Pro Asn Leu Ile Ile Lys Gln Pro
 35 40 45
 Asp Glu Leu Leu Asp Ser Met Ser Asp Trp Cys Lys Glu His His Gly
 50 55 60
 Lys Ser Gly Leu Thr Lys Ala Val Lys Glu Ser Thr Ile Thr Leu Gln
 65 70 75 80
 60 Gln Ala Glu Tyr Glu Phe Leu Ser Phe Val Arg Gln Gln Thr Pro Pro

650

85 90 95
 Gly Leu Cys Pro Leu Ala Gly Asn Ser Val His Glu Asp Lys Lys Phe
 100 105 110
 5 Leu Asp Lys Tyr Met Pro Gln Phe Met Lys His Leu His Tyr Arg Ile
 115 120 125
 10 Ile Asp Val Ser Thr Val Lys Glu Leu Cys Arg Arg Trp Tyr Pro Glu
 130 135 140
 Glu Tyr Glu Phe Ala Pro Lys Lys Ala Ala Ser His Arg Ala Leu Asp
 15 145 150 155 160
 Asp Ile Ser Glu Ser Ile Lys Glu Leu Gln Phe Tyr Arg Asn Asn Ile
 165 170 175
 Phe Lys Lys Lys Ile Asp Glu Lys Lys Arg Lys Ile Ile Glu Asn Gly
 20 180 185 190
 Glu Asn Glu Lys Thr Val Ser Xaa
 195 200
 25
 (2) INFORMATION FOR SEQ ID NO: 489:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 351 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 489:
 30 Met Ala Thr Thr Ala Ala Pro Ala Gly Gly Ala Arg Asn Gly Ala Gly
 1 5 10 15
 Pro Glu Trp Gly Gly Phe Glu Glu Asn Ile Gln Gly Gly Gly Ser Ala
 20 25 30
 40 Val Ile Asp Met Glu Asn Met Asp Asp Thr Ser Gly Ser Ser Phe Glu
 35 40 45
 Asp Met Gly Glu Leu His Gln Arg Leu Arg Glu Glu Glu Val Asp Ala
 45 50 55 60
 Asp Ala Ala Asp Ala Ala Ala Ala Glu Glu Glu Asp Gly Glu Phe Leu
 65 70 75 80
 Gly Met Lys Gly Phe Lys Gly Gln Leu Ser Arg Gln Val Ala Asp Gln
 50 85 90 95
 Met Trp Gln Ala Gly Lys Arg Gln Ala Ser Arg Ala Phe Ser Leu Tyr
 100 105 110
 55 Ala Asn Ile Asp Ile Leu Arg Pro Tyr Phe Asp Val Glu Pro Ala Gln
 115 120 125
 Val Arg Thr Gly Leu Leu Glu Ser Met Ile Pro Ile Lys Met Val Asn
 130 135 140
 60

651

Phe Pro Gln Lys Ile Ala Gly Glu Leu Tyr Gly Pro Leu Met Leu Val
 145 150 155 160
 5 Phe Thr Leu Val Ala Ile Leu Leu His Gly Met Lys Thr Ser Asp Thr
 165 170 175
 Ile Ile Arg Glu Gly Thr Leu Met Gly Thr Ala Ile Gly Thr Cys Phe
 180 185 190
 10 Gly Tyr Trp Leu Gly Val Ser Ser Phe Ile Tyr Phe Leu Ala Tyr Leu
 195 200 205
 Cys Asn Ala Gln Ile Thr Met Leu Gln Met Leu Ala Leu Leu Gly Tyr
 210 215 220
 15 Gly Leu Phe Gly His Cys Ile Val Leu Phe Ile Thr Tyr Asn Ile His
 225 230 235 240
 Leu His Ala Leu Phe Tyr Leu Phe Trp Leu Leu Val Gly Gly Leu Ser
 20 245 250 255
 Thr Leu Arg Met Val Ala Val Leu Val Ser Arg Thr Val Gly Pro Thr
 260 265 270
 25 Gln Arg Leu Leu Leu Cys Gly Thr Leu Ala Ala Leu His Met Leu Phe
 275 280 285
 Leu Leu Tyr Leu His Phe Ala Tyr His Lys Val Val Glu Gly Ile Leu
 290 295 300
 30 Asp Thr Leu Glu Gly Pro Asn Ile Pro Pro Ile Gln Arg Val Pro Arg
 305 310 315 320
 Asp Ile Pro Ala Met Leu Pro Ala Ala Arg Leu Pro Thr Thr Val Leu
 35 325 330 335
 Asn Ala Thr Ala Lys Ala Val Ala Val Thr Leu Gln Ser His Xaa
 340 345 350

40

(2) INFORMATION FOR SEQ ID NO: 490:

- 45 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 265 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 490:

50 Met Arg Gly Ser Arg Gly Gly Trp Ala Gly Glu Met Ala Ala Ser Gly
 1 5 10 15
 Glu Ser Gly Thr Ser Gly Gly Gly Gly Ser Thr Glu Glu Ala Phe Met
 20 25 30
 55 Thr Phe Tyr Ser Glu Val Lys Gln Ile Glu Lys Arg Asp Ser Val Leu
 35 40 45
 60 Thr Ser Lys Asn Gln Ile Glu Arg Leu Thr Arg Pro Gly Ser Ser Tyr
 50 55 60

652

Phe Asn Leu Asn Pro Phe Glu Val Leu Gln Ile Asp Pro Glu Val Thr
 65 70 75 80
 5 Asp Glu Glu Ile Lys Lys Arg Phe Arg Gln Leu Ser Ile Leu Val His
 85 90 95
 Pro Asp Lys Asn Gln Asp Asp Ala Asp Arg Ala Gln Lys Ala Phe Glu
 100 105 110
 10 Ala Val Asp Lys Ala Tyr Lys Leu Leu Leu Asp Gln Glu Gln Lys Lys
 115 120 125
 Arg Ala Leu Asp Val Ile Gln Ala Gly Lys Glu Tyr Val Glu His Thr
 15 130 135 140
 Val Lys Glu Arg Lys Lys Gln Leu Lys Lys Glu Gly Lys Pro Thr Ile
 145 150 155 160
 20 Val Glu Glu Asp Asp Pro Glu Leu Phe Lys Gln Ala Val Tyr Lys Gln
 165 170 175
 Thr Met Lys Leu Phe Ala Glu Leu Glu Ile Lys Arg Lys Glu Arg Glu
 180 185 190
 25 Ala Lys Glu Met His Glu Arg Lys Arg Gln Arg Glu Glu Glu Ile Glu
 195 200 205
 Ala Gln Glu Lys Ala Lys Arg Glu Arg Glu Trp Gln Lys Asn Phe Glu
 30 210 215 220
 Glu Ser Arg Asp Gly Arg Val Asp Ser Trp Arg Asn Phe Gln Ala Asn
 225 230 235 240
 35 Thr Lys Gly Lys Lys Glu Lys Lys Asn Arg Thr Phe Leu Arg Pro Pro
 245 250 255
 Lys Val Lys Met Glu Gln Arg Glu Xaa
 260 265
 40

(2) INFORMATION FOR SEQ ID NO: 491:

- 45 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 25 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 491:

Asp Ser Met Pro Thr Cys Pro Leu Xaa Ala Ser Leu Glu Cys Gly Pro
 1 5 10 15
 55 Leu Leu Pro Val Arg Leu Cys Cys Leu
 20 25

(2) INFORMATION FOR SEQ ID NO: 492:

60

653

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 159 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 492:

Met Asn Glu Tyr Arg Val Pro Glu Leu Asn Val Gln Asn Gly Val Leu
 1 5 10 15

10 Lys Ser Leu Ser Phe Leu Phe Glu Tyr Ile Gly Glu Met Gly Lys Asp
 20 25 30

Tyr Ile Tyr Ala Val Thr Pro Leu Leu Glu Asp Ala Leu Met Asp Arg
 35 40 45

15 Asp Leu Val His Arg Gln Thr Ala Ser Ala Val Val Gln His Met Ser
 50 55 60

20 Leu Gly Val Tyr Gly Phe Gly Cys Glu Asp Ser Leu Asn His Leu Leu
 65 70 75 80

Asn Tyr Val Trp Pro Asn Val Phe Glu Thr Ser Pro His Val Ile Gln
 85 90 95

25 Ala Val Met Gly Ala Leu Glu Gly Leu Arg Val Ala Ile Gly Pro Cys
 100 105 110

Arg Met Leu Gln Tyr Cys Leu Gln Gly Leu Phe His Pro Ala Arg Lys
 115 120 125

30 Val Arg Asp Val Tyr Trp Lys Ile Tyr Asn Ser Ile Tyr Ile Gly Ser
 130 135 140

35 Gln Asp Ala Leu Ile Ala His Tyr Pro Arg Ile Tyr Gln Arg Xaa
 145 150 155

40 (2) INFORMATION FOR SEQ ID NO: 493:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 279 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 493:

Met Ile Ser Asp Asn Ser Ala Glu Asn Ile Ala Leu Val Thr Ser Met
 1 5 10 15

50 Tyr Asp Gly Leu Leu Gln Ala Gly Ala Arg Leu Cys Pro Thr Val Gln
 20 25 30

Leu Glu Asp Ile Arg Asn Leu Gln Asp Leu Thr Pro Leu Lys Leu Ala
 35 40 45

55 Ala Lys Glu Gly Lys Ile Glu Ile Phe Arg His Ile Leu Gln Arg Glu
 50 55 60

60 Phe Ser Gly Leu Ser His Leu Ser Arg Lys Phe Thr Glu Trp Cys Tyr
 65 70 75 80

654

Gly Pro Val Arg Val Ser Leu Tyr Asp Leu Ala Ser Val Asp Ser Cys
 85 90 95
 5 Glu Glu Asn Ser Val Leu Glu Ile Ile Ala Phe His Cys Lys Ser Pro
 100 105 110
 His Arg His Arg Met Val Val Leu Glu Pro Leu Asn Lys Leu Leu Gln
 115 120 125
 10 Ala Lys Trp Asp Leu Leu Ile Pro Lys Phe Phe Leu Asn Phe Leu Cys
 130 135 140
 Asn Leu Ile Tyr Met Phe Ile Phe Thr Ala Val Ala Tyr His Gln Pro
 15 145 150 155 160
 Thr Leu Lys Lys Gln Ala Ala Pro His Leu Lys Ala Glu Val Gly Asn
 165 170 175
 20 Ser Met Leu Leu Thr Gly His Ile Leu Ile Leu Leu Gly Gly Ile Tyr
 180 185 190
 Leu Leu Val Gly Gln Leu Trp Tyr Phe Trp Arg Arg His Val Phe Ile
 195 200 205
 25 Trp Ile Ser Phe Ile Asp Ser Tyr Phe Glu Ile Leu Phe Leu Phe Gln
 210 215 220
 Ala Leu Leu Thr Val Val Ser Gln Val Leu Cys Phe Leu Xaa Ile Glu
 30 225 230 235 240
 Trp Tyr Leu Pro Leu Leu Val Ser Ala Leu Val Leu Gly Trp Leu Asn
 245 250 255
 35 Leu Leu Tyr Tyr Thr Arg Gly Phe Gln His Thr Gly Ile Tyr Ser Val
 260 265 270
 Met Ile Gln Lys Pro Trp Xaa
 275
 40

(2) INFORMATION FOR SEQ ID NO: 494:

45 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 193 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 494:
 50 Met Ile Arg Cys Gly Leu Ala Cys Glu Arg Cys Arg Trp Ile Leu Pro
 1 5 10 15
 55 Leu Leu Leu Leu Ser Ala Ile Ala Phe Asp Ile Ile Ala Leu Ala Gly
 20 25 30
 Arg Gly Trp Leu Gln Ser Ser Asp His Gly Gln Thr Ser Ser Leu Trp
 35 40 45
 60 Trp Lys Cys Ser Gln Glu Gly Gly Gly Ser Gly Ser Tyr Glu Glu Gly

655

[illegible]

30

(2) INFORMATION FOR SEQ ID NO: 495:

35 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 205 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 495:

40 Met Ala Ala Gly Asp Gln Val Phe Ser Gly Ala Gly His Val Xaa Glu
1 5 10 15

His Val Ala Gly Gly Arg His Ala Trp Leu Leu Thr Trp Gln Ser Ala
20 25 30

45 Cys Pro Ala Asn Arg Leu Ser Leu Val Pro Leu Val Pro Ser Ala Ser
35 40 45

50 Met Thr Arg Leu Met Arg Xaa Arg Thr Ala Ser Gly Ser Ser Val Ile
50 55 60

Leu Trp Met Ala Pro Ala Ala Ala Pro Thr Pro Ala Arg Ala Pro Glu
65 70 75 80

55 Ala Ala Pro Thr Pro Ala Arg Ala Pro Ala Ala Ala Arg Thr Pro Ala
85 90 95

Arg Gly Pro Thr Trp Thr Ser Pro Pro Thr Arg Val Leu Leu Gly Thr
100 105 110

60

656

Xaa Pro Gly Pro Ser Pro Trp Arg Ser Pro Ala Arg Arg Pro Ala Gln
 115 120 125
 5 Leu Pro Pro Pro Asp Ser Asp Leu Cys Ser Gly Pro Leu Leu Pro Gly
 130 135 140
 Pro Phe Ser Pro Pro Ala Cys His Thr Ala Pro Asn Ser Val Leu Ile
 145 150 155 160
 10 Gln Ser Leu Phe Cys Lys Ser Glu Leu Trp Trp Arg Gln Met Arg Ser
 165 170 175
 Ile Thr Trp Val Pro Ser Pro Lys Ala Gly Trp Arg Trp Thr Lys Gly
 180 185 190
 15 Arg Lys Gln Ala Ser Pro His Arg Ile Leu Phe His Xaa
 195 200 205
 20
 (2) INFORMATION FOR SEQ ID NO: 496:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 147 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 496:
 25 Met Ala Leu Thr Leu Leu Pro Ser Val Ser Arg Leu Pro Gly Glu Arg
 1 5 10 15
 Met Ala Ala Ser Gly Leu Pro Tyr Val Leu His His Lys Ser Ser Leu
 20 25 30
 35 Met Lys Val Ile Phe Phe Pro Tyr Pro Val Leu Pro Leu Pro Ala Pro
 35 40 45
 Asn Gly Thr Trp Val Pro Arg Leu Val Leu Gly Leu Gly Ser Gly Asp
 50 55 60
 40 Gln Val His Tyr Leu Pro Ile Ser Ser Ser Ile Val Asn Tyr Gly Thr
 65 70 75 80
 Ser Val Ser Gly Lys Ser Trp Val Phe Leu Val Tyr Pro Leu His Pro
 85 90 95
 45 Thr Pro Thr Trp Ser Thr Arg Cys Phe Gln Val Trp Asp Leu Leu Ser
 100 105 110
 50 Val Glu Leu Pro Asp Lys Gly Glu Gly Asn Thr Arg Arg Ala Ser Gly
 115 120 125
 Val Pro Gly Leu Ser Gln Leu Pro Thr Ser His Lys Pro Ile Lys Gln
 130 135 140
 55 Glu Tyr Xaa
 145
 60

(2) INFORMATION FOR SEQ ID NO: 497:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 64 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 497:

5 Met Val Trp Val Leu Trp Ser Ala Pro Ser Leu Ala Pro Pro Trp Val
 10 1 5 10 15
 Gly Pro Cys Trp Pro Ser Thr Gly Asn Cys Cys Leu Cys Glu Val Gly
 20 25 30
 15 Ala Ala Leu Pro Pro Arg Gly Pro Ser Leu Ser Asp Cys Leu Gly Leu
 35 40 45
 Pro Pro Trp Thr Pro Trp Gly Pro Ala Trp Thr Leu Ala Gln Ser Xaa
 50 55 60
 20

25

(2) INFORMATION FOR SEQ ID NO: 498:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 94 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 498:

35 Met Ser Thr Gly Ala Leu Asn Thr Ser Pro Pro Ala Ser Asn Arg Leu
 1 5 10 15
 Glu Ser Thr Leu Asn Glu Tyr Leu Ile Gln Pro Gln Leu His Cys Ser
 20 25 30
 40 Ser Val Gln Arg Leu Thr Leu Lys Trp Gly Cys Ser Ser Leu Gln Arg
 35 40 45
 Asp Gly Gln Ala Val Pro Trp Gly Leu Trp Gln Arg Ala Tyr Pro Ser
 50 55 60
 45 Leu Leu Pro Thr Leu Pro Ser Asp Leu Leu Arg Pro His Ala Val Thr
 65 70 75 80
 Pro Ser Val Ser Val Ser Val His Thr Cys Glu Ser Ser Xaa
 85 90
 50

55

(2) INFORMATION FOR SEQ ID NO: 499:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 22 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 499:

60

658

Met Phe Leu Ile Phe Val Tyr Phe Leu Lys Xaa Leu Phe Ser Ser Ser
1 5 10 15

5 Leu Pro Phe Leu Trp Leu
20

10 (2) INFORMATION FOR SEQ ID NO: 500:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 33 amino acids

(B) TYPE: amino acid

15 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 500:

Arg Gly Gly Leu Cys Pro Leu Leu Val Pro Gly Pro Leu Ala Arg Gln
1 5 10 15

20 Glu Pro Ser Pro Ser Leu Gln Gly Cys Ser Glu Ser Pro Val Gly Met
20 25 30

25 Asp

30 (2) INFORMATION FOR SEQ ID NO: 501:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 28 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 501:

Met Gln Phe Leu Leu Thr Ala Phe Leu Leu Val Pro Leu Leu Ala Leu
1 5 10 15

40 Cys Asp Val Pro Ile Ser Leu Gly Phe Ser Pro Ser
20 25

45 (2) INFORMATION FOR SEQ ID NO: 502:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 15 amino acids

(B) TYPE: amino acid

50 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 502:

Pro Gly Lys Pro Gln Ala Cys Pro Glu Leu Thr Ser Val Leu Pro
1 5 10 15

55

(2) INFORMATION FOR SEQ ID NO: 503:

60 (i) SEQUENCE CHARACTERISTICS:

659

(A) LENGTH: 19 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 503:

5

Asn Lys Ser Leu Xaa Ser Cys Leu Phe Val Leu His Phe Val Leu His
 1 5 10 15

Cys Xaa Phe

10

(2) INFORMATION FOR SEQ ID NO: 504:

15

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 29 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 504:

Met Glu Lys Thr His Arg Leu Arg Ile Arg Asn Pro Cys Leu Gln Phe
 1 5 10 15

25

Ser Ile Leu Asn Leu Phe Leu Leu Lys Met Ile Val Ser
 20 25

30

(2) INFORMATION FOR SEQ ID NO: 505:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 75 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 505:

Met Val Asp Ile Ser Lys Met His Met Ile Leu Tyr Asp Leu Gln Gln
 1 5 10 15

40

Asn Leu Ser Ser Ser His Arg Ala Leu Glu Lys Gln Ile Asp Thr Leu
 20 25 30

Ala Gly Lys Leu Asp Ala Leu Thr Glu Leu Leu Ser Thr Ala Leu Gly
 35 40 45

45

Pro Ser Ser Phe Gln Asn Pro Ala Ser Ser Pro Ser Ser Trp Thr His
 50 55 60

50

Glu Glu Glu Pro Gly Tyr Phe Pro Gln Tyr Xaa
 65 70 75

55

(2) INFORMATION FOR SEQ ID NO: 506:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 10 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

60

660

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 506:

Leu Pro Leu Ala Glu Leu Lys Asn Trp Val
 1 5 10

5

(2) INFORMATION FOR SEQ ID NO: 507:

10

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 207 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 507:

15

Met Leu Trp Phe Gly Gly Cys Ser Ala Val Asn Ala Thr Gly His Leu
 1 5 10 15

20

Ser Asp Thr Leu Trp Leu Ile Pro Ile Thr Phe Leu Thr Ile Gly Tyr
 20 25 30

Gly Asp Val Val Pro Gly Thr Met Trp Gly Lys Ile Val Cys Leu Cys
 35 40 45

25

Thr Gly Val Met Gly Val Cys Cys Thr Ala Leu Leu Val Ala Val Val
 50 55 60

Ala Arg Lys Leu Glu Phe Asn Lys Ala Glu Lys His Val His Asn Phe
 65 70 75 80

30

Met Met Asp Ile Gln Tyr Thr Lys Glu Met Lys Glu Ser Ala Ala Arg
 85 90 95

35

Val Leu Gln Glu Ala Trp Met Phe Tyr Lys His Thr Arg Arg Lys Glu
 100 105 110

Ser His Ala Ala Arg Arg His Gln Arg Xaa Leu Leu Ala Ala Ile Asn
 115 120 125

40

Ala Phe Arg Gln Val Arg Leu Lys His Arg Lys Leu Arg Glu Gln Val
 130 135 140

Asn Ser Met Val Asp Ile Ser Lys Met His Met Ile Leu Tyr Asp Leu
 145 150 155 160

45

Gln Gln Asn Leu Ser Ser Ser His Arg Ala Leu Glu Lys Gln Ile Asp
 165 170 175

50

Thr Leu Ala Gly Lys Leu Asp Ala Leu Thr Glu Leu Leu Ser Thr Ala
 180 185 190

Leu Gly Pro Arg Gln Leu Pro Glu Pro Ser Gln Gln Ser Lys Xaa
 195 200 205

55

(2) INFORMATION FOR SEQ ID NO: 508:

60

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 36 amino acids

661

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 508:

5 Met Trp Arg Cys Arg Gly Lys Leu Ser Phe Pro Leu Phe Ala Val Val
 1 5 10 15
 Ile Val Ser Cys Arg Lys Asp Gly Pro Asp Ala Ala Ala Ala Pro Ala
 20 25 30
 10 Val Xaa Lys Lys
 35

15

(2) INFORMATION FOR SEQ ID NO: 509:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 19 amino acids

20

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 509:

25 Met Ala Leu Val Ala Leu Phe Thr Gln Leu Met Arg Xaa Leu Gly Arg
 1 5 10 15
 Cys Pro Gln

30

(2) INFORMATION FOR SEQ ID NO: 510:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 32 amino acids

35

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 510:

40 Met Thr Phe Pro Phe Glu Lys Glu Asn Ser Cys Phe Gln Cys Leu Leu
 1 5 10 15
 Phe Asp Ser Trp Arg Glu Gln Thr Arg Thr Asn Ile Gln Pro Gln Arg
 20 25 30
 45

50

(2) INFORMATION FOR SEQ ID NO: 511:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 28 amino acids

55

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 511:

60 Met His Leu Leu Asp Phe Phe Arg Asp Leu Val Leu Leu Val Leu Leu
 1 5 10 15

662

Ala Leu Leu Asp Ser Phe Trp Leu Glu Val Gln Lys
 20 25

5

(2) INFORMATION FOR SEQ ID NO: 512:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 26 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 512:

10

Met Cys Leu Ile His Phe Ile Lys Ile Ile Leu Val Phe Ile Leu Lys
 1 5 10 15

Leu Trp Leu Tyr Ser Gln Lys Cys Pro Lys
 20 25

20

(2) INFORMATION FOR SEQ ID NO: 513:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 33 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 513:

25

30

Met Ile His Val His Glu Trp Asn Asp Gln Met Leu Met Val Tyr Ile
 1 5 10 15

35

Phe Leu Tyr Pro Val Ser Ile Thr Phe Leu Asn Leu Cys Ser Leu Thr
 20 25 30

Cys

40

(2) INFORMATION FOR SEQ ID NO: 514:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 47 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 514:

45

50

Leu Asn Glu Ser Tyr Val Ser Arg Ala Gly Gly Trp Phe Ser Met Phe
 1 5 10 15

Xaa Leu Ile Phe Phe Leu Leu Ala Leu Gly Ser Xaa Leu Cys Leu Leu
 20 25 30

55

Leu Cys Leu Pro Ser Phe Asn Lys Thr Arg Arg Lys Gln Lys Pro
 35 40 45

60

663

(2) INFORMATION FOR SEQ ID NO: 515:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 43 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 515:

5 Ser Ser Lys Thr Pro Leu Pro Ser Glu Arg Arg Trp Ile Ser Gly Ser
 10 1 5 10 15
 Ser Leu Met Ala Pro Arg Pro Trp Leu Leu Gly Ile Ala Leu Leu Gly
 20 25 30
 15 Leu Trp Ala Leu Glu Pro Ala Leu Gly His Trp
 35 40

20 (2) INFORMATION FOR SEQ ID NO: 516:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 3 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 516:

25 Leu Asn Trp
 30 1

(2) INFORMATION FOR SEQ ID NO: 517:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 174 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 517:

35 Phe Ala Phe Cys Ala Glu Leu Met Ile Gln Asn Trp Thr Leu Gly Ala
 1 5 10 15
 40 Val Asp Ser Gln Met Asp Asp Met Asp Met Asp Leu Asp Lys Glu Phe
 20 25 30
 Leu Gln Asp Leu Lys Glu Leu Lys Val Leu Val Ala Asp Lys Asp Leu
 35 40 45
 50 Leu Asp Leu His Lys Ser Leu Val Cys Thr Ala Leu Arg Gly Lys Leu
 50 55 60
 Gly Val Phe Ser Glu Met Glu Ala Asn Phe Lys Asn Leu Ser Arg Gly
 65 70 75 80
 55 Leu Val Asn Val Ala Ala Lys Leu Thr His Asn Lys Asp Val Arg Asp
 85 90 95
 60 Leu Phe Val Asp Leu Val Glu Lys Phe Val Glu Pro Cys Arg Ser Asp
 100 105 110

664

His Trp Pro Leu Ser Asp Val Arg Phe Phe Leu Asn Gln Tyr Ser Ala
115 120 125

5 Ser Val His Ser Leu Asp Gly Phe Arg His Gln Ala Ser Gly Thr Ala
130 135 140

Thr Trp Ala Pro Ser Ala Ala Ala Ser Cys Ala Cys Ile Met Thr Glu
145 150 155 160

10

Val Pro Pro Asn Ala Pro Pro Thr Leu Thr Ile Lys Leu Leu
165 170

15

(2) INFORMATION FOR SEQ ID NO: 518:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 43 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 518:

25 Met Trp Lys Asn Leu Gly Ser Gly Ser Val Phe Val Thr Trp Phe Ser
1 5 10 15

Leu Val Met Ile Leu Ser Gly Ile Gly Pro Leu Gly Asp Ala Glu Asp
20 25 30

30 Ser Ile Ser Asp Val Ser His Arg Leu Arg Pro
35 40

35

(2) INFORMATION FOR SEQ ID NO: 519:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 13 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 519:

Phe Gln Phe Pro Leu Leu Thr Ile Ala Leu Gln Phe Leu
1 5 10

45

(2) INFORMATION FOR SEQ ID NO: 520:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 30 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 520:

55

Met His Tyr Val Ile Val Leu Ser Leu Phe Val Val Leu Glu Lys Lys
1 5 10 15

60

Asn Lys Met Gly Ser Asp Gly Cys Leu Arg Lys Asn Gly Ser
20 25 30

(2) INFORMATION FOR SEQ ID NO: 521:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 47 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 521:

Met Ser Arg Ser Ile Val Leu Arg Gly Ser Leu Phe Leu Phe Phe Ser
1 5 10 15

His Tyr Thr Leu Lys Leu Leu Ser Val Ile Lys Gln Thr Asn Arg Lys
20 25 30

Ile Val Trp Glu Lys Pro Cys Ile Arg Leu Phe Tyr Xaa Val Leu
35 40 45

(2) INFORMATION FOR SEQ ID NO: 522:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 26 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 522:

Met Pro Leu Pro Val Leu Leu Cys Leu Thr Leu Pro Met Pro Leu Pro
1 5 10 15

Ser Ala Thr Ala Arg Gly Gly Asn Arg Thr
20 25

(2) INFORMATION FOR SEQ ID NO: 523:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 58 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 523:

Ser Ser Ile Pro Val Ser Ile Leu Ile Gly Met Lys Leu Ile Leu Tyr
1 5 10 15

Leu Leu Ile Thr Glu Ser Gly Ser His Glu Lys Lys Ser Phe Tyr Pro
20 25 30

Ser Phe Lys Tyr Met Phe Lys Ile Ile Ile Tyr Val Ser Ala Tyr Cys
35 40 45

Arg Thr Ala Leu Arg Ala Thr Val Ser His
50 55

666

(2) INFORMATION FOR SEQ ID NO: 524:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 19 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 524:

Asn Arg Thr Leu Leu Phe Leu Ile Leu Phe Val Leu Phe Gly Leu Gly
 1 5 10 15

Tyr Gly Phe

(2) INFORMATION FOR SEQ ID NO: 525:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 40 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 525:

Met Phe Leu Leu Val Leu Ser Val Phe Cys Asp Phe Met Cys Ser Ile
 1 5 10 15

Ala Pro Arg Cys His Ala Leu Ser Leu Val Ser Leu Arg Ala Gln His
 20 25 30

Leu Ser Leu Phe Ile Thr Cys His
 35 40

(2) INFORMATION FOR SEQ ID NO: 526:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 57 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 526:

Met Leu Leu Phe Ile Leu Leu Thr Leu Ser Ser Gly Cys Arg Leu Leu
 1 5 10 15

Val Ser Ser Trp Lys Thr Phe Leu Pro His Phe Ser Leu Pro Gly Pro
 20 25 30

Arg Glu His Pro Glu Gly Ser Arg Thr Trp Phe Phe Arg Tyr Trp Glu
 35 40 45

Pro Gly Ala His Cys Leu His Cys Ala
 50 55

(2) INFORMATION FOR SEQ ID NO: 527:

(i) SEQUENCE CHARACTERISTICS:

667

(A) LENGTH: 21 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 527:

5

Ala Arg Leu Leu Leu Phe Leu Ser Ser Val His Pro Ser Ile Met Pro
 1 5 10 15

10

Ser Cys Asn Gln Leu
 20

(2) INFORMATION FOR SEQ ID NO: 528:

15

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 39 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 528:

Met Ser Leu Thr Ser Ser Leu Thr Phe Leu Ser His Ile Leu Leu Leu
 1 5 10 15

25

Pro Gln Lys Leu Gln Phe Leu Ser Trp Met Glu Arg Gln Gln Arg Cys
 20 25 30

Thr Gly Val Ala Lys Tyr Ala
 35

30

(2) INFORMATION FOR SEQ ID NO: 529:

35

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 128 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 529:

40

Met Val Leu Arg Leu Ile Gln Leu Ile Phe Leu Ile Phe Phe Ile His
 1 5 10 15

45

Ile Ile Ile Leu Leu Ile Pro Gly Ser Arg Pro Cys Gly Ser Trp Val
 20 25 30

Asn Asp Arg Xaa Leu Gly Leu Arg Asp Val Thr His Leu Ile Tyr Leu
 35 40 45

50

His Trp Val His Gly His Leu Pro Trp Cys His Pro Tyr Ile Gln Val
 50 55 60

55

Glu Phe Ser Ala Leu Ile Glu Ser Thr Ala Gln Leu Gly Leu Pro Phe
 65 70 75 80

Ser Trp Val Arg Val Ile His Pro Phe Leu Val Leu Pro Cys Leu Tyr
 85 90 95

60

Ser Pro Gly Leu Lys Asn Gly Ile Phe Leu Phe Leu Leu Arg Ala Met
 100 105 110

Pro Gly Gly Met Phe Pro Gly Asn Leu Glu Ala Phe Arg Val Pro Val
 115 120 125

5

10 (2) INFORMATION FOR SEQ ID NO: 530:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 82 amino acids

(B) TYPE: amino acid

15 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 530:

Met Gly Ser Ser Val Leu Pro Phe Cys Val Cys Val Thr Ser Pro Ser
 1 5 10 15

20

Leu Gly Gly Arg Cys Ile Gln Gly Arg Phe Ala Ser His Ser Lys Phe
 20 25 30

25

Trp Gly Phe Gly Xaa Lys Thr Ala Ser Phe Gly Ala Val Gly Glu Thr
 35 40 45

Pro Pro Asp Gln Glu Pro Gln Lys Glu Thr Glu Pro Ala Thr Ser Ser
 50 55 60

30

His Ala Arg Pro Trp Ala Arg Val Ile Gly Leu Arg Ile Trp Pro Gln
 65 70 75 80

Pro Asn

35

(2) INFORMATION FOR SEQ ID NO: 531:

40 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 531:

Met Leu Leu Ser Val Ala Ile Phe Ile Leu Leu Thr Leu Val Tyr Ala
 1 5 10 15

50

Tyr Trp Thr Met
 20

(2) INFORMATION FOR SEQ ID NO: 532:

55

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 75 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

60 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 532:

669

Asn Cys Glu Ile Leu Glu Tyr Cys Tyr Tyr Leu Thr Gln Leu Lys Ile
 1 5 10 15
 5 Ser Met Gly Lys Tyr Leu Ser Ile Pro Thr Val Leu Leu Lys Ile Ile
 20 25 30
 Arg Cys Ser Ile Thr Ala Val Ser Asp Ser Ser Thr Ser Trp Ala Ile
 35 40 45
 10 Lys Ala Gln Leu Lys Ile Glu Asn Lys Asp Leu Asp Asn Lys Thr Ala
 50 55 60
 15 Lys Gly Gly Gly Gln Glu Ala Leu Thr Cys Thr
 65 70 75

(2) INFORMATION FOR SEQ ID NO: 533:
 20 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 60 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 533:

Met Phe Leu Met Arg Met His Leu Cys Phe Cys Lys Tyr Cys Cys Ser
 1 5 10 15
 30 Phe Ile Val Thr Pro Thr Ser Thr Ser Asn Thr Xaa Ser Tyr Leu Trp
 20 25 30
 Pro Trp Ile Ser Ala Ser Met Ala Gly Arg Gly Ser Xaa Trp Ala Cys
 35 40 45
 35 Thr Leu Asn Ala Val Thr Arg Glu Gly Leu Pro Glu
 50 55 60

40 (2) INFORMATION FOR SEQ ID NO: 534:
 (i) SEQUENCE CHARACTERISTICS:
 45 (A) LENGTH: 39 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 534:

50 Met Ser Leu Leu Asn Thr His Thr Leu Cys Phe Val Leu Phe Cys Phe
 1 5 10 15
 Thr Leu Ser Ile Asn Gln Glu Lys Leu Ala Asn His Leu Ala Phe Arg
 20 25 30
 55 Ile Leu Phe Phe Ile Val Phe
 35

60 (2) INFORMATION FOR SEQ ID NO: 535:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 535:

Met Leu

1

(2) INFORMATION FOR SEQ ID NO: 536:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 36 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 536:

Met Asp Gln Phe Lys Ile Phe Tyr Phe Leu Lys Ala Phe Phe Ala Cys
1 5 10 15Cys Asn Val Gln Asp Pro Ser Pro Phe Met Gly Glu Thr Gly Ser Tyr
20 25 30Leu Asn Ile Gly
35

(2) INFORMATION FOR SEQ ID NO: 537:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 14 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 537:

Met Phe Asp Phe Leu Ser Tyr Phe Lys Asp Leu Leu Ser Cys
1 5 10

(2) INFORMATION FOR SEQ ID NO: 538:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 18 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 538:

Met Gly Phe Gly Phe Val Leu Asn Ile Phe Ser Phe Phe Leu Xaa Pro
1 5 10 15

Pro Leu

(2) INFORMATION FOR SEQ ID NO: 539:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 11 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 539:

Leu Leu Leu Trp Thr Leu Leu Ala Xaa Tyr Xaa
 1 5 10

(2) INFORMATION FOR SEQ ID NO: 540:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 108 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 540:

Met Ala Ala Gln Lys Asp Gln Gln Lys Asp Ala Glu Ala Glu Gly Leu
 1 5 10 15

Ser Gly Thr Thr Leu Leu Pro Lys Leu Ile Pro Ser Gly Ala Gly Arg
 20 25 30

Glu Trp Leu Glu Arg Arg Arg Ala Thr Ile Arg Pro Trp Ser Thr Phe
 35 40 45

Val Asp Gln Gln Arg Phe Ser Arg Pro Arg Asn Leu Gly Glu Leu Cys
 50 55 60

Gln Arg Leu Val Arg Asn Val Glu Tyr Tyr Gln Ser Asn Tyr Val Phe
 65 70 75 80

Val Phe Leu Gly Leu Ile Leu Tyr Cys Val Val Thr Ser Pro Met Leu
 85 90 95

Leu Val Ala Leu Ala Val Phe Phe Gly Ala Cys Xaa
 100 105

(2) INFORMATION FOR SEQ ID NO: 541:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 106 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 541:

Phe Val Phe Leu Gly Leu Ile Leu Tyr Cys Val Val Thr Ser Pro Met
 1 5 10 15

Leu Leu Val Ala Leu Ala Val Phe Phe Gly Ala Cys Tyr Ile Leu Tyr
 20 25 30

Leu Arg Thr Leu Glu Ser Lys Leu Val Leu Phe Gly Arg Glu Val Ser
 35 40 45

672

Pro Ala His Gln Tyr Ala Leu Ala Gly Gly Ile Ser Phe Pro Phe Phe
 50 55 60
 5 Trp Leu Ala Gly Ala Gly Ser Ala Val Phe Trp Val Leu Gly Ala Thr
 65 70 75 80
 Leu Val Val Ile Gly Ser His Ala Ala Phe His Gln Ile Glu Ala Val
 85 90 95
 10 Asp Gly Glu Glu Leu Gln Met Glu Pro Val
 100 105
 15
 (2) INFORMATION FOR SEQ ID NO: 542:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 136 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 542:
 20 Met Asp Arg Phe Thr Val Ala Gly Val Leu Pro Asp Ile Glu Gln Phe
 1 5 10 15
 Phe Asn Ile Gly Asp Ser Ser Ser Gly Leu Ile Gln Thr Val Phe Ile
 20 25 30
 30 Ser Ser Tyr Met Val Leu Ala Pro Val Phe Gly Tyr Leu Gly Asp Arg
 35 40 45
 Tyr Asn Arg Lys Tyr Leu Met Cys Gly Gly Ile Ala Phe Trp Ser Leu
 50 55 60
 35 Val Thr Leu Gly Ser Ser Phe Ile Pro Gly Glu His Phe Trp Leu Leu
 65 70 75 80
 Leu Leu Thr Arg Gly Leu Val Gly Val Gly Glu Ala Ser Tyr Ser Thr
 85 90 95
 40 Ile Ala Pro Thr Leu Ile Ala Asp Leu Phe Val Ala Asp Gln Arg Thr
 100 105 110
 45 Gly Cys Ser Ala Ser Ser Thr Leu Pro Phe Arg Trp Ala Val Val Trp
 115 120 125
 Ala Thr Leu Gln Ala Pro Lys Xaa
 130 135
 50

(2) INFORMATION FOR SEQ ID NO: 543:
 55 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 424 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 543:
 60

673

Met Ala Gly Asp Trp His Trp Ala Leu Arg Val Thr Pro Gly Leu Gly
 1 5 10 15
 Val Val Ala Val Leu Leu Leu Phe Leu Val Val Arg Glu Pro Pro Arg
 5 20 25 30
 Gly Ala Val Glu Arg His Ser Asp Leu Pro Pro Leu Asn Pro Thr Ser
 35 40 45
 Trp Trp Ala Asp Leu Arg Ala Leu Ala Arg Asn Pro Ser Phe Val Leu
 10 50 55 60
 Ser Ser Leu Gly Phe Thr Ala Val Ala Phe Val Thr Gly Ser Leu Ala
 65 70 75 80
 15 Leu Trp Ala Pro Ala Phe Leu Leu Arg Ser Arg Val Val Leu Gly Glu
 85 90 95
 Thr Pro Pro Cys Leu Pro Gly Asp Ser Cys Ser Ser Ser Asp Ser Leu
 20 100 105 110
 Ile Phe Gly Leu Ile Thr Cys Leu Thr Gly Val Leu Gly Val Gly Leu
 115 120 125
 25 Gly Val Glu Ile Ser Arg Arg Xaa Arg His Ser Asn Pro Arg Ala Asp
 130 135 140
 Pro Leu Val Cys Ala Thr Gly Leu Leu Gly Ser Ala Pro Phe Leu Phe
 145 150 155 160
 30 Leu Ser Leu Ala Cys Ala Arg Gly Ser Ile Val Ala Thr Tyr Ile Phe
 165 170 175
 Ile Phe Ile Gly Glu Thr Leu Leu Ser Met Asn Trp Ala Ile Val Ala
 35 180 185 190
 Asp Ile Leu Leu Tyr Val Val Ile Pro Thr Arg Arg Ser Thr Ala Glu
 195 200 205
 40 Ala Phe Gln Ile Val Leu Ser His Leu Leu Gly Asp Ala Gly Ser Pro
 210 215 220
 Tyr Leu Ile Gly Leu Ile Ser Asp Arg Leu Arg Arg Asn Trp Pro Pro
 225 230 235 240
 45 Ser Phe Leu Ser Glu Phe Arg Ala Leu Gln Phe Ser Leu Met Leu Cys
 245 250 255
 Ala Phe Val Gly Ala Leu Gly Gly Ala Leu Ser Trp Ala Pro Xaa Ser
 50 260 265 270
 Ser Leu Arg Pro Thr Ala Gly Gly His Ser Cys Thr Cys Arg Ala Cys
 275 280 285
 55 Cys Thr Lys Gln Gly Pro Gln Thr Thr Gly Leu Trp Cys Pro Ser Gly
 290 295 300
 Ala Ala Pro Pro Ala Cys Pro Trp Pro Val Cys Ser Ser Glu Arg Leu
 305 310 315 320
 60

[illegible]

(2) INFORMATION FOR SEQ ID NO: 544:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 39 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 544:

Met Phe Arg Phe Val Ile Cys Leu Phe Leu Trp Leu Val Leu Cys Arg
1 5 10 15
35 Asp Ser Thr Ser Ala Ser Arg Ile Ala Leu Tyr Tyr Arg Ile Val Phe
20 25 30
Leu Ile His Gln Cys Ser Ser
35

(2) INFORMATION FOR SEQ ID NO: 545:

45 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 58 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 545:

Met Leu Pro Trp Xaa Ala Gln Leu Leu Asp Arg Thr Ile Gly Pro Leu
1 5 10 15

55 Tyr Leu Leu Phe Val Gln Phe Ser Pro Ala Phe Ser Arg Thr Ser Pro
20 25 30

Trp Arg Ser Pro Lys Asn Phe Arg Arg Leu Tyr Pro Pro Cys Thr Thr
35 40 45

60 Ser Gly Cys Ala Ala Arg Trp Leu Phe Ser

50

55

5 (2) INFORMATION FOR SEQ ID NO: 546:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 33 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 546:

Met Gly Leu Ser Val Leu Leu Pro Leu Cys Leu Leu Gly Pro Gly Arg
 1 5 10 15

15

Phe Thr Ser Gly Gln Lys Pro Leu Asp Thr Pro Gly Leu Gly Val Pro
 20 25 30

Phe

20

25 (2) INFORMATION FOR SEQ ID NO: 547:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 367 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 547:

Met Ala Lys Pro Gln Val Val Val Ala Pro Val Leu Met Ser Lys Leu
 1 5 10 15

35

Ser Val Asn Ala Pro Glu Phe Tyr Pro Ser Gly Tyr Ser Ser Ser Tyr
 20 25 30

Thr Glu Ser Tyr Glu Asp Gly Cys Glu Asp Tyr Pro Thr Leu Ser Glu
 35 40 45

40

Tyr Val Gln Asp Phe Leu Asn His Leu Thr Glu Gln Pro Gly Ser Phe
 50 55 60

Glu Thr Glu Ile Glu Gln Phe Ala Glu Thr Leu Asn Gly Cys Val Thr
 65 70 75 80

45

Thr Asp Asp Ala Leu Gln Glu Leu Val Glu Leu Ile Tyr Gln Gln Ala
 85 90 95

Thr Ser Ile Pro Asn Phe Ser Tyr Met Gly Ala Arg Leu Cys Asn Tyr
 100 105 110

50

Leu Ser His His Leu Thr Ile Ser Pro Gln Ser Gly Asn Phe Arg Gln
 115 120 125

55

Leu Leu Leu Gln Arg Cys Arg Thr Glu Tyr Glu Val Lys Asp Gln Ala
 130 135 140

Ala Lys Gly Asp Glu Val Thr Arg Lys Arg Phe His Ala Phe Val Leu
 145 150 155 160

60

676

Phe Leu Gly Glu Leu Tyr Leu Asn Leu Glu Ile Lys Gly Thr Asn Gly
 165 170 175
 5 Gln Val Thr Arg Ala Asp Ile Leu Gln Val Gly Leu Arg Glu Leu Leu
 180 185 190
 Asn Ala Leu Phe Ser Asn Pro Met Asp Asp Asn Leu Ile Cys Ala Val
 195 200 205
 10 Lys Leu Leu Lys Leu Thr Gly Ser Val Leu Glu Asp Ala Trp Lys Glu
 210 215 220
 Lys Gly Lys Met Asp Met Glu Glu Ile Ile Gln Arg Ile Glu Asn Val
 15 225 230 235 240
 Val Leu Asp Ala Asn Cys Ser Arg Asp Val Lys Gln Met Leu Leu Lys
 245 250 255
 20 Leu Val Glu Leu Arg Ser Ser Asn Trp Gly Arg Val His Ala Thr Ser
 260 265 270
 Thr Tyr Arg Glu Ala Thr Pro Glu Asn Asp Pro Asn Tyr Phe Met Asn
 275 280 285
 25 Glu Pro Thr Phe Tyr Thr Ser Asp Gly Val Pro Phe Thr Ala Ala Asp
 290 295 300
 Pro Asp Tyr Gln Glu Lys Tyr Gln Glu Leu Leu Glu Arg Glu Asp Phe
 30 305 310 315 320
 Phe Pro Asp Tyr Glu Glu Asn Gly Thr Asp Leu Ser Gly Ala Gly Asp
 325 330 335
 35 Pro Tyr Leu Asp Asp Ile Asp Asp Glu Met Asp Pro Glu Ile Glu Glu
 340 345 350
 Ala Tyr Glu Lys Phe Cys Leu Glu Ser Glu Arg Lys Arg Lys Gln
 355 360 365
 40

(2) INFORMATION FOR SEQ ID NO: 548:

45 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 77 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 548:
 50 Met Leu Arg Leu Asp Ile Ile Asn Ser Leu Val Thr Thr Val Phe Met
 1 5 10 15
 55 Leu Ile Val Ser Val Leu Ala Leu Ile Pro Glu Thr Thr Thr Leu Thr
 20 25 30
 Val Gly Gly Gly Val Phe Ala Leu Val Thr Ala Val Cys Cys Leu Ala
 35 40 45
 60 Asp Gly Ala Leu Ile Tyr Arg Lys Leu Leu Phe Asn Pro Ser Gly Pro

677

Tyr Gln Lys Lys Pro Val His Glu Lys Lys Glu Val Leu
65 70 75

(2) INFORMATION FOR SEQ ID NO: 549:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 47 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 549:

Met Leu Lys Gln Val Met Phe Val Phe Ser Gly Met Gly Pro Arg Ser
1 5 10 15

His Cys Trp Gly Leu Pro Leu Ala Cys Gly Thr Phe Val Gln Gly His
20 25 30

Gln Ala Asp Ser Ser His Leu Leu Pro Leu Lys His Gln Gly Ala
35 40 45

(2) INFORMATION FOR SEQ ID NO: 550:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 168 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 550:

Met Leu Leu Ser Leu Ala Ala Phe Ser Val Ile Ser Val Val Ser Tyr
1 5 10 15

Leu Ile Leu Ala Leu Leu Ser Val Thr Ile Ser Phe Arg Ile Tyr Lys
20 25 30

Ser Val Ile Gln Ala Val Gln Lys Ser Glu Glu Gly His Pro Phe Lys
35 40 45

Ala Tyr Leu Asp Val Asp Ile Thr Leu Ser Ser Glu Ala Phe His Asn
50 55 60

Tyr Met Asn Ala Ala Met Val His Ile Asn Arg Ala Leu Lys Leu Ile
65 70 75 80

Ile Arg Leu Phe Leu Val Glu Asp Leu Val Asp Ser Leu Lys Leu Ala
85 90 95

Val Phe Met Trp Leu Met Thr Tyr Val Gly Ala Val Phe Asn Gly Ile
100 105 110

Thr Leu Leu Ile Leu Ala Glu Leu Leu Ile Phe Ser Val Pro Ile Val
115 120 125

Tyr Glu Lys Tyr Lys Thr Gln Ile Asp His Tyr Val Gly Ile Ala Arg
130 135 140

Asp Gln Thr Lys Ser Ile Val Glu Lys Ile Gln Ala Lys Leu Pro Gly
145 150 155 160

5 Ile Ala Lys Lys Lys Ala Glu Xaa
165

10 (2) INFORMATION FOR SEQ ID NO: 551:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 124 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 551:

Ser Val Pro Phe His Leu Leu Val Val Leu Arg Ser Arg Ala Val Arg
1 5 10 15

20 Ala Arg Arg Arg Arg Glu Pro Arg Ser Leu Pro Arg Pro Gly Asp Glu
20 25 30

25 Glu Leu Gln Leu Leu Leu Cys Gly Ala Arg Ser Asp Phe Leu Glu Arg
35 40 45

Cys Glu Glu Asp Trp Val Cys Leu Trp His His Ala Asp His Ala Ala
50 55 60

30 Phe Pro Gly Ser Phe Gln Cys His Gln Cys Gly Phe Leu Pro His Pro
65 70 75 80

Gly Ser Ser Leu Cys His His Gln Leu Gln Asp Leu Gln Val Arg His
85 90 95

35 Pro Ser Cys Thr Glu Val Arg Arg Arg Pro Ser Ile Gln Ser Leu Pro
100 105 110

40 Gly Arg Arg His Tyr Ser Val Leu Arg Ser Phe Pro
115 120

(2) INFORMATION FOR SEQ ID NO: 552:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 177 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 552:

Met Val His Leu Leu Val Leu Ser Gly Ala Trp Gly Met Gln Met Trp
1 5 10 15

55 Val Thr Phe Val Ser Gly Phe Leu Leu Phe Arg Ser Leu Pro Arg His
20 25 30

Thr Phe Gly Leu Val Gln Ser Lys Leu Phe Pro Phe Tyr Phe His Ile
35 40 45

60

679

Ser Met Gly Cys Ala Phe Ile Asn Leu Cys Ile Leu Ala Ser Gln His
 50 55 60
 5 Ala Trp Ala Gln Leu Thr Phe Trp Glu Ala Ser Gln Leu Tyr Leu Leu
 65 70 75 80
 Phe Leu Ser Leu Thr Leu Ala Thr Val Asn Ala Arg Trp Leu Glu Pro
 85 90 95
 10 Arg Thr Thr Ala Ala Met Trp Ala Leu Gln Thr Val Glu Lys Glu Arg
 100 105 110
 Gly Leu Gly Gly Glu Val Pro Gly Ser His Gln Gly Pro Asp Pro Tyr
 115 120 125
 15 Arg Gln Leu Arg Glu Lys Asp Pro Lys Tyr Ser Ala Leu Arg Gln Asn
 130 135 140
 20 Phe Phe Arg Tyr His Gly Leu Ser Ser Leu Cys Asn Leu Gly Cys Val
 145 150 155 160
 Leu Ser Asn Gly Leu Cys Leu Ala Gly Leu Ala Leu Glu Ile Arg Ser
 165 170 175
 25 Leu

30 (2) INFORMATION FOR SEQ ID NO: 553:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 72 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 553:

Met Ala Phe Ile Leu Leu Phe Tyr Cys Leu Met Thr Phe Leu Ser Leu
 1 5 10 15
 40 Glu Gln Asn Ser Ala Thr Val Glu Pro Ser Ser His Glu Ile Leu His
 20 25 30
 45 Leu Leu Gln Asn Cys Phe Glu Leu Leu Arg Thr Ser Thr Ser Gln Cys
 35 40 45
 Thr Glu Gly Ile Pro Cys Ala Lys Ile Pro Glu Trp Val Thr His Leu
 50 55 60
 50 Thr Trp Gln Thr Leu Lys Asn Ser
 65 70

55 (2) INFORMATION FOR SEQ ID NO: 554:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 45 amino acids

(B) TYPE: amino acid

60 (D) TOPOLOGY: linear

680

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 554:

5 Val Leu Arg Ile Ile Cys Leu Trp Pro Cys Gly Thr Thr Leu Pro Leu
 1 5 10 15
 Val Glu Lys Ala His Asp Ser His Ser Ala Asp Pro Val Cys Pro Gly
 20 25 30
 10 Leu Thr Ala His Leu Pro Val Leu Leu Tyr Val Gln Leu
 35 40 45

(2) INFORMATION FOR SEQ ID NO: 555:

15

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 251 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 555:

Met Lys His Ala Asp Pro Arg Ile Gln Gly Tyr Pro Leu Met Gly Ser
 1 5 10 15
 25 Pro Leu Leu Met Thr Ser Ile Leu Leu Thr Tyr Val Tyr Phe Val Leu
 20 25 30
 Ser Leu Gly Pro Arg Ile Met Ala Asn Arg Lys Pro Phe Gln Leu Arg
 35 40 45
 30 Gly Phe Met Ile Val Tyr Asn Phe Ser Leu Val Ala Leu Ser Leu Tyr
 50 55 60
 Ile Val Tyr Glu Phe Leu Met Ser Gly Trp Leu Ser Thr Tyr Thr Trp
 35 65 70 75 80
 Arg Cys Asp Pro Gln Asp Cys Thr Leu Gly Gln Cys Pro Ser Val Pro
 85 90 95
 40 Ser Pro Xaa Thr Pro Val Thr Lys Ala Tyr Val Val Arg Thr Glu Gln
 100 105 110
 Gly Thr Gly Pro Pro Leu Pro Thr Ala Ala Leu Gln Gly Pro Arg Leu
 115 120 125
 45 Trp Phe Leu Thr His Phe Pro Arg Ala Ala Pro Gly Met Trp Pro His
 130 135 140
 Cys Cys Leu Pro Leu Gln Ser Trp Gly Leu Lys Gly Leu Tyr Ser Tyr
 50 145 150 155 160
 Phe Pro Leu Pro Ala Leu Lys Leu Gly Arg Gly Ala Leu Arg Ala Gly
 165 170 175
 55 Pro Thr Lys Gly Leu Val Ala Phe Phe Leu Thr Gln Lys Arg Ser Ala
 180 185 190
 Ile Met Ser Leu Trp Thr Gln Ser His Ser Ser Thr Pro His Thr Glu
 195 200 205
 60

681

Ala Val Ala Ser Gly Pro Lys Val Arg Val Gly Gly Gly Leu Gly Ile
 210 215 220

5 Gln Pro Val Glu Ala Ala Tyr Ser Thr Cys Val Leu Ile Lys Ser Asp
 225 230 235 240

Arg Gly Asn His Glu Lys Lys Lys Lys Lys Lys
 245 250

10

(2) INFORMATION FOR SEQ ID NO: 556:

15 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 19 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 556:

20 Gly Leu Ala Gly Leu Cys Gly Gln Leu Ser Ser Pro Ala Leu Cys Val
 1 5 10 15

Asn Arg Leu

25

(2) INFORMATION FOR SEQ ID NO: 557:

30 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 217 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 557:

35 Met Ile Thr Glu Lys Trp Gly Leu Asn Met Glu Tyr Cys Arg Gly Gln
 1 5 10 15

40 Ala Tyr Ile Xaa Ser Ser Gly Phe Ser Ser Lys Met Lys Val Val Ala
 20 25 30

Ser Arg Leu Leu Glu Lys Tyr Pro Gln Ala Ile Tyr Thr Leu Cys Ser
 35 40 45

45 Ser Cys Ala Leu Asn Met Trp Leu Ala Lys Ser Val Pro Val Met Gly
 50 55 60

50 Val Ser Val Ala Leu Gly Thr Ile Glu Glu Val Cys Ser Phe Phe His
 65 70 75 80

Arg Ser Pro Gln Leu Leu Glu Leu Asp Asn Val Ile Ser Val Leu
 85 90 95

55 Phe Gln Asn Ser Lys Glu Arg Gly Lys Glu Leu Lys Glu Ile Cys His
 100 105 110

Ser Gln Trp Thr Gly Arg His Asp Ala Phe Glu Ile Leu Val Glu Leu
 115 120 125

60 Leu Gln Ala Leu Val Leu Cys Leu Asp Gly Ile Asn Ser Asp Thr Asn

682

130 135 140

Ile Arg Trp Asn Asn Tyr Ile Ala Gly Arg Ala Phe Val Leu Cys Ser
145 150 155 160

5 Ala Val Ser Asp Phe Asp Phe Ile Val Thr Ile Val Val Leu Lys Asn
165 170 175

10 Val Leu Ser Phe Thr Arg Ala Phe Gly Lys Asn Leu Gln Gly Gln Thr
180 185 190

Ser Asp Val Phe Phe Ala Ala Gly Ser Leu Thr Ala Val Leu His Ser
195 200 205

15 Leu Asn Glu Val Ile Gly Lys Tyr Xaa
210 215

20 (2) INFORMATION FOR SEQ ID NO: 558:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 82 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 558:

Leu Leu Lys Val Leu Cys Ile Leu Pro Val Met Lys Val Glu Asn Glu
1 5 10 15

30 Arg Tyr Glu Asn Gly Arg Lys Arg Leu Lys Ala Tyr Leu Arg Asn Thr
20 25 30

35 Leu Thr Asp Gln Arg Ser Ser Asn Leu Ala Leu Leu Asn Ile Asn Phe
35 40 45

Asp Ile Lys His Asp Leu Asp Leu Met Val Asp Thr Tyr Ile Lys Leu
50 55 60

40 Tyr Thr Ser Lys Ser Glu Leu Pro Thr Asp Asn Ser Glu Thr Val Glu
65 70 75 80

Asn Thr

45

(2) INFORMATION FOR SEQ ID NO: 559:

50 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 95 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 559:

55 Met Val Leu Ile Leu Leu Asn Leu Leu Leu Gly Gln Phe Ser Cys Met
1 5 10 15

60 Ser Pro Ala Ser His His Cys His Pro Leu Pro Thr Glu Met Pro Cys
20 25 30

683

Ser Ser Asp Trp Gly Phe Asp Ser His Thr Val Tyr Pro Ser Cys Val
 35 40 45

5 Asp Ala Leu Leu Pro Lys Pro Ser Ala Asn Ser Phe Pro Asn Gly Ser
 50 55 60

Cys His Cys Gln Gly Leu Tyr Asn Gln Gln Gln Gln Asn Leu His Ala
 65 70 75 80

10 Ala Glu Gly Pro Ala Ser Leu Arg Cys Asn Lys Tyr Val Ser Thr
 85 90 95

15

(2) INFORMATION FOR SEQ ID NO: 560:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 54 amino acids

20

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 560:

25 Met Ile Pro Ala Tyr Ser Lys Asn Arg Ala Tyr Ala Ile Phe Phe Ile
 1 5 10 15

Val Phe Thr Val Ile Gly Asp Ala Pro Gly Ala Val Leu Ser Cys Ala
 20 25 30

30 Gly His Pro Cys Val Gly Phe Ala Ala Val Leu Val Ala Pro Leu Thr
 35 40 45

Val Ala Val Ser Ser Xaa
 50

35

(2) INFORMATION FOR SEQ ID NO: 561:

40

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 108 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 561:

45

Met Glu Val Pro Pro Pro Ala Pro Arg Ser Phe Leu Cys Arg Ala Leu
 1 5 10 15

50 Cys Leu Phe Pro Arg Val Phe Ala Ala Glu Ala Val Thr Ala Asp Ser
 20 25 30

Glu Val Leu Glu Glu Arg Gln Lys Arg Leu Pro Tyr Val Pro Glu Pro
 35 40 45

55 Tyr Tyr Pro Glu Ser Gly Trp Asp Arg Leu Arg Glu Leu Phe Gly Lys
 50 55 60

Asp Thr Val Asn Thr Ser Leu Asn Val Tyr Arg Asn Lys Asp Ala Leu
 65 70 75 80

60

684

Ser His Phe Val Ile Ala Gly Ala Val Thr Gly Ser Leu Phe Arg Ile
85 90 95

Asn Val Gly Leu Arg Gly Trp Trp Leu Val Ala Xaa
100 105

(2) INFORMATION FOR SEQ ID NO: 562:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 562:

Met Asn Trp Gly Leu Ser Ile Trp Leu His Tyr Tyr Glu Lys Lys Lys
1 5 10 15

Glu Gln Val Phe Leu Val Ile Leu Ala His Val Val Arg Arg Cys Ala
20 25 30

Ser Asp Gly Ile Leu Gln Phe Glu Ser Ser Leu Leu Lys Met Arg Arg
35 40 45

Ala Pro
50

(2) INFORMATION FOR SEQ ID NO: 563:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 253 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 563:

Met Val Lys Val Cys Asn Asp Ser Asp Arg Trp Ser Leu Ile Ser Leu
1 5 10 15

Ser Asn Asn Ser Gly Lys Asn Val Glu Leu Lys Phe Val Asp Ser Leu
20 25 30

Arg Arg Gln Phe Glu Phe Ser Val Asp Ser Phe Gln Ile Lys Leu Asp
35 40 45

Ser Leu Leu Leu Phe Tyr Glu Cys Ser Glu Asn Pro Met Thr Glu Thr
50 55 60

Phe His Pro Thr Ile Ile Gly Glu Ser Val Tyr Gly Asp Phe Gln Glu
65 70 75 80

Ala Phe Asp His Leu Cys Asn Lys Ile Ile Ala Thr Arg Asn Pro Glu
85 90 95

Glu Ile Arg Gly Gly Gly Leu Leu Lys Tyr Cys Asn Leu Leu Val Arg
100 105 110

Gly Phe Arg Pro Ala Ser Asp Glu Ile Lys Thr Leu Gln Arg Tyr Met

685

115 120 125
 Cys Ser Arg Phe Phe Ile Asp Phe Ser Asp Ile Gly Glu Gln Gln Arg
 130 135 140
 5 Lys Leu Glu Ser Tyr Leu Gln Asn His Phe Val Gly Leu Glu Asp Arg
 145 150 155 160
 10 Lys Tyr Glu Tyr Leu Met Thr Leu His Gly Val Val Asn Glu Ser Thr
 165 170 175
 Val Cys Leu Met Gly His Glu Arg Arg Gln Thr Leu Asn Leu Ile Thr
 180 185 190
 15 Met Leu Ala Ile Arg Val Leu Ala Asp Gln Asn Val Ile Pro Asn Val
 195 200 205
 Ala Asn Val Thr Cys Tyr Tyr Gln Pro Ala Pro Tyr Val Ala Asp Ala
 210 215 220
 20 Asn Phe Ser Asn Tyr Tyr Ile Ala Gln Val Gln Pro Val Phe Thr Cys
 225 230 235 240
 25 Gln Gln Gln Thr Tyr Ser Thr Trp Leu Pro Cys Asn Xaa
 245 250

30 (2) INFORMATION FOR SEQ ID NO: 564:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 18 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 564:

Met Ser Phe Leu Met Trp Leu Met Ser Leu Ala Ile Thr Ser Gln Pro
 1 5 10 15

40 Pro Met

45 (2) INFORMATION FOR SEQ ID NO: 565:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 80 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 565:

Met Ala Pro Lys Gly Lys Val Gly Thr Arg Gly Lys Lys Gln Ile Phe
 1 5 10 15

55 Glu Glu Asn Arg Glu Thr Leu Lys Phe Tyr Leu Arg Ile Ile Leu Gly
 20 25 30

60 Ala Asn Ala Ile Tyr Cys Leu Val Thr Leu Val Phe Phe Tyr Ser Ser
 35 40 45

686

Ala Ser Phe Trp Ala Trp Leu Ala Leu Gly Phe Ser Leu Ala Val Tyr
 50 55 60

5 Gly Ala Ser Tyr His Ser Met Ser Ser Met Ala Arg Ala Ala Phe Phe
 65 70 75 80

10

(2) INFORMATION FOR SEQ ID NO: 566:

15 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 73 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 566:

20

His Leu Lys Asp Val Ile Leu Leu Thr Ala Ile Val Gln Val Leu Ser
 1 5 10 15

25

Cys Phe Ser Leu Tyr Val Trp Ser Phe Trp Leu Leu Ala Pro Gly Arg
 20 25 30

Ala Leu Tyr Leu Leu Trp Val Asn Val Leu Gly Pro Trp Phe Thr Ala
 35 40 45

30

Asp Ser Gly Thr Pro Ala Pro Glu His Asn Glu Lys Arg Gln Arg Arg
 50 55 60

Gln Glu Arg Arg Gln Met Lys Arg Leu
 65 70

35

(2) INFORMATION FOR SEQ ID NO: 567:

40 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 263 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 567:

45

Met Asp Cys Pro Ala Leu Pro Pro Gly Trp Lys Lys Glu Glu Val Ile
 1 5 10 15

50

Arg Lys Ser Gly Leu Ser Ala Gly Lys Ser Asp Val Tyr Tyr Phe Ser
 20 25 30

Pro Ser Gly Lys Lys Phe Arg Ser Lys Pro Gln Leu Ala Arg Tyr Leu
 35 40 45

55

Gly Asn Thr Val Asp Leu Ser Ser Phe Asp Phe Arg Thr Gly Lys Met
 50 55 60

Met Pro Ser Lys Leu Gln Lys Asn Lys Gln Arg Leu Arg Asn Asp Pro
 65 70 75 80

60

687

Leu Asn Gln Asn Lys Gly Lys Pro Asp Leu Asn Thr Thr Leu Pro Ile
 85 90 95
 5 Arg Gln Thr Ala Ser Ile Phe Lys Gln Pro Val Thr Lys Val Thr Asn
 100 105 110
 His Pro Ser Asn Lys Val Lys Ser Asp Pro Gln Arg Met Asn Glu Gln
 115 120 125
 10 Pro Arg Gln Leu Phe Trp Glu Lys Arg Leu Gln Gly Leu Ser Ala Ser
 130 135 140
 Asp Val Thr Glu Gln Ile Ile Lys Thr Met Glu Leu Pro Lys Gly Leu
 145 150 155 160
 15 Gln Gly Val Gly Pro Gly Ser Asn Asp Glu Thr Leu Leu Ser Ala Val
 165 170 175
 Ala Ser Ala Leu His Thr Ser Ser Ala Pro Ile Thr Gly Gln Val Ser
 180 185 190
 Ala Ala Val Glu Lys Asn Pro Ala Val Trp Leu Asn Thr Ser Gln Pro
 195 200 205
 25 Leu Cys Lys Ala Phe Ile Val Thr Asp Glu Asp Ile Arg Lys Gln Glu
 210 215 220
 Glu Arg Val Gln Gln Val Arg Lys Lys Leu Glu Glu Ala Leu Met Ala
 225 230 235 240
 30 Asp Ile Leu Ser Arg Ala Ala Asp Thr Glu Glu Met Asp Ile Glu Met
 245 250 255
 Asp Ser Gly Asp Glu Ala Xaa
 260

40 (2) INFORMATION FOR SEQ ID NO: 568:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 70 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 568:

Met Met Arg Pro Phe Tyr Leu Leu Leu Pro Val Leu Cys Thr Gln Ala
 1 5 10 15
 50 Leu Arg Gln Ser Gln Gly Lys Ser Pro Leu Leu Trp Lys Arg Thr Leu
 20 25 30
 Leu Phe Gly Leu Thr His Leu Asn Pro Ser Ala Lys Leu Leu Ser
 35 40 45
 55 Gln Met Lys Thr Ser Gly Asn Arg Lys Ser Glu Tyr Ser Lys Tyr Ala
 50 55 60
 60 Arg Asn Trp Lys Lys His
 65 70

(2) INFORMATION FOR SEQ ID NO: 569:

5

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 34 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 569:

Met Pro Val Thr Ser Lys Arg Thr Leu Phe Phe Pro Asp Pro Cys Ser
 1 5 10 15

15

Tyr Asp Thr Pro Pro Pro Asp Cys His Cys His Ser Phe Arg Ala Glu
 20 25 30

Leu Leu

20

(2) INFORMATION FOR SEQ ID NO: 570:

25

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 104 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 570:

Met Asn Ser Arg Gly Met Trp Leu Thr Tyr Ala Leu Gly Val Gly Leu
 1 5 10 15

35

Leu His Ile Val Leu Leu Ser Ile Pro Phe Phe Ser Val Pro Val Ala
 20 25 30

Trp Thr Leu Thr Asn Ile Ile His Asn Leu Gly Met Tyr Val Phe Leu
 35 40 45

40

His Ala Val Lys Gly Thr Pro Phe Glu Thr Pro Asp Gln Gly Lys Ser
 50 55 60

45

Lys Ala Pro Asn Ser Leu Gly Thr Thr Gly Leu Trp Ser Thr Val Tyr
 65 70 75 80

Ile Phe Thr Glu Val Phe His Asn Phe Ser Asn Asn Ser Ile Phe Ser
 85 90 95

50

Gly Lys Phe Leu Tyr Glu Val Xaa
 100

(2) INFORMATION FOR SEQ ID NO: 571:

55

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 132 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

60

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 571:

689

Met Trp Leu Thr Tyr Ala Leu Gly Val Gly Leu Leu His Ile Val Leu
 1 5 10 15
 5 Leu Ser Ile Pro Phe Phe Ser Val Pro Val Ala Trp Thr Leu Thr Asn
 20 25 30
 Ile Ile His Asn Leu Gly Met Tyr Val Phe Leu His Ala Val Lys Gly
 35 40 45
 10 Thr Pro Phe Glu Thr Pro Asp Gln Gly Lys Ala Arg Leu Leu Thr His
 50 55 60
 Trp Glu Gln Leu Asp Tyr Gly Val Gln Phe Thr Ser Ser Arg Lys Phe
 15 65 70 75 80
 Phe Thr Ile Ser Pro Ile Ile Leu Tyr Phe Leu Ala Ser Phe Tyr Thr
 85 90 95
 20 Lys Tyr Asp Pro Thr His Phe Ile Leu Asn Thr Ala Ser Leu Leu Ser
 100 105 110
 Val Leu Ile Pro Lys Met Pro Gln Leu His Gly Val Arg Ile Phe Gly
 115 120 125
 25 Ile Asn Lys Tyr
 130

30

(2) INFORMATION FOR SEQ ID NO: 572:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 32 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 572:

35

Met Asn Lys Trp Ile Cys Glu Met His Cys Tyr Leu Val Leu Leu Ser
 1 5 10 15

40

Val Cys Ser Pro Ser Ala Leu Arg Arg Val Arg His Thr Leu Ser Arg
 20 25 30

45

50

(2) INFORMATION FOR SEQ ID NO: 573:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 28 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 573:

55

Met Pro Val Leu Ser Leu Leu Cys Thr Leu Ile Val Ser Phe Gln Ser
 1 5 10 15

60

Ala Asp Ser Cys Glu Val Phe Leu Asn Cys Ser Leu
20 25

5

(2) INFORMATION FOR SEQ ID NO: 574:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 40 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 574:

10

Met Lys Val Ser Thr Met Leu Trp Phe Leu Cys Trp Glu Gln Ser His
1 5 10 15

Phe Leu Arg Glu Trp Glu Asp Leu Ser Thr Phe Leu Ile Leu Ile Gln
20 25 30

20

Met Glu Cys Gln Tyr Gly Asn Ser
35 40

25

(2) INFORMATION FOR SEQ ID NO: 575:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 30 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 575:

30

Met Gly Leu Pro Leu Met Ala Leu Met Trp Ser Thr Leu Pro Ala Ser
1 5 10 15

35

Ala Gly Val Asn Phe Ile Leu Ala Leu Pro Leu Leu Xaa Leu
20 25 30

40

(2) INFORMATION FOR SEQ ID NO: 576:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 29 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 576:

45

Met Lys Arg Gly Cys Leu Gly Leu Leu Phe Phe Ser Cys Cys Ser Ser
1 5 10 15

50

Ala Pro Thr Met Leu Leu Cys Asp Tyr Leu Asn Trp Phe
20 25

55

(2) INFORMATION FOR SEQ ID NO: 577:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 92 amino acids

60

691

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 577:

5 Met Lys Leu Leu Leu Gly Ile Ala Leu Leu Ala Tyr Val Ala Ser Val
 1 5 10 15
 Trp Gly Asn Phe Val Asn Met Arg Ser Ile Gln Glu Asn Gly Glu Leu
 20 25 30
 10 Lys Ile Glu Ser Lys Ile Glu Glu Met Val Glu Pro Leu Arg Glu Lys
 35 40 45
 Ile Arg Asp Leu Glu Lys Ser Phe Thr Gln Lys Tyr Pro Pro Val Lys
 15 50 55 60
 Phe Leu Ser Glu Lys Asp Arg Lys Arg Ile Leu Xaa Asn Arg Arg Arg
 65 70 75 80
 20 Xaa Val Arg Gly Leu Pro Ser Xaa Leu Thr Asn Ser
 85 90

25 (2) INFORMATION FOR SEQ ID NO: 578:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 42 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 578:

Met Lys Phe Ser Leu Val Leu Leu Ile Lys Ile Ile Ser Phe Glu Arg
 1 5 10 15
 35 Leu Leu Ile Phe Leu Phe Pro Leu Ser Phe Leu Pro Asn Ile Trp Arg
 20 25 30
 Arg Val Met Val Asn Leu Asn Ile Leu Phe
 40 35 40

45 (2) INFORMATION FOR SEQ ID NO: 579:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 70 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 579:

Leu Ala Gln Glu Cys Pro Pro His Ile Pro Ser Ser Phe Phe Leu Val
 1 5 10 15
 55 Lys Leu Leu Phe Ile Pro Trp Leu Ala Ser Leu Leu Pro Pro Leu Ser
 20 25 30
 Thr Phe Thr Ser Asp Phe Tyr Phe Met Glu Phe Gly Ile Glu Val Lys
 35 40 45
 60

692

Leu Gln Gln Cys Arg Gln His Gln Val Leu Gln Glu Lys Asn Thr Lys
 50 55 60

5 Lys Phe Asn Lys Lys Lys
 65 70

(2) INFORMATION FOR SEQ ID NO: 580:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 110 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 580:

Met Leu Arg Leu Leu Leu Val Ala Phe Ala Leu Val Val Val Leu
 1 5 10 15

20 Phe His Val Leu Leu Ala Pro Ile Thr Ala Leu Phe His Thr His Phe
 20 25 30

25 Tyr Asp Arg Leu Gln Asp Ala Gly Ser Arg Trp Pro Glu Leu Tyr Leu
 35 40 45

Tyr Ser Arg Ala Asp Glu Val Val Leu Ala Arg Asp Ile Glu Arg Met
 50 55 60

30 Val Glu Ala Arg Leu Ala Arg Arg Val Leu Ala Arg Ser Val Asp Phe
 65 70 75 80

Val Ser Ser Ala His Val Ser His Leu Arg Asp Tyr Pro Thr Tyr Tyr
 85 90 95

35 Thr Ser Leu Cys Val Asp Phe Met Arg Asn Cys Val Arg Cys
 100 105 110

(2) INFORMATION FOR SEQ ID NO: 581:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 30 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 581:

Met Phe Lys Leu Glu Glu Cys Gly Lys Thr Thr Phe Leu Leu Ser Met
 1 5 10 15

Ala Leu Tyr Phe Trp Trp Ile Val Gln Thr Thr Lys Gly Cys
 20 25 30

(2) INFORMATION FOR SEQ ID NO: 582:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 71 amino acids

(B) TYPE: amino acid

693

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 582:

5 Met Glu Ser Asp Ala Leu Leu Leu Thr Ile Phe Trp Ile Ile Ala Arg
 1 5 10 15
 Ser Ser Val Arg Ser Val Gly Lys Ser Ser Gln Arg Ser Phe Thr Thr
 20 25 30
 10 Ile Thr Gln Leu Arg Ser Thr His Thr Gly Pro Ser Arg Arg Ser Tyr
 35 40 45
 Leu Ile Trp Trp Asn Gly Gly Pro Lys Arg Thr Ile Ser Tyr Val Ser
 50 55 60
 15 Arg Arg Phe Arg Ser Phe Arg
 65 70

20

(2) INFORMATION FOR SEQ ID NO: 583:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 47 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 583:

30 Val Gly Leu Phe Gln Pro Lys Thr Phe Gln Val Pro Val Thr Asp Leu
 1 5 10 15
 Tyr Ile Phe Ile Lys Ile Tyr Ser Glu Ile Gly Pro Ile Met His Val
 20 25 30
 35 Leu Cys Pro Gly Tyr Ser Gln Ser Pro Ser Thr Pro Pro Trp Thr
 35 40 45

40

(2) INFORMATION FOR SEQ ID NO: 584:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 39 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 584:

50 Met Trp Phe Gly Ser Asp Arg Ser Asp Leu Arg Ile Gly Thr Ala Phe
 1 5 10 15
 Leu Phe Asp Leu Val Cys Asp Leu Cys Ile His Ala Trp Lys Pro Pro
 20 25 30
 55 Gly Leu Val Arg Phe Ser Phe
 35

60

(2) INFORMATION FOR SEQ ID NO: 585:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 19 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 585:

Met Leu Asn Thr Ala Ser Leu Asn Leu Pro Trp Lys Val Gln Leu Phe
1 5 10 15

10 Ala His Ala

15 (2) INFORMATION FOR SEQ ID NO: 586:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 23 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 586:

Met Ser Ala Cys Leu Leu Leu Phe Leu Ala Phe Ser Trp Lys Arg Lys
1 5 10 15

25 Gly Leu Trp Ser Gly Pro Gly
20

30 (2) INFORMATION FOR SEQ ID NO: 587:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 69 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 587:

40 Met Leu Pro Pro Phe Ser Leu Val Tyr Thr His Phe Leu Val Ala Ser
1 5 10 15

Leu Leu Pro Val Ile Leu Ala Val Phe Pro Asp Ser Ala Gln Ile Val
20 25 30

45 Pro Leu Leu Lys Pro Ile Pro Arg Pro Gln Pro Glu Val Ile Phe Pro
35 40 45

Ser Ser Glu Leu Leu Glu Gln Leu Leu Ser Val Gln Phe Val Trp Gln
50 55 60

50 Ala His Thr Val Ala
65

55 (2) INFORMATION FOR SEQ ID NO: 588:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 77 amino acids

(B) TYPE: amino acid

60

695

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 588:

5 Met Gly Pro Pro Met Leu Gln Glu Ile Ser Asn Leu Phe Leu Ile Leu
1 5 10 15

Leu Met Met Gly Ala Ile Phe Thr Leu Ala Ala Leu Lys Glu Ser Leu
20 25 30

10 Ser Thr Cys Ile Pro Ala Ile Val Cys Leu Gly Phe Leu Leu Leu Leu
35 40 45

Asn Val Gly Gln Leu Leu Ala Gln Thr Lys Lys Val Val Arg Pro Thr
50 55 60

15 Arg Lys Lys Thr Leu Ser Thr Phe Lys Glu Ser Trp Lys
65 70 75

20

(2) INFORMATION FOR SEQ ID NO: 589:

(i) SEQUENCE CHARACTERISTICS:

25 (A) LENGTH: 155 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 589:

30 Met Ala Leu Leu Leu Ser Val Leu Arg Val Leu Leu Gly Gly Phe Phe
1 5 10 15

Ala Leu Val Gly Leu Ala Lys Leu Ser Glu Glu Ile Ser Ala Pro Val
20 25 30

35 Ser Glu Arg Met Asn Ala Leu Phe Val Gln Phe Ala Glu Val Phe Pro
35 40 45

Leu Lys Val Phe Gly Tyr Gln Pro Asp Pro Leu Asn Tyr Gln Ile Ala
50 55 60

40 Val Gly Phe Leu Glu Leu Leu Ala Gly Leu Leu Leu Val Met Gly Pro
65 70 75 80

45 Pro Met Leu Gln Glu Ile Ser Asn Leu Phe Leu Ile Leu Leu Met Met
85 90 95

Gly Ala Ile Phe Thr Leu Ala Ala Leu Lys Glu Ser Leu Ser Thr Cys
100 105 110

50 Ile Pro Ala Ile Val Cys Leu Gly Phe Leu Leu Leu Leu Asn Val Gly
115 120 125

Gln Leu Leu Ala Gln Thr Lys Lys Val Val Arg Pro Thr Arg Lys Lys
130 135 140

55 Thr Leu Ser Thr Phe Lys Glu Ser Trp Lys Xaa
145 150 155

60

696

(2) INFORMATION FOR SEQ ID NO: 590:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 24 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 590:

Met Pro Glu Thr Arg Leu Gly His Arg Gln Gln Phe Ala Val Phe His
 1 5 10 15

Leu Xaa Pro Val Pro Pro Cys Gly
 20

(2) INFORMATION FOR SEQ ID NO: 591:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 38 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 591:

Met Leu Thr Phe Leu Phe Ser Ala Cys Ala Thr Cys Leu Gly Lys Leu
 1 5 10 15

Ala Ser Pro Leu Ala Pro Val Gly Pro Gln Gln Arg Gly Xaa Pro Pro
 20 25 30

Gly Pro Pro Leu Leu Ser
 35

(2) INFORMATION FOR SEQ ID NO: 592:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 69 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 592:

Met Asp Pro Phe His Tyr Asp Tyr Gln Thr Leu Arg Ile Gly Gly Leu
 1 5 10 15

Val Phe Ala Val Val Leu Phe Ser Val Gly Ile Leu Leu Ile Leu Ser
 20 25 30

Arg Arg Cys Lys Cys Ser Phe Asn Gln Lys Pro Arg Ala Pro Gly Asp
 35 40 45

Glu Glu Ala Gln Val Glu Asn Leu Ile Thr Ala Asn Ala Thr Glu Pro
 50 55 60

Gln Lys Ala Glu Asn
 65

(2) INFORMATION FOR SEQ ID NO: 593:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 308 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 593:

5
10 Asn Leu Arg Val Arg Leu Gly Asp Val Ile Ser Ile Gln Pro Cys Pro
1 5 10 15
Asp Val Lys Tyr Gly Lys Arg Ile His Val Leu Pro Ile Asp Asp Thr
20 25 30
15 Val Glu Gly Ile Thr Gly Asn Leu Phe Glu Val Tyr Leu Lys Pro Tyr
35 40 45
Phe Leu Glu Ala Tyr Arg Pro Ile Arg Lys Gly Asp Ile Phe Leu Val
50 55 60
20 Arg Gly Gly Met Arg Ala Val Glu Phe Lys Val Val Glu Thr Asp Pro
65 70 75 80
25 Ser Pro Tyr Cys Ile Val Ala Pro Asp Thr Val Ile His Cys Glu Gly
85 90 95
Glu Pro Ile Lys Arg Glu Asp Glu Glu Glu Ser Leu Asn Glu Val Gly
100 105 110
30 Tyr Asp Asp Ile Gly Gly Cys Arg Lys Gln Leu Ala Gln Ile Lys Glu
115 120 125
Met Val Glu Leu Pro Leu Arg His Pro Ala Leu Phe Lys Ala Ile Gly
130 135 140
35 Val Lys Pro Pro Arg Gly Ile Leu Leu Tyr Gly Pro Pro Gly Thr Gly
145 150 155 160
40 Lys Thr Leu Ile Ala Arg Ala Val Ala Asn Glu Thr Gly Ala Phe Phe
165 170 175
Phe Leu Ile Asn Gly Pro Glu Ile Met Ser Lys Leu Ala Gly Glu Ser
180 185 190
45 Glu Ser Asn Leu Arg Lys Ala Phe Glu Glu Ala Glu Lys Asn Ala Pro
195 200 205
Ala Ile Ile Phe Ile Asp Glu Leu Asp Ala Ile Ala Pro Lys Arg Glu
210 215 220
50 Lys Thr His Gly Glu Val Glu Arg Arg Ile Val Ser Gln Leu Leu Thr
225 230 235 240
Leu Met Asp Gly Leu Lys Gln Arg Ala His Val Ile Val Met Ala Ala
245 250 255
55 Thr Asn Arg Pro Asn Ser Ile Asp Pro Ala Leu Arg Arg Phe Gly Arg
260 265 270
60 Phe Asp Arg Glu Val Asp Ile Gly Ile Pro Asp Ala Thr Gly Arg Leu

698

275 280 285

Glu Ile Leu Gln Ile His Thr Lys Asn Met Lys Leu Ala Asp Asp Val
 290 295 300

5 Asp Leu Glu Gln
 305

10

(2) INFORMATION FOR SEQ ID NO: 594:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 22 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 594:

15

Met Gln Ile Lys Leu Leu Lys Ser Val Lys Thr Val Phe Ala Ile Thr
 20 1 5 10 15

Leu Leu Val Leu Phe Leu
 20

25

(2) INFORMATION FOR SEQ ID NO: 595:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 24 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 595:

30

Met Phe Pro Lys Phe Cys Pro Ile Leu Ser Leu Val Asp Phe Ile Ser
 35 1 5 10 15

His Arg Asp Lys Pro Glu Thr Glu
 40 20

40

(2) INFORMATION FOR SEQ ID NO: 596:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 24 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 596:

50

Met Leu Ile Glu Cys Ala Trp Gln Leu Met Phe Leu Leu Leu Lys Val
 1 5 10 15

55

Glu Gln Leu Gly Ile Leu Asp Lys
 20

60

(2) INFORMATION FOR SEQ ID NO: 597:

699

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 597:

Met
1

10

(2) INFORMATION FOR SEQ ID NO: 598:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 8 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 598:

20 Met Cys Ile Met Ser Ala Leu Val
1 5

25 (2) INFORMATION FOR SEQ ID NO: 599:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 599:

Met Phe Leu Val Trp Phe Phe Trp Gly Leu Ile Ser Ala Leu Ser Asn
1 5 10 15

35

Val His Thr Pro Ser Arg Leu Pro Ala
20 25

40

(2) INFORMATION FOR SEQ ID NO: 600:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 600:

50 Met Xaa Gly Leu Ser Leu Ile Leu Thr Val Thr Leu Leu Ala Val Ser
1 5 10 15

Asp Ser Ala Ala Thr Cys Ile Val Ala Lys Gly
20 25

55

(2) INFORMATION FOR SEQ ID NO: 601:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 61 amino acids

60

700

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 601:

5 Met Trp Thr Arg Ser Ser Arg Cys Leu Leu Leu Cys Ile Pro Gly Xaa
 1 5 10 15
 Ser Arg Arg Arg Arg Ala Gly Ser Gly Met Lys Pro Arg Ser Trp Ser
 20 25 30
 10 Ala Trp Arg Pro Ser Gly Gly Thr Gly Thr Ser Ser Ser Gln Ser Ser
 35 40 45
 Thr Gln Ser Arg Thr Leu Ser Ala Thr Ala Ser Pro Ala
 15 50 55 60

(2) INFORMATION FOR SEQ ID NO: 602:

20

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 29 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 602:

Met Arg Glu Thr Ser Ile Arg Val Leu Leu Met Leu Pro Ala Leu Glu
 1 5 10 15
 30 Ser Thr Ser Gly Leu Ser Ala Phe Met Gly Leu Gly Thr
 20 25

(2) INFORMATION FOR SEQ ID NO: 603:

35

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 69 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 603:

Met Pro Pro Lys Gln Glu Leu Gly Ser Gly Val Gly Glu Leu Ala Lys
 1 5 10 15
 45 Asn Ser Lys Arg Gln His Trp Asn His Arg Trp Lys Lys Tyr Leu Lys
 20 25 30
 Leu Ile Arg Trp Glu Asp Gly Leu Leu Leu Glu Gly Leu Leu Leu Val
 35 40 45
 Leu Glu His Cys Ala Thr Met Ala Trp Asp Cys Leu Met Arg Leu Glu
 50 55 60
 55 Leu Leu Lys Arg Leu
 65

(2) INFORMATION FOR SEQ ID NO: 604:

60

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 24 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 604:

Lys Ile Val Tyr Ile Leu Gly Asn Pro Leu Lys Phe Asn Ser Arg Val
 1 5 10 15

Ile His His Leu Val Leu Leu Gln
 20

(2) INFORMATION FOR SEQ ID NO: 605:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 35 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 605:

Met Asn Leu His Gln Arg Arg Leu Leu Leu Ile Gly His Leu Met Thr
 1 5 10 15

Leu Val Lys Ala Ser Lys Ser Phe Ser Phe Thr Glu Ile Thr Ser Ser
 20 25 30

Arg Lys Lys
 35

(2) INFORMATION FOR SEQ ID NO: 606:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 130 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 606:

Leu Leu Gly Tyr Gly Leu Phe Gly His Cys Ile Val Leu Phe Ile Thr
 1 5 10 15

Tyr Asn Ile His Leu His Ala Leu Phe Tyr Leu Phe Trp Leu Leu Val
 20 25 30

Gly Gly Leu Ser Thr Leu Arg Met Val Ala Val Leu Val Ser Arg Thr
 35 40 45

Val Gly Pro Thr Gln Arg Leu Leu Leu Cys Gly Thr Leu Ala Ala Leu
 50 55 60

His Met Leu Phe Leu Leu Tyr Leu His Phe Ala Tyr His Lys Val Xaa
 65 70 75 80

Glu Gly Ile Leu Asp Thr Leu Glu Gly Pro Asn Ile Pro Pro Ile Gln
 85 90 95

Arg Val Pro Arg Asp Ile Pro Ala Met Leu Pro Ala Ala Arg Leu Pro
 100 105 110

5 Thr Thr Val Leu Asn Ala Thr Ala Lys Ala Val Ala Val Thr Leu Gln
 115 120 125

Ser His
 130

10

(2) INFORMATION FOR SEQ ID NO: 607:

15 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 23 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 607:

20 Met Leu Val Ile Phe Leu Phe Thr Ser Leu Leu Lys Ile Pro Ser Ser
 1 5 10 15

Val Pro Gly Leu Ile Asn Val
 20

25

(2) INFORMATION FOR SEQ ID NO: 608:

30 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 6 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 608:

35

Glu Leu Asp Tyr Ile Leu
 1 5

40

(2) INFORMATION FOR SEQ ID NO: 609:

45 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 232 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 609:

50 Met Ala Pro Pro Gly Trp Gln Xaa Xaa Xaa Xaa Xaa Trp Leu Ala Cys
 1 5 10 15

Pro Asp Arg Gly Glu Leu Ser Ser Arg Ser Pro Pro Cys Arg Leu Ala
 20 25 30

55 Arg Trp Ala Glu Gly Asp Arg Glu Thr Arg Thr Cys Leu Leu Glu Leu
 35 40 45

Ser Ala Gln Ser Trp Gly Gly Arg Phe Arg Arg Ser Ser Ala Val Ser
 50 55 60

60

703

Ala Gly Ser Pro Ser Arg Leu His Phe Leu Pro Gln Pro Leu Leu Leu
65 70 75 80

Arg Ser Ser Gly Ile Pro Ala Ala Ala Thr Pro Trp Pro Gln Pro Ala
5 85 90 95

Gly Leu Pro Val Arg Pro Thr Pro Thr Arg Thr Gly Glu Glu Asp Arg
100 105 110

Thr Leu Asp Ile Ser Ile Cys Thr Glu Val Leu Ala Gly Thr Glu Gln
10 115 120 125

Pro Pro Pro Pro Arg Met Thr Ser Pro Ser Ser Ser Pro Val Phe Arg
130 135 140

15 Leu Glu Thr Leu Asp Gly Gly Gln Glu Asp Gly Ser Glu Ala Asp Arg
145 150 155 160

Gly Lys Leu Asp Phe Gly Ser Gly Leu Pro Pro Met Glu Ser Gln Phe
20 165 170 175

Gln Gly Glu Asp Arg Lys Phe Ala Pro Ser Asp Lys Ser Gln Pro Pro
180 185 190

25 Thr Thr Glu Arg Glu Gln Val Pro Val Ser Arg Ile Gln Thr Asp Leu
195 200 205

Thr Glu Ile Gly Ser Ser Met Arg Ser Pro Gly Val Ser Pro Arg Ile
210 215 220

30 Trp Leu Asp Phe Gln Ser Thr Xaa
225 230

35

(2) INFORMATION FOR SEQ ID NO: 610:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 34 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 610:

45

Met Val Leu Leu Leu Leu Leu Ala Tyr Val Leu Leu Thr Tyr Ile Leu
1 5 10 15

Leu Leu Asn Met Leu Ile Ala Leu Met Xaa Arg Asp Arg Gln Gln Cys
20 25 30

50

Arg His

55

(2) INFORMATION FOR SEQ ID NO: 611:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 21 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

60

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 611:

Met Val Phe Glu Gly Phe Ser Ser Ala Phe Cys Leu Ser Ser Thr Ala
1 5 10 15
Pro Thr Ser His Pro
20

10

(2) INFORMATION FOR SEQ ID NO: 612:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 9 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 612:

Gly Lys Lys Asn Gln Leu Leu Val Ile
1 5
20

25

(2) INFORMATION FOR SEQ ID NO: 613:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 29 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 613:

Met Val Trp Val Leu Trp Ser Ala Pro Ser Leu Ala Pro Pro Trp Val
1 5 10 15

35

Gly Pro Cys Trp Pro Ser Thr Gly Asn Cys Cys Leu Cys
20 25

40

(2) INFORMATION FOR SEQ ID NO: 614:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 30 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 614:

Met Ala Lys Arg Ser Pro Gly Gly Cys Gly Ser Gly Leu Ile Leu Leu
1 5 10 15

50

Cys Cys Gln Pro Cys Arg Pro Thr Ser Ser Ala Pro Met Arg
20 25 30

55

(2) INFORMATION FOR SEQ ID NO: 615:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 113 amino acids

(B) TYPE: amino acid

60

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 615:

5	Ile Thr	Ile Ala	Ile Gln	Met	Ile Cys	Leu Val	Asn Xaa	Glu Leu	Tyr
	1		5			10		15	
	Pro Thr	Phe Val	Arg Asn	Xaa Gly	Val Met	Val Cys	Ser Ser	Leu Cys	
		20			25		30		
10	Asp Ile	Gly Gly	Ile Ile	Thr	Pro Phe	Ile Val	Phe Arg	Leu Arg	Glu
		35			40		45		
	Val Trp	Gln Ala	Leu Pro	Leu Ile	Leu Phe	Ala Val	Leu Gly	Leu Leu	
		50		55		60			
15	Ala Ala	Gly Val	Thr Leu	Leu Leu	Pro Glu	Thr Lys	Gly Val	Ala Leu	
		65		70		75		80	
	Pro Glu	Thr Met	Lys Asp	Ala Glu	Asn Leu	Gly Arg	Lys Ala	Lys Pro	
			85		90		95		
20	Lys Glu	Asn Thr	Ile Tyr	Leu Lys	Val Gln	Thr Ser	Glu Pro	Ser Gly	
		100			105		110		
25	Thr								

30 (2) INFORMATION FOR SEQ ID NO: 616:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 18 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 616:

40 Thr Met Lys Asp Ala Glu Asn Leu Gly Arg Lys Ala Lys Pro Lys Glu
1 5 10 15
Asn Thr

45 (2) INFORMATION FOR SEQ ID NO: 617:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 21 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 617:

55 Pro Arg Val Arg Asn Ser Pro Glu Asp Leu Gly Leu Ser Leu Thr Gly
 1 5 10 15

Asp Ser Cys Lys Leu
 20

(2) INFORMATION FOR SEQ ID NO: 618:

- 5 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 52 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 618:

10 Gln Ala Asp Asp Leu Gln Ala Thr Val Ala Ala Leu Cys Val Leu Arg
 1 5 10 15
 Gly Gly Gly Pro Trp Ala Gly Ser Trp Leu Ser Pro Lys Thr Pro Gly
 20 25 30
 15 Ala Met Gly Gly Asp Leu Val Leu Gly Leu Gly Ala Leu Arg Arg Arg
 35 40 45
 Lys Arg Leu Leu
 20 50

(2) INFORMATION FOR SEQ ID NO: 619:

- 25 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 232 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 619:

Glu Gln Glu Lys Ser Leu Ala Gly Trp Ala Leu Val Leu Ala Xaa Xaa
 1 5 10 15
 35 Gly Ile Gly Leu Met Val Leu His Ala Glu Met Leu Trp Phe Gly Gly
 20 25 30
 Cys Ser Ala Val Asn Ala Thr Gly His Leu Ser Asp Thr Leu Trp Leu
 35 40 45
 40 Ile Pro Ile Thr Phe Leu Thr Ile Gly Tyr Gly Asp Val Val Pro Gly
 50 55 60
 Thr Met Trp Gly Lys Ile Val Cys Leu Cys Thr Gly Val Met Gly Val
 45 65 70 75 80
 Cys Cys Thr Ala Leu Leu Val Ala Val Val Ala Arg Lys Leu Glu Phe
 85 90 95
 50 Asn Lys Ala Glu Lys His Val His Asn Phe Met Met Asp Ile Gln Tyr
 100 105 110
 Thr Lys Glu Met Lys Glu Ser Ala Ala Arg Val Leu Gln Glu Ala Trp
 115 120 125
 55 Met Phe Tyr Lys His Thr Arg Arg Lys Glu Ser His Ala Ala Arg Xaa
 130 135 140
 60 His Gln Arg Xaa Leu Leu Ala Ala Ile Asn Ala Phe Arg Gln Val Arg
 145 150 155 160

Leu Lys His Arg Lys Leu Arg Glu Gln Val Asn Ser Met Val Asp Ile
 165 170 175
 5 Ser Lys Met His Met Ile Leu Tyr Asp Leu Gln Gln Asn Leu Ser Ser
 180 185 190
 Ser His Arg Ala Leu Glu Lys Gln Ile Asp Thr Leu Ala Gly Lys Leu
 195 200 205
 10 Asp Ala Leu Thr Glu Leu Leu Ser Thr Ala Leu Gly Pro Arg Gln Leu
 210 215 220
 Pro Glu Pro Ser Gln Gln Ser Lys
 15 225 230

20 (2) INFORMATION FOR SEQ ID NO: 620:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 36 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 620:

Tyr Gln Ala His His Val Ser Arg Asn Lys Arg Gly Gln Val Val Gly
 1 5 10 15
 30 Thr Arg Gly Gly Phe Arg Gly Cys Thr Val Trp Leu Thr Gly Leu Ser
 20 25 30
 Gly Ala Gly Lys
 35
 35

(2) INFORMATION FOR SEQ ID NO: 621:
 40 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 57 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 621:

Leu Gln Cys Glu Ile Cys Gly Phe Thr Cys Arg Gln Lys Ala Ser Leu
 1 5 10 15
 50 Asn Trp His Met Lys Lys His Asp Ala Asp Ser Phe Tyr Gln Phe Ser
 20 25 30
 Cys Asn Ile Cys Gly Lys Lys Phe Glu Lys Lys Asp Ser Val Val Ala
 35 40 45
 55 His Lys Ala Lys Ser His Pro Glu Val
 50 55

60 (2) INFORMATION FOR SEQ ID NO: 622:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 19 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 622:

Ile Thr Ser Thr Asp Ile Leu Gly Thr Asn Pro Glu Ser Leu Thr Gln
 1 5 10 15

Pro Ser Asp

(2) INFORMATION FOR SEQ ID NO: 623:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 19 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 623:

Asn Ser Thr Ser Gly Glu Cys Leu Leu Leu Glu Ala Glu Gly Met Ser
 1 5 10 15

Lys Ser Tyr

(2) INFORMATION FOR SEQ ID NO: 624:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 51 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 624:

Cys Ser Gly Thr Glu Arg Val Ser Leu Met Ala Asp Gly Lys Ile Phe
 1 5 10 15

Val Gly Ser Gly Ser Ser Gly Gly Thr Glu Gly Leu Val Met Asn Ser
 20 25 30

Asp Ile Leu Gly Ala Thr Thr Glu Val Leu Ile Glu Asp Ser Asp Ser
 35 40 45

Ala Gly Pro
 50

(2) INFORMATION FOR SEQ ID NO: 625:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 60 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 625:

Ile Gln Tyr Val Arg Cys Glu Met Glu Gly Cys Gly Thr Val Leu Ala
 1 5 10 15
 5 His Pro Arg Tyr Leu Gln His His Ile Lys Tyr Gln His Leu Leu Lys
 20 25 30
 Lys Lys Tyr Val Cys Pro His Pro Ser Cys Gly Arg Leu Phe Arg Leu
 35 40 45
 10 Gln Lys Gln Leu Leu Arg His Ala Lys His His Thr
 50 55 60

15

(2) INFORMATION FOR SEQ ID NO: 626:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 31 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 626:

25 Asp Gln Arg Asp Tyr Ile Cys Glu Tyr Cys Ala Arg Ala Phe Lys Ser
 1 5 10 15
 Ser His Asn Leu Ala Val His Arg Met Ile His Thr Gly Glu Lys
 20 25 30

30

(2) INFORMATION FOR SEQ ID NO: 627:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 25 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 627:

40 Arg Ser Ser Arg Ser Lys Thr Gly Ser Leu Gln Leu Ile Cys Lys Ser
 1 5 10 15
 Glu Pro Asn Thr Asp Gln Leu Asp Tyr
 20 25
 45

50

(2) INFORMATION FOR SEQ ID NO: 628:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 183 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 628:

55

Leu Gln Cys Glu Ile Cys Gly Phe Thr Cys Arg Gln Lys Ala Ser Leu
 1 5 10 15
 Asn Trp His Met Lys Lys His Asp Ala Asp Ser Phe Tyr Gln Phe Ser
 20 25 30
 60

710

Cys Asn Ile Cys Gly Lys Lys Phe Glu Lys Lys Asp Ser Val Val Ala
 35 40 45
 5 His Lys Ala Lys Ser His Pro Glu Val Xaa Ile Thr Ser Thr Asp Ile
 50 55 60
 Leu Gly Thr Asn Pro Glu Ser Leu Thr Gln Pro Ser Asp Xaa Asn Ser
 65 70 75 80
 10 Thr Ser Gly Glu Cys Leu Leu Leu Glu Ala Glu Gly Met Ser Lys Ser
 85 90 95
 Tyr Xaa Cys Ser Gly Thr Glu Arg Val Ser Leu Met Ala Asp Gly Lys
 100 105 110
 15 Ile Phe Val Gly Ser Gly Ser Ser Gly Gly Thr Glu Gly Leu Val Met
 115 120 125
 20 Asn Ser Asp Ile Leu Gly Ala Thr Thr Glu Val Leu Ile Glu Asp Ser
 130 135 140
 Asp Ser Ala Gly Pro Xaa Gln Arg Asp Tyr Ile Cys Glu Tyr Cys Ala
 145 150 155 160
 25 Arg Ala Phe Lys Ser Ser His Asn Leu Ala Val His Arg Met Ile His
 165 170 175
 30 Thr Gly Glu Lys His Tyr Xaa
 180

(2) INFORMATION FOR SEQ ID NO: 629:

35

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 60 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 629:

Gln Tyr Val Arg Cys Glu Met Glu Gly Cys Gly Thr Val Leu Ala His
 1 5 10 15
 45 Pro Arg Tyr Leu Gln His His Ile Lys Tyr Gln His Leu Leu Lys Lys
 20 25 30
 Lys Tyr Val Cys Pro His Pro Ser Cys Gly Arg Leu Phe Arg Leu Gln
 35 40 45
 50 Lys Gln Leu Leu Arg His Ala Lys His His Thr Asp
 50 55 60

55

(2) INFORMATION FOR SEQ ID NO: 630:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 27 amino acids
 (B) TYPE: amino acid

60

711

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 630:

5 Pro Phe Lys Asp Asp Pro Arg Asp Glu Thr Tyr Lys Pro His Leu Glu
 1 5 10 15

Arg Glu Thr Pro Lys Pro Arg Arg Lys Ser Gly
 20 25

10

(2) INFORMATION FOR SEQ ID NO: 631:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 110 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 631:

20 Glu Met Phe Asp Ser Leu Ser Tyr Phe Lys Gly Ser Ser Leu Leu Leu
 1 5 10 15

Met Leu Lys Thr Tyr Leu Ser Glu Asp Val Phe Gln His Ala Val Val
 20 25 30

25

Leu Tyr Leu His Asn His Ser Tyr Ala Ser Ile Gln Ser Asp Asp Leu
 35 40 45

30

Trp Asp Ser Phe Asn Glu Val Thr Asn Gln Thr Leu Asp Val Lys Arg
 50 55 60

Met Met Lys Thr Trp Thr Leu Gln Lys Gly Phe Pro Leu Val Thr Val
 65 70 75 80

35

Gln Lys Lys Gly Lys Glu Leu Phe Ile Gln Gln Glu Arg Phe Phe Leu
 85 90 95

Asn Met Lys Pro Glu Ile Gln Pro Ser Asp Thr Arg Tyr Met
 100 105 110

40

(2) INFORMATION FOR SEQ ID NO: 632:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 24 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 632:

50

Leu Glu Lys Val Ala Ser Val Gly Asn Ser Arg Pro Thr Gly Gln Gln
 1 5 10 15

55

Leu Glu Ser Leu Gly Leu Leu Ala
 20

60

(2) INFORMATION FOR SEQ ID NO: 633:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 18 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 633:

Val His Arg Glu Glu Ala Ser Cys Tyr Cys Gln Ala Glu Pro Ser Gly
 1 5 10 15

10 Asp Leu

15 (2) INFORMATION FOR SEQ ID NO: 634:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 22 amino acids

(B) TYPE: amino acid

20 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 634:

Arg Pro Ala Leu Arg Gln Ala Gly Gly Gly Thr Arg Glu Pro Arg Gln
 1 5 10 15

25 Lys Arg Trp Ala Gly Leu
 20

30 (2) INFORMATION FOR SEQ ID NO: 635:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 12 amino acids

35 (B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 635:

40 Ala Val Asn Phe Arg Pro Gln Arg Ser Gln Ser Met
 1 5 10

45 (2) INFORMATION FOR SEQ ID NO: 636:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 37 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 636:

Met Ile Thr Asp Val Gln Leu Ala Ile Phe Ala Asn Met Leu Gly Val
 1 5 10 15

55 Ser Leu Phe Leu Leu Val Val Leu Tyr His Tyr Val Ala Val Asn Asn
 20 25 30

Pro Lys Lys Gln Glu
 35

60

(2) INFORMATION FOR SEQ ID NO: 637:

5

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 342 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 637:

10

Glu Glu Met Ala Asp Ser Val Lys Thr Phe Leu Gln Asp Leu Ala Arg
1 5 10 15

15

Gly Ile Lys Asp Ser Ile Trp Gly Ile Cys Thr Ile Ser Lys Leu Asp
20 25 30

Ala Arg Ile Gln Gln Lys Arg Glu Gln Arg Arg Arg Arg Ala Ser
35 40 45

20

Ser Val Leu Ala Gln Arg Arg Ala Gln Ser Ile Glu Arg Lys Gln Glu
50 55 60

25

Ser Glu Pro Arg Ile Val Ser Arg Ile Phe Gln Cys Cys Ala Trp Asn
65 70 75 80

Gly Gly Val Phe Trp Phe Ser Leu Leu Leu Phe Tyr Arg Val Phe Ile
85 90 95

30

Pro Val Leu Gln Ser Val Thr Ala Arg Ile Ile Gly Asp Pro Ser Leu
100 105 110

His Gly Asp Val Trp Ser Trp Leu Glu Phe Phe Leu Thr Ser Ile Phe
115 120 125

35

Ser Ala Leu Trp Val Leu Pro Leu Phe Val Leu Ser Lys Val Val Asn
130 135 140

40

Ala Ile Trp Phe Gln Asp Ile Ala Asp Leu Ala Phe Glu Val Ser Gly
145 150 155 160

Arg Lys Pro His Pro Phe Pro Ser Val Ser Lys Ile Ile Ala Asp Met
165 170 175

45

Leu Phe Asn Leu Leu Leu Gln Ala Leu Phe Leu Ile Gln Gly Met Phe
180 185 190

Val Ser Leu Phe Pro Ile His Leu Val Gly Gln Leu Val Ser Leu Leu
195 200 205

50

His Met Ser Leu Leu Tyr Ser Leu Tyr Cys Phe Glu Tyr Arg Trp Phe
210 215 220

55

Asn Lys Gly Ile Glu Met His Gln Arg Leu Ser Asn Ile Glu Arg Asn
225 230 235 240

Trp Pro Tyr Tyr Phe Gly Phe Gly Leu Pro Leu Ala Phe Leu Thr Ala
245 250 255

60

Met Gln Ser Ser Tyr Ile Ile Ser Gly Cys Leu Phe Ser Ile Leu Phe
260 265 270

Pro Leu Phe Ile Ile Ser Ala Asn Glu Ala Lys Thr Pro Gly Lys Ala
 275 280 285

5 Tyr Leu Phe Gln Leu Arg Leu Phe Ser Leu Val Val Phe Leu Ser Asn
 290 295 300

Arg Leu Phe His Lys Thr Val Tyr Leu Gln Ser Ala Leu Ser Ser Ser
 305 310 315 320

10 Thr Ser Ala Glu Lys Phe Pro Ser Pro His Pro Ser Pro Ala Lys Leu
 325 330 335

15 Lys Ala Thr Ala Gly His
 340

(2) INFORMATION FOR SEQ ID NO: 638:

20

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 529 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 638:

Met Ala Lys Phe Met Thr Pro Val Ile Gln Asp Asn Pro Ser Gly Trp
 1 5 10 15

30 Gly Pro Cys Ala Val Pro Glu Gln Phe Arg Asp Met Pro Tyr Gln Pro
 20 25 30

Phe Ser Lys Gly Asp Arg Leu Gly Lys Val Ala Asp Trp Thr Gly Ala
 35 40 45

35 Thr Tyr Gln Asp Lys Arg Tyr Thr Asn Lys Tyr Ser Ser Gln Phe Gly
 50 55 60

40 Gly Gly Ser Gln Tyr Ala Tyr Phe His Glu Glu Asp Glu Ser Ser Phe
 65 70 75 80

Gln Leu Val Asp Thr Ala Arg Thr Gln Lys Thr Ala Tyr Gln Arg Asn
 85 90 95

45 Arg Met Arg Phe Ala Gln Arg Asn Leu Arg Arg Asp Lys Asp Arg Arg
 100 105 110

Asn Met Leu Gln Phe Asn Leu Gln Ile Leu Pro Lys Ser Ala Lys Gln
 115 120 125

50 Lys Glu Arg Glu Arg Ile Arg Leu Gln Lys Lys Phe Gln Lys Gln Phe
 130 135 140

55 Gly Val Arg Gln Lys Trp Asp Gln Lys Ser Gln Lys Pro Arg Asp Ser
 145 150 155 160

Ser Val Glu Val Arg Ser Asp Trp Glu Val Lys Glu Glu Met Asp Phe
 165 170 175

60 Pro Gln Leu Met Lys Met Arg Tyr Leu Glu Val Ser Glu Pro Gln Asp

	180	185	190
	Ile Glu Cys Cys Gly Ala Leu Glu Tyr Tyr Asp Lys Ala Phe Asp Arg		
	195	200	205
5	Ile Thr Thr Arg Ser Glu Lys Pro Leu Arg Xaa Xaa Lys Arg Ile Phe		
	210	215	220
	His Thr Val Thr Thr Thr Asp Asp Pro Val Ile Arg Lys Leu Ala Lys		
10	225	230	235 240
	Thr Gln Gly Asn Val Phe Ala Thr Asp Ala Ile Leu Ala Thr Leu Met		
		245	250 255
15	Ser Cys Thr Arg Ser Val Tyr Ser Trp Asp Ile Val Val Gln Arg Val		
		260	265 270
	Gly Ser Lys Leu Phe Phe Asp Lys Arg Asp Asn Ser Asp Phe Asp Leu		
		275	280 285
20	Leu Thr Val Ser Glu Thr Ala Asn Glu Pro Pro Gln Asp Glu Gly Asn		
		290	295 300
	Ser Phe Asn Ser Pro Arg Asn Leu Ala Met Glu Ala Thr Tyr Ile Asn		
25	305	310	315 320
	His Asn Phe Ser Gln Gln Cys Leu Arg Met Gly Lys Glu Arg Tyr Asn		
		325	330 335
30	Phe Pro Asn Pro Asn Pro Phe Val Glu Asp Asp Met Asp Lys Asn Glu		
		340	345 350
	Ile Ala Ser Val Ala Tyr Arg Tyr Arg Ser Gly Lys Leu Gly Asp Asp		
		355	360 365
35	Ile Asp Leu Ile Val Arg Cys Glu His Asp Gly Val Met Thr Gly Ala		
		370	375 380
	Asn Gly Glu Val Ser Phe Ile Asn Ile Lys Thr Leu Asn Glu Trp Asp		
40	385	390	395 400
	Ser Arg His Cys Asn Gly Val Asp Trp Arg Gln Lys Leu Asp Ser Gln		
		405	410 415
45	Arg Gly Ala Val Ile Ala Thr Glu Leu Lys Asn Asn Ser Tyr Lys Leu		
		420	425 430
	Ala Arg Trp Thr Cys Cys Ala Leu Leu Ala Gly Ser Glu Tyr Leu Lys		
		435	440 445
50	Leu Gly Tyr Val Ser Arg Tyr His Val Lys Asp Ser Ser Arg His Val		
		450	455 460
	Ile Leu Gly Thr Gln Gln Phe Lys Pro Asn Glu Phe Ala Ser Gln Ile		
55	465	470	475 480
	Asn Leu Ser Val Glu Asn Ala Trp Gly Ile Leu Arg Cys Val Ile Asp		
		485	490 495
60	Ile Cys Met Lys Leu Glu Glu Gly Lys Tyr Leu Ile Leu Lys Asp Pro		

500 505 510

Asn Lys Gln Val Ile Arg Val Tyr Ser Leu Pro Asp Gly Thr Phe Ser
 515 520 525

5 Ser

10 (2) INFORMATION FOR SEQ ID NO: 639:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 194 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 639:

20 Lys Lys Arg His Thr Asp Val Gln Phe Tyr Thr Glu Val Gly Glu Ile
 1 5 10 15

Thr Thr Asp Leu Gly Lys His Gln His Met His Asp Arg Asp Asp Leu
 20 25 30

25 Tyr Ala Glu Gln Met Glu Arg Glu Met Arg His Lys Leu Lys Thr Ala
 35 40 45

Phe Lys Asn Phe Ile Glu Lys Val Glu Ala Leu Thr Lys Glu Glu Leu
 50 55 60

30 Glu Phe Glu Val Pro Phe Arg Asp Leu Gly Phe Asn Gly Ala Pro Tyr
 65 70 75 80

35 Arg Ser Thr Cys Leu Leu Gln Pro Thr Ser Ser Ala Leu Val Asn Ala
 85 90 95

Thr Glu Trp Pro Pro Phe Val Val Thr Leu Asp Glu Val Glu Leu Ile
 100 105 110

40 His Phe Xaa Arg Val Gln Phe His Leu Lys Asn Phe Asp Met Val Ile
 115 120 125

Val Tyr Lys Asp Tyr Ser Lys Lys Val Thr Met Ile Asn Ala Ile Pro
 130 135 140

45 Val Ala Ser Leu Asp Pro Ile Lys Glu Trp Leu Asn Ser Cys Asp Leu
 145 150 155 160

50 Lys Tyr Thr Glu Gly Val Gln Ser Leu Asn Trp Thr Lys Ile Met Lys
 165 170 175

Thr Ile Val Asp Asp Pro Glu Gly Phe Phe Glu Gln Gly Gly Trp Ser
 180 185 190

55 Phe Leu

60 (2) INFORMATION FOR SEQ ID NO: 640:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 70 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 640:

Arg Ser Gly Leu Gly Leu Gly Ile Thr Ile Ala Phe Leu Ala Thr Leu
 1 5 10 15
 Ile Thr Gln Phe Leu Val Tyr Asn Gly Val Tyr Gln Tyr Thr Ser Pro
 20 25 30
 Asp Phe Leu Tyr Ile Arg Ser Trp Leu Pro Cys Ile Phe Phe Ser Gly
 35 40 45
 Gly Val Thr Val Gly Asn Ile Gly Arg Gln Leu Ala Met Gly Val Pro
 50 55 60
 Glu Lys Pro His Ser Asp
 65 70

(2) INFORMATION FOR SEQ ID NO: 641:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 101 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 641:

Val Thr Gln Pro Lys His Leu Ser Ala Ser Met Gly Gly Ser Val Glu
 1 5 10 15
 Ile Pro Phe Ser Phe Tyr Tyr Pro Trp Glu Leu Ala Xaa Xaa Pro Xaa
 20 25 30
 Val Arg Ile Ser Trp Arg Arg Gly His Phe His Gly Gln Ser Phe Tyr
 35 40 45
 Ser Thr Arg Pro Pro Ser Ile His Lys Asp Tyr Val Asn Arg Leu Phe
 50 55 60
 Leu Asn Trp Thr Glu Gly Gln Glu Ser Gly Phe Leu Arg Ile Ser Asn
 65 70 75 80
 Leu Arg Lys Glu Asp Gln Ser Val Tyr Phe Cys Arg Val Glu Leu Asp
 85 90 95
 Thr Arg Arg Ser Gly
 100

(2) INFORMATION FOR SEQ ID NO: 642:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 233 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 642:

5 Met Glu Ala Gln Gln Val Asn Glu Ala Glu Ser Ala Arg Glu Gln Leu
 1 5 10 15
 Gln Xaa Leu His Asp Gln Ile Ala Gly Gln Lys Ala Ser Lys Gln Glu
 20 25 30
 10 Leu Glu Thr Glu Leu Glu Arg Leu Lys Gln Glu Phe His Tyr Ile Glu
 35 40 45
 Glu Asp Leu Tyr Arg Thr Lys Asn Thr Leu Gln Ser Arg Ile Lys Asp
 50 55 60
 15 Arg Asp Glu Glu Ile Gln Lys Leu Arg Asn Gln Leu Thr Asn Lys Thr
 65 70 75 80
 Leu Ser Asn Ser Ser Gln Ser Glu Leu Glu Asn Arg Leu His Gln Leu
 85 90 95
 Thr Glu Thr Leu Ile Gln Lys Gln Thr Met Leu Glu Ser Leu Ser Thr
 100 105 110
 25 Glu Lys Asn Ser Leu Val Phe Gln Leu Glu Arg Leu Glu Gln Gln Met
 115 120 125
 Asn Ser Ala Ser Gly Ser Ser Ser Asn Gly Ser Ser Ile Asn Met Ser
 130 135 140
 30 Gly Ile Asp Asn Gly Glu Gly Thr Arg Leu Arg Asn Val Pro Val Leu
 145 150 155 160
 Phe Asn Asp Thr Glu Thr Asn Leu Ala Gly Met Tyr Gly Lys Val Arg
 165 170 175
 Lys Ala Ala Ser Ser Ile Asp Gln Phe Ser Ile Arg Leu Gly Ile Phe
 180 185 190
 40 Leu Arg Arg Tyr Pro Ile Ala Arg Val Phe Val Ile Ile Tyr Met Ala
 195 200 205
 Leu Leu His Leu Trp Val Met Ile Val Leu Leu Thr Tyr Thr Pro Glu
 210 215 220
 45 Met His His Asp Gln Pro Tyr Gly Lys
 225 230

50

(2) INFORMATION FOR SEQ ID NO: 643:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 43 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 643:

60 Ile Arg His Glu Gln His Pro Asn Phe Ser Leu Glu Met His Ser Lys
 1 5 10 15

Gly Ser Ser Leu Leu Leu Phe Leu Pro Gln Leu Ile Leu Ile Leu Pro
 20 25 30

5 Val Cys Ala His Leu His Glu Glu Leu Asn Cys
 35 40

10 (2) INFORMATION FOR SEQ ID NO: 644:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 63 amino acids

(B) TYPE: amino acid

15 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 644:

Ser Phe Phe Ile Ser Glu Glu Lys Gly His Leu Leu Leu Gln Ala Glu
 1 5 10 15

20 Arg His Pro Trp Val Ala Gly Ala Leu Val Gly Val Ser Gly Gly Leu
 20 25 30

25 Thr Leu Thr Thr Cys Ser Gly Pro Thr Glu Lys Pro Ala Thr Lys Asn
 35 40 45

Tyr Phe Leu Lys Arg Leu Leu Gln Glu Met His Ile Arg Ala Asn
 50 55 60

30

35

INDICATIONS RELATING TO A DEPOSITED MICROORGANISM

(PCT Rule 13bis)

A. The indications made below relate to the microorganism referred to in the description on page <u>116</u> , line <u>N/A</u>	
B. IDENTIFICATION OF DEPOSIT Further deposits are identified on an additional sheet <input type="checkbox"/>	
Name of depositary institution <div style="text-align: center;">American Type Culture Collection</div>	
Address of depositary institution (including postal code and country) 12301 Parklawn Drive Rockville, Maryland 20852 United States of America	
Date of deposit February 26, 1997	Accession Number 97897
C. ADDITIONAL INDICATIONS (leave blank if not applicable) This information is continued on an additional sheet <input type="checkbox"/>	
D. DESIGNATED STATES FOR WHICH INDICATIONS ARE MADE (if the indications are not for all designated States)	
E. SEPARATE FURNISHING OF INDICATIONS (leave blank if not applicable)	
The indications listed below will be submitted to the International Bureau later (specify the general nature of the indications, e.g., "Accession Number of Deposit")	

For receiving Office use only

<input checked="checked" type="checkbox"/> This sheet was received with the international application
Authorized officer <div style="text-align: center;">Susan White PCT International Division</div>

For International Bureau use only

<input type="checkbox"/> This sheet was received by the International Bureau on:
Authorized officer

INDICATIONS RELATING TO A DEPOSITED MICROORGANISM

(PCT Rule 13bis)

A. The indications made below relate to the microorganism referred to in the description on page <u>116</u> , line <u>N/A</u>	
B. IDENTIFICATION OF DEPOSIT Further deposits are identified on an additional sheet <input type="checkbox"/>	
Name of depositary institution <div style="text-align: center;">American Type Culture Collection</div>	
Address of depositary institution (including postal code and country) 12301 Parklawn Drive Rockville, Maryland 20852 United States of America	
Date of deposit May 15, 1997	Accession Number 209043
C. ADDITIONAL INDICATIONS (leave blank if not applicable) This information is continued on an additional sheet <input type="checkbox"/>	
D. DESIGNATED STATES FOR WHICH INDICATIONS ARE MADE (if the indications are not for all designated States)	
E. SEPARATE FURNISHING OF INDICATIONS (leave blank if not applicable)	
The indications listed below will be submitted to the International Bureau later (specify the general nature of the indications, e.g., "Accession Number of Deposit")	

<div style="border-bottom: 1px solid black; margin-bottom: 5px;">For receiving Office use only</div> <div style="display: flex; align-items: center; margin-bottom: 10px;"><input checked="checked" type="checkbox"/> This sheet was received with the international application</div> <div style="border-bottom: 1px solid black; margin-bottom: 10px;">Authorized officer</div> <div style="text-align: center;">Susan White PCT International Division</div>	<div style="border-bottom: 1px solid black; margin-bottom: 5px;">For International Bureau use only</div> <div style="display: flex; align-items: center; margin-bottom: 10px;"><input type="checkbox"/> This sheet was received by the International Bureau on:</div> <div style="border-bottom: 1px solid black; margin-bottom: 10px;">Authorized officer</div>
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INDICATIONS RELATING TO A DEPOSITED MICROORGANISM

(PCT Rule 13bis)

A. The indications made below relate to the microorganism referred to in the description on page <u>119</u> , line <u>N/A</u>	
B. IDENTIFICATION OF DEPOSIT Further deposits are identified on an additional sheet <input type="checkbox"/>	
Name of depositary institution <div style="text-align: center;">American Type Culture Collection</div>	
Address of depositary institution (including postal code and country) 12301 Parklawn Drive Rockville, Maryland 20852 United States of America	
Date of deposit September 4, 1997	Accession Number 209235
C. ADDITIONAL INDICATIONS (leave blank if not applicable) This information is continued on an additional sheet <input type="checkbox"/>	
D. DESIGNATED STATES FOR WHICH INDICATIONS ARE MADE (if the indications are not for all designated States)	
E. SEPARATE FURNISHING OF INDICATIONS (leave blank if not applicable)	
The indications listed below will be submitted to the International Bureau later (specify the general nature of the indications, e.g., "Accession Number of Deposit")	

For receiving Office use only	For International Bureau use only
<input checked="checked" type="checkbox"/> This sheet was received with the international application	<input type="checkbox"/> This sheet was received by the International Bureau on:
Authorized officer <div style="text-align: center;">Susan White PCT International Division</div>	Authorized officer

INDICATIONS RELATING TO A DEPOSITED MICROORGANISM

(PCT Rule 13bis)

A. The indications made below relate to the microorganism referred to in the description on page <u>122</u> , line <u>N/A</u>	
B. IDENTIFICATION OF DEPOSIT Further deposits are identified on an additional sheet <input type="checkbox"/>	
Name of depositary institution <div style="text-align: center;">American Type Culture Collection</div>	
Address of depositary institution (including postal code and country) 12301 Parklawn Drive Rockville, Maryland 20852 United States of America	
Date of deposit February 26, 1997	Accession Number 97898
C. ADDITIONAL INDICATIONS (leave blank if not applicable) This information is continued on an additional sheet <input type="checkbox"/>	
D. DESIGNATED STATES FOR WHICH INDICATIONS ARE MADE (if the indications are not for all designated States)	
E. SEPARATE FURNISHING OF INDICATIONS (leave blank if not applicable)	
The indications listed below will be submitted to the International Bureau later (specify the general nature of the indications, e.g., "Accession Number of Deposit")	

For receiving Office use only	For International Bureau use only
<input checked="checked" type="checkbox"/> This sheet was received with the international application	<input type="checkbox"/> This sheet was received by the International Bureau on:
Authorized officer <div style="text-align: center;">Susan White PCT International Division</div>	Authorized officer

INDICATIONS RELATING TO A DEPOSITED MICROORGANISM

(PCT Rule 13bis)

A. The indications made below relate to the microorganism referred to in the description on page <u>122</u> , line <u>N/A</u>	
B. IDENTIFICATION OF DEPOSIT Further deposits are identified on an additional sheet <input type="checkbox"/>	
Name of depositary institution <div style="text-align: center;">American Type Culture Collection</div>	
Address of depositary institution (including postal code and country) 12301 Parklawn Drive Rockville, Maryland 20852 United States of America	
Date of deposit May 15, 1997	Accession Number 209044
C. ADDITIONAL INDICATIONS (leave blank if not applicable) This information is continued on an additional sheet <input type="checkbox"/>	
D. DESIGNATED STATES FOR WHICH INDICATIONS ARE MADE (if the indications are not for all designated States)	
E. SEPARATE FURNISHING OF INDICATIONS (leave blank if not applicable)	
The indications listed below will be submitted to the International Bureau later (specify the general nature of the indications, e.g., "Accession Number of Deposit")	

<div style="border-bottom: 1px solid black; margin-bottom: 5px;">For receiving Office use only</div> <div style="display: flex; align-items: center; margin-bottom: 10px;"><input checked="checked" type="checkbox"/> This sheet was received with the international application</div> <div style="border-bottom: 1px solid black; margin-bottom: 10px;">Authorized officer</div> <div style="text-align: center;">Susan White PCT International Division</div>	<div style="border-bottom: 1px solid black; margin-bottom: 5px;">For International Bureau use only</div> <div style="display: flex; align-items: center; margin-bottom: 10px;"><input type="checkbox"/> This sheet was received by the International Bureau on:</div> <div style="border-bottom: 1px solid black; margin-bottom: 10px;">Authorized officer</div>
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INDICATIONS RELATING TO A DEPOSITED MICROORGANISM

(PCT Rule 13bis)

A. The indications made below relate to the microorganism referred to in the description on page <u>126</u> , line <u>N/A</u>	
B. IDENTIFICATION OF DEPOSIT Further deposits are identified on an additional sheet <input type="checkbox"/>	
Name of depositary institution <div style="text-align: center;">American Type Culture Collection</div>	
Address of depositary institution (including postal code and country) 12301 Parklawn Drive Rockville, Maryland 20852 United States of America	
Date of deposit February 26, 1997	Accession Number 97899
C. ADDITIONAL INDICATIONS (leave blank if not applicable) This information is continued on an additional sheet <input type="checkbox"/>	
D. DESIGNATED STATES FOR WHICH INDICATIONS ARE MADE (if the indications are not for all designated States)	
E. SEPARATE FURNISHING OF INDICATIONS (leave blank if not applicable)	
The indications listed below will be submitted to the International Bureau later (specify the general nature of the indications, e.g., "Accession Number of Deposit")	

<div style="text-align: center;">For receiving Office use only</div> <div style="border: 1px solid black; padding: 5px; margin-top: 5px;"><input checked="checked" type="checkbox"/> This sheet was received with the international application</div> <div style="border: 1px solid black; padding: 5px; margin-top: 5px;">Authorized officer <div style="text-align: center;">Susan White PCT International Division</div></div>	<div style="text-align: center;">For International Bureau use only</div> <div style="border: 1px solid black; padding: 5px; margin-top: 5px;"><input type="checkbox"/> This sheet was received by the International Bureau on:</div> <div style="border: 1px solid black; padding: 5px; margin-top: 5px;">Authorized officer</div>
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INDICATIONS RELATING TO A DEPOSITED MICROORGANISM

(PCT Rule 13bis)

A. The indications made below relate to the microorganism referred to in the description on page <u>126</u> , line <u>N/A</u>	
B. IDENTIFICATION OF DEPOSIT Further deposits are identified on an additional sheet <input type="checkbox"/>	
Name of depositary institution <div style="text-align: center;">American Type Culture Collection</div>	
Address of depositary institution (including postal code and country) 12301 Parklawn Drive Rockville, Maryland 20852 United States of America	
Date of deposit May 15, 1997	Accession Number 209045
C. ADDITIONAL INDICATIONS (leave blank if not applicable) This information is continued on an additional sheet <input type="checkbox"/>	
D. DESIGNATED STATES FOR WHICH INDICATIONS ARE MADE (If the indications are not for all designated States)	
E. SEPARATE FURNISHING OF INDICATIONS (leave blank if not applicable)	
The indications listed below will be submitted to the International Bureau later (specify the general nature of the indications, e.g., "Accession Number of Deposit")	

<div style="text-align: center;">For receiving Office use only</div> <div style="padding: 10px;"><input checked="checked" type="checkbox"/> This sheet was received with the international application</div> <div style="padding: 5px;">Authorized officer <div style="text-align: center;">Susan White POT International Division</div></div>	<div style="text-align: center;">For International Bureau use only</div> <div style="padding: 10px;"><input type="checkbox"/> This sheet was received by the International Bureau on:</div> <div style="padding: 5px;">Authorized officer</div>
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INDICATIONS RELATING TO A DEPOSITED MICROORGANISM

(PCT Rule 13bis)

A. The indications made below relate to the microorganism referred to in the description on page <u>130</u> , line <u>N/A</u>	
B. IDENTIFICATION OF DEPOSIT Further deposits are identified on an additional sheet <input type="checkbox"/>	
Name of depositary institution <div style="text-align: center;">American Type Culture Collection</div>	
Address of depositary institution (including postal code and country) 12301 Parklawn Drive Rockville, Maryland 20852 United States of America	
Date of deposit April 28, 1997	Accession Number 209011
C. ADDITIONAL INDICATIONS (leave blank if not applicable) This information is continued on an additional sheet <input type="checkbox"/>	
D. DESIGNATED STATES FOR WHICH INDICATIONS ARE MADE (if the indications are not for all designated States)	
E. SEPARATE FURNISHING OF INDICATIONS (leave blank if not applicable)	
The indications listed below will be submitted to the International Bureau later (specify the general nature of the indications, e.g., "Accession Number of Deposit")	

<div style="border-bottom: 1px solid black; margin-bottom: 5px;">For receiving Office use only</div> <div style="display: flex; align-items: center; margin-bottom: 10px;"><input checked="checked" type="checkbox"/> This sheet was received with the international application</div> <div style="border-bottom: 1px solid black; margin-bottom: 10px;">Authorized officer</div> <div style="text-align: center;">Susan White PCT International Division</div>	<div style="border-bottom: 1px solid black; margin-bottom: 5px;">For International Bureau use only</div> <div style="display: flex; align-items: center; margin-bottom: 10px;"><input type="checkbox"/> This sheet was received by the International Bureau on:</div> <div style="border-bottom: 1px solid black; margin-bottom: 10px;">Authorized officer</div>
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INDICATIONS RELATING TO A DEPOSITED MICROORGANISM

(PCT Rule 13bis)

A. The indications made below relate to the microorganism referred to in the description on page <u>131</u> , line <u>N/A</u>	
B. IDENTIFICATION OF DEPOSIT Further deposits are identified on an additional sheet <input type="checkbox"/>	
Name of depositary institution <p style="text-align: center;">American Type Culture Collection</p>	
Address of depositary institution (including postal code and country) 12301 Parklawn Drive Rockville, Maryland 20852 United States of America	
Date of deposit February 26, 1997	Accession Number 97900
C. ADDITIONAL INDICATIONS (leave blank if not applicable) This information is continued on an additional sheet <input type="checkbox"/>	
D. DESIGNATED STATES FOR WHICH INDICATIONS ARE MADE (If the indications are not for all designated States)	
E. SEPARATE FURNISHING OF INDICATIONS (leave blank if not applicable)	
The indications listed below will be submitted to the International Bureau later (specify the general nature of the indications, e.g., "Accession Number of Deposit")	

<p style="text-align: center;">For receiving Office use only</p> <div style="border: 1px solid black; padding: 5px; margin-bottom: 5px;"> <input checked="" type="checkbox"/> This sheet was received with the international application </div> <div style="border: 1px solid black; padding: 5px;"> Authorized officer <p style="text-align: center;">Susan White PCT International Division</p> </div>	<p style="text-align: center;">For International Bureau use only</p> <div style="border: 1px solid black; padding: 5px; margin-bottom: 5px;"> <input type="checkbox"/> This sheet was received by the International Bureau on: </div> <div style="border: 1px solid black; padding: 5px;"> Authorized officer </div>
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INDICATIONS RELATING TO A DEPOSITED MICROORGANISM

(PCT Rule 13bis)

A. The indications made below relate to the microorganism referred to in the description on page <u>137</u> , line <u>N/A</u>	
B. IDENTIFICATION OF DEPOSIT Further deposits are identified on an additional sheet <input type="checkbox"/>	
Name of depositary institution <div style="text-align: center;">American Type Culture Collection</div>	
Address of depositary institution (including postal code and country) 12301 Parklawn Drive Rockville, Maryland 20852 United States of America	
Date of deposit February 26, 1997	Accession Number 97901
C. ADDITIONAL INDICATIONS (leave blank if not applicable) This information is continued on an additional sheet <input type="checkbox"/>	
D. DESIGNATED STATES FOR WHICH INDICATIONS ARE MADE (if the indications are not for all designated States)	
E. SEPARATE FURNISHING OF INDICATIONS (leave blank if not applicable)	
The indications listed below will be submitted to the International Bureau later (specify the general nature of the indications, e.g., "Accession Number of Deposit")	

<div style="border-bottom: 1px solid black; margin-bottom: 5px;">For receiving Office use only</div> <div style="display: flex; align-items: center; margin-bottom: 10px;"><input checked="checked" type="checkbox"/> This sheet was received with the international application</div> <div style="display: flex; justify-content: space-between; margin-top: 10px;"><div style="width: 60%;">Authorized officer</div><div style="text-align: center;">Susan White PCT International Division</div></div>	<div style="border-bottom: 1px solid black; margin-bottom: 5px;">For International Bureau use only</div> <div style="display: flex; align-items: center; margin-bottom: 10px;"><input type="checkbox"/> This sheet was received by the International Bureau on:</div> <div style="display: flex; justify-content: space-between; margin-top: 10px;"><div style="width: 60%;">Authorized officer</div><div></div></div>
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INDICATIONS RELATING TO A DEPOSITED MICROORGANISM

(PCT Rule 13bis)

A. The indications made below relate to the microorganism referred to in the description on page <u>131</u> , line <u>N/A</u>	
B. IDENTIFICATION OF DEPOSIT Further deposits are identified on an additional sheet <input type="checkbox"/>	
Name of depositary institution <div style="text-align: center;">American Type Culture Collection</div>	
Address of depositary institution (including postal code and country) 12301 Parklawn Drive Rockville, Maryland 20852 United States of America	
Date of deposit May 15, 1997	Accession Number 209046
C. ADDITIONAL INDICATIONS (leave blank if not applicable) This information is continued on an additional sheet <input type="checkbox"/>	
D. DESIGNATED STATES FOR WHICH INDICATIONS ARE MADE (if the indications are not for all designated States)	
E. SEPARATE FURNISHING OF INDICATIONS (leave blank if not applicable)	
The indications listed below will be submitted to the International Bureau later (specify the general nature of the indications, e.g., "Accession Number of Deposit")	

<div style="border-bottom: 1px solid black; margin-bottom: 5px;">For receiving Office use only</div> <div style="display: flex; align-items: center; margin-bottom: 10px;"><input checked="checked" type="checkbox"/> This sheet was received with the international application</div> <div style="border-bottom: 1px solid black; margin-bottom: 10px;">Authorized officer</div> <div style="text-align: center;">Susan White PCT International Division</div>	<div style="border-bottom: 1px solid black; margin-bottom: 5px;">For International Bureau use only</div> <div style="display: flex; align-items: center; margin-bottom: 10px;"><input type="checkbox"/> This sheet was received by the International Bureau on:</div> <div style="border-bottom: 1px solid black; margin-bottom: 10px;">Authorized officer</div>
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INDICATIONS RELATING TO A DEPOSITED MICROORGANISM

(PCT Rule 13bis)

A. The indications made below relate to the microorganism referred to in the description on page <u>137</u> , line <u>N/A</u>	
B. IDENTIFICATION OF DEPOSIT Further deposits are identified on an additional sheet <input type="checkbox"/>	
Name of depositary institution <div style="text-align: center;">American Type Culture Collection</div>	
Address of depositary institution (including postal code and country) 12301 Parklawn Drive Rockville, Maryland 20852 United States of America	
Date of deposit May 15, 1997	Accession Number 209047
C. ADDITIONAL INDICATIONS (leave blank if not applicable) This information is continued on an additional sheet <input type="checkbox"/>	
D. DESIGNATED STATES FOR WHICH INDICATIONS ARE MADE (if the indications are not for all designated States)	
E. SEPARATE FURNISHING OF INDICATIONS (leave blank if not applicable)	
The indications listed below will be submitted to the International Bureau later (specify the general nature of the indications, e.g., "Accession Number of Deposit")	

<div style="text-align: center; border-bottom: 1px solid black;">For receiving Office use only</div> <div style="padding: 10px;"><input checked="checked" type="checkbox"/> This sheet was received with the international application</div> <div style="border-top: 1px solid black; padding: 5px;">Authorized officer Susan White PCT International Division</div>	<div style="text-align: center; border-bottom: 1px solid black;">For International Bureau use only</div> <div style="padding: 10px;"><input type="checkbox"/> This sheet was received by the International Bureau on:</div> <div style="border-top: 1px solid black; padding: 5px;">Authorized officer</div>
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INDICATIONS RELATING TO A DEPOSITED MICROORGANISM

(PCT Rule 13bis)

A. The indications made below relate to the microorganism referred to in the description on page <u>137</u> , line <u>N/A</u>	
B. IDENTIFICATION OF DEPOSIT Further deposits are identified on an additional sheet <input type="checkbox"/>	
Name of depositary institution <div style="text-align: center;">American Type Culture Collection</div>	
Address of depositary institution (including postal code and country) 12301 Parklawn Drive Rockville, Maryland 20852 United States of America	
Date of deposit May 22, 1997	Accession Number 209076
C. ADDITIONAL INDICATIONS (leave blank if not applicable) This information is continued on an additional sheet <input type="checkbox"/>	
D. DESIGNATED STATES FOR WHICH INDICATIONS ARE MADE (if the indications are not for all designated States)	
E. SEPARATE FURNISHING OF INDICATIONS (leave blank if not applicable)	
The indications listed below will be submitted to the International Bureau later (specify the general nature of the indications, e.g., "Accession Number of Deposit")	

For receiving Office use only	For International Bureau use only
<input checked="checked" type="checkbox"/> This sheet was received with the international application	<input type="checkbox"/> This sheet was received by the International Bureau on
Authorized officer <div style="text-align: center;">Susan White PCT International Division</div>	Authorized officer

INDICATIONS RELATING TO A DEPOSITED MICROORGANISM

(PCT Rule 13bis)

A. The indications made below relate to the microorganism referred to in the description on page <u>140</u> , line <u>N/A</u>	
B. IDENTIFICATION OF DEPOSIT Further deposits are identified on an additional sheet <input type="checkbox"/>	
Name of depositary institution <div style="text-align: center;">American Type Culture Collection</div>	
Address of depositary institution (including postal code and country) 12301 Parklawn Drive Rockville, Maryland 20852 .. United States of America	
Date of deposit August 21, 1997	Accession Number 209215
C. ADDITIONAL INDICATIONS (leave blank if not applicable) This information is continued on an additional sheet <input type="checkbox"/>	
D. DESIGNATED STATES FOR WHICH INDICATIONS ARE MADE (if the indications are not for all designated States)	
E. SEPARATE FURNISHING OF INDICATIONS (leave blank if not applicable)	
The indications listed below will be submitted to the International Bureau later (specify the general nature of the indications, e.g., "Accession Number of Deposit")	

<div style="border-bottom: 1px solid black; margin-bottom: 5px;">For receiving Office use only</div> <div style="display: flex; align-items: center; margin-bottom: 10px;"><input checked="checked" type="checkbox"/> This sheet was received with the international application</div> <div style="border-bottom: 1px solid black; margin-bottom: 10px;">Authorized officer</div> <div style="text-align: center;">Susan White PCT International Division</div>	<div style="border-bottom: 1px solid black; margin-bottom: 5px;">For International Bureau use only</div> <div style="display: flex; align-items: center; margin-bottom: 10px;"><input type="checkbox"/> This sheet was received by the International Bureau on:</div> <div style="border-bottom: 1px solid black; margin-bottom: 10px;">Authorized officer</div>
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INDICATIONS RELATING TO A DEPOSITED MICROORGANISM

(PCT Rule 13bis)

A. The indications made below relate to the microorganism referred to in the description on page <u>160</u> , line <u>N/A</u>	
B. IDENTIFICATION OF DEPOSIT Further deposits are identified on an additional sheet <input type="checkbox"/>	
Name of depositary institution <div style="text-align: center;">American Type Culture Collection</div>	
Address of depositary institution (including postal code and country) 12301 Parklawn Drive Rockville, Maryland 20852 United States of America	
Date of deposit February 26, 1997	Accession Number 97904
C. ADDITIONAL INDICATIONS (leave blank if not applicable) This information is continued on an additional sheet <input type="checkbox"/>	
D. DESIGNATED STATES FOR WHICH INDICATIONS ARE MADE (if the indications are not for all designated States)	
E. SEPARATE FURNISHING OF INDICATIONS (leave blank if not applicable)	
The indications listed below will be submitted to the International Bureau later (specify the general nature of the indications, e.g., "Accession Number of Deposit")	

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INDICATIONS RELATING TO A DEPOSITED MICROORGANISM

(PCT Rule 13bis)

A. The indications made below relate to the microorganism referred to in the description on page <u>154</u> , line <u>N/A</u>	
B. IDENTIFICATION OF DEPOSIT Further deposits are identified on an additional sheet <input type="checkbox"/>	
Name of depositary institution <div style="text-align: center;">American Type Culture Collection</div>	
Address of depositary institution (including postal code and country) 12301 Parklawn Drive Rockville, Maryland 20852 United States of America	
Date of deposit July 3, 1997	Accession Number 209139
C. ADDITIONAL INDICATIONS (leave blank if not applicable) This information is continued on an additional sheet <input type="checkbox"/>	
D. DESIGNATED STATES FOR WHICH INDICATIONS ARE MADE (if the indications are not for all designated States)	
E. SEPARATE FURNISHING OF INDICATIONS (leave blank if not applicable)	
The indications listed below will be submitted to the International Bureau later (specify the general nature of the indications, e.g., "Accession Number of Deposit")	

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INDICATIONS RELATING TO A DEPOSITED MICROORGANISM

(PCT Rule 13bis)

A. The indications made below relate to the microorganism referred to in the description on page <u>153</u> , line <u>N/A</u>	
B. IDENTIFICATION OF DEPOSIT Further deposits are identified on an additional sheet <input type="checkbox"/>	
Name of depositary institution <div style="text-align: center;">American Type Culture Collection</div>	
Address of depositary institution (including postal code and country) 12301 Parklawn Drive Rockville, Maryland 20852 United States of America	
Date of deposit May 15, 1997	Accession Number 209049
C. ADDITIONAL INDICATIONS (leave blank if not applicable) This information is continued on an additional sheet <input type="checkbox"/>	
D. DESIGNATED STATES FOR WHICH INDICATIONS ARE MADE (if the indications are not for all designated States)	
E. SEPARATE FURNISHING OF INDICATIONS (leave blank if not applicable)	
The indications listed below will be submitted to the International Bureau later (specify the general nature of the indications, e.g., "Accession Number of Deposit")	

<div style="text-align: center; border-bottom: 1px solid black; margin-bottom: 5px;">For receiving Office use only</div> <div style="padding: 5px;"><input checked="checked" type="checkbox"/> This sheet was received with the international application</div> <div style="padding: 5px;">Authorized officer <div style="text-align: center; margin-top: 10px;">Susan White PCT International Division</div></div>	<div style="text-align: center; border-bottom: 1px solid black; margin-bottom: 5px;">For International Bureau use only</div> <div style="padding: 5px;"><input type="checkbox"/> This sheet was received by the International Bureau on:</div> <div style="padding: 5px;">Authorized officer</div>
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INDICATIONS RELATING TO A DEPOSITED MICROORGANISM

(PCT Rule 13bis)

A. The indications made below relate to the microorganism referred to in the description on page <u>153</u> , line <u>N/A</u>	
B. IDENTIFICATION OF DEPOSIT Further deposits are identified on an additional sheet <input type="checkbox"/>	
Name of depositary institution <div style="text-align: center;">American Type Culture Collection</div>	
Address of depositary institution (including postal code and country) 12301 Parklawn Drive Rockville, Maryland 20852 United States of America	
Date of deposit February 26, 1997	Accession Number 97903
C. ADDITIONAL INDICATIONS (leave blank if not applicable) This information is continued on an additional sheet <input type="checkbox"/>	
D. DESIGNATED STATES FOR WHICH INDICATIONS ARE MADE (if the indications are not for all designated States)	
E. SEPARATE FURNISHING OF INDICATIONS (leave blank if not applicable)	
The indications listed below will be submitted to the International Bureau later (specify the general nature of the indications, e.g., "Accession Number of Deposit")	

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INDICATIONS RELATING TO A DEPOSITED MICROORGANISM

(PCT Rule 13bis)

A. The indications made below relate to the microorganism referred to in the description on page <u>142</u> , line <u>N/A</u>	
B. IDENTIFICATION OF DEPOSIT Further deposits are identified on an additional sheet <input type="checkbox"/>	
Name of depositary institution <p style="text-align: center;">American Type Culture Collection</p>	
Address of depositary institution (including postal code and country) 12301 Parklawn Drive Rockville, Maryland 20852 United States of America	
Date of deposit <u>June 12, 1997</u>	Accession Number <u>209119</u>
C. ADDITIONAL INDICATIONS (leave blank if not applicable) This information is continued on an additional sheet <input type="checkbox"/>	
D. DESIGNATED STATES FOR WHICH INDICATIONS ARE MADE (if the indications are not for all designated States)	
E. SEPARATE FURNISHING OF INDICATIONS (leave blank if not applicable)	
The indications listed below will be submitted to the International Bureau later (specify the general nature of the indications, e.g., "Accession Number of Deposit")	

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INDICATIONS RELATING TO A DEPOSITED MICROORGANISM

(PCT Rule 13bis)

A. The indications made below relate to the microorganism referred to in the description on page <u>146</u> , line <u>N/A</u>	
B. IDENTIFICATION OF DEPOSIT Further deposits are identified on an additional sheet <input type="checkbox"/>	
Name of depositary institution <div style="text-align: center;">American Type Culture Collection</div>	
Address of depositary institution (including postal code and country) 12301 Parklawn Drive Rockville, Maryland 20852 United States of America	
Date of deposit February 26, 1997	Accession Number 97902
C. ADDITIONAL INDICATIONS (leave blank if not applicable) This information is continued on an additional sheet <input type="checkbox"/>	
D. DESIGNATED STATES FOR WHICH INDICATIONS ARE MADE (if the indications are not for all designated States)	
E. SEPARATE FURNISHING OF INDICATIONS (leave blank if not applicable)	
The indications listed below will be submitted to the International Bureau later (specify the general nature of the indications, e.g., "Accession Number of Deposit")	

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INDICATIONS RELATING TO A DEPOSITED MICROORGANISM

(PCT Rule 13bis)

A. The indications made below relate to the microorganism referred to in the description on page <u>146</u> , line <u>N/A</u>	
B. IDENTIFICATION OF DEPOSIT Further deposits are identified on an additional sheet <input type="checkbox"/>	
Name of depositary institution <div style="text-align: center;">American Type Culture Collection</div>	
Address of depositary institution (including postal code and country) 12301 Parklawn Drive Rockville, Maryland 20852 United States of America	
Date of deposit May 15, 1997	Accession Number 209048
C. ADDITIONAL INDICATIONS (leave blank if not applicable) This information is continued on an additional sheet <input type="checkbox"/>	
D. DESIGNATED STATES FOR WHICH INDICATIONS ARE MADE (if the indications are not for all designated States)	
E. SEPARATE FURNISHING OF INDICATIONS (leave blank if not applicable)	
The indications listed below will be submitted to the International Bureau later (specify the general nature of the indications, e.g., "Accession Number of Deposit")	

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INDICATIONS RELATING TO A DEPOSITED MICROORGANISM

(PCT Rule 13bis)

A. The indications made below relate to the microorganism referred to in the description on page <u>160</u> , line <u>N/A</u>	
B. IDENTIFICATION OF DEPOSIT Further deposits are identified on an additional sheet <input type="checkbox"/>	
Name of depositary institution <div style="text-align: center;">American Type Culture Collection</div>	
Address of depositary institution (including postal code and country) 12301 Parklawn Drive Rockville, Maryland 20852 United States of America	
Date of deposit May 15, 1997	Accession Number 209050
C. ADDITIONAL INDICATIONS (leave blank if not applicable) This information is continued on an additional sheet <input type="checkbox"/>	
D. DESIGNATED STATES FOR WHICH INDICATIONS ARE MADE (if the indications are not for all designated States)	
E. SEPARATE FURNISHING OF INDICATIONS (leave blank if not applicable)	
The indications listed below will be submitted to the International Bureau later (specify the general nature of the indications, e.g., "Accession Number of Deposit")	

<div style="border-bottom: 1px solid black; margin-bottom: 5px;">For receiving Office use only</div> <div style="display: flex; align-items: center; margin-bottom: 10px;"><input checked="checked" type="checkbox"/> This sheet was received with the international application</div> <div style="border-top: 1px solid black; padding-top: 5px;">Authorized officer <div style="text-align: center;">Susan White PCT International Division</div></div>	<div style="border-bottom: 1px solid black; margin-bottom: 5px;">For International Bureau use only</div> <div style="display: flex; align-items: center; margin-bottom: 10px;"><input type="checkbox"/> This sheet was received by the International Bureau on:</div> <div style="border-top: 1px solid black; padding-top: 5px;">Authorized officer</div>
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INDICATIONS RELATING TO A DEPOSITED MICROORGANISM

(PCT Rule 13bis)

A. The indications made below relate to the microorganism referred to in the description on page <u>142</u> , line <u>N/A</u>	
B. IDENTIFICATION OF DEPOSIT Further deposits are identified on an additional sheet <input checked="" type="checkbox"/>	
Name of depositary institution <u>American Type Culture Collection</u>	
Address of depositary institution (including postal code and country) <u>12301 Parklawn Drive</u> <u>Rockville, Maryland 20852</u> <u>United States of America</u>	
Date of deposit <u>February 12, 1998</u>	Accession Number <u>209627</u>
C. ADDITIONAL INDICATIONS (leave blank if not applicable) This information is continued on an additional sheet <input type="checkbox"/>	
D. DESIGNATED STATES FOR WHICH INDICATIONS ARE MADE (If the indications are not for all designated States)	
E. SEPARATE FURNISHING OF INDICATIONS (leave blank if not applicable)	
The indications listed below will be submitted to the International Bureau later (specify the general nature of the indications, e.g., "Accession Number of Deposit") 	

For receiving Office use only	For International Bureau use only
<input checked="" type="checkbox"/> This sheet was received with the international application	<input type="checkbox"/> This sheet was received by the International Bureau on:
Authorized officer Susan White PCT International Division	Authorized officer

What Is Claimed Is:

1. An isolated nucleic acid molecule comprising a polynucleotide having a nucleotide sequence at least 95% identical to a sequence selected from the group
5 consisting of:

(a) a polynucleotide fragment of SEQ ID NO:X or a polynucleotide fragment of the cDNA sequence included in ATCC Deposit No:Z, which is hybridizable to SEQ ID NO:X;

10 (b) a polynucleotide encoding a polypeptide fragment of SEQ ID NO:Y or a polypeptide fragment encoded by the cDNA sequence included in ATCC Deposit No:Z, which is hybridizable to SEQ ID NO:X;

(c) a polynucleotide encoding a polypeptide domain of SEQ ID NO:Y or a polypeptide domain encoded by the cDNA sequence included in ATCC Deposit No:Z, which is hybridizable to SEQ ID NO:X;

15 (d) a polynucleotide encoding a polypeptide epitope of SEQ ID NO:Y or a polypeptide epitope encoded by the cDNA sequence included in ATCC Deposit No:Z, which is hybridizable to SEQ ID NO:X;

(e) a polynucleotide encoding a polypeptide of SEQ ID NO:Y or the cDNA sequence included in ATCC Deposit No:Z, which is hybridizable to SEQ ID NO:X,
20 having biological activity;

(f) a polynucleotide which is a variant of SEQ ID NO:X;

(g) a polynucleotide which is an allelic variant of SEQ ID NO:X;

(h) a polynucleotide which encodes a species homologue of the SEQ ID NO:Y;

25 (i) a polynucleotide capable of hybridizing under stringent conditions to any one of the polynucleotides specified in (a)-(h), wherein said polynucleotide does not hybridize under stringent conditions to a nucleic acid molecule having a nucleotide sequence of only A residues or of only T residues.

2. The isolated nucleic acid molecule of claim 1, wherein the
30 polynucleotide fragment comprises a nucleotide sequence encoding a secreted protein.

3. The isolated nucleic acid molecule of claim 1, wherein the polynucleotide fragment comprises a nucleotide sequence encoding the sequence identified as SEQ ID NO:Y or the polypeptide encoded by the cDNA sequence included
35 in ATCC Deposit No:Z, which is hybridizable to SEQ ID NO:X.

4. The isolated nucleic acid molecule of claim 1, wherein the polynucleotide fragment comprises the entire nucleotide sequence of SEQ ID NO:X or the cDNA sequence included in ATCC Deposit No:Z, which is hybridizable to SEQ ID NO:X.

5. The isolated nucleic acid molecule of claim 2, wherein the nucleotide sequence comprises sequential nucleotide deletions from either the C-terminus or the N-terminus.

6. The isolated nucleic acid molecule of claim 3, wherein the nucleotide sequence comprises sequential nucleotide deletions from either the C-terminus or the N-terminus.

7. A recombinant vector comprising the isolated nucleic acid molecule of claim 1.

8. A method of making a recombinant host cell comprising the isolated nucleic acid molecule of claim 1.

9. A recombinant host cell produced by the method of claim 8.

10. The recombinant host cell of claim 9 comprising vector sequences.

11. An isolated polypeptide comprising an amino acid sequence at least 95% identical to a sequence selected from the group consisting of:

(a) a polypeptide fragment of SEQ ID NO:Y or the encoded sequence included in ATCC Deposit No:Z;

(b) a polypeptide fragment of SEQ ID NO:Y or the encoded sequence included in ATCC Deposit No:Z, having biological activity;

(c) a polypeptide domain of SEQ ID NO:Y or the encoded sequence included in ATCC Deposit No:Z;

(d) a polypeptide epitope of SEQ ID NO:Y or the encoded sequence included in ATCC Deposit No:Z;

(e) a secreted form of SEQ ID NO:Y or the encoded sequence included in ATCC Deposit No:Z;

(f) a full length protein of SEQ ID NO:Y or the encoded sequence included in ATCC Deposit No:Z;

- (g) a variant of SEQ ID NO:Y;
- (h) an allelic variant of SEQ ID NO:Y; or
- (i) a species homologue of the SEQ ID NO:Y.

12. The isolated polypeptide of claim 11, wherein the secreted form or the
5 full length protein comprises sequential amino acid deletions from either the C-terminus
or the N-terminus.

13. An isolated antibody that binds specifically to the isolated polypeptide of
claim 11.

10

14. A recombinant host cell that expresses the isolated polypeptide of claim
11.

15. A method of making an isolated polypeptide comprising:

15

- (a) culturing the recombinant host cell of claim 14 under conditions such that
said polypeptide is expressed; and
- (b) recovering said polypeptide.

16. The polypeptide produced by claim 15.

20

17. A method for preventing, treating, or ameliorating a medical condition,
comprising administering to a mammalian subject a therapeutically effective amount of
the polypeptide of claim 11 or the polynucleotide of claim 1.

25

18. A method of diagnosing a pathological condition or a susceptibility to a
pathological condition in a subject comprising:

(a) determining the presence or absence of a mutation in the polynucleotide of
claim 1; and

30

(b) diagnosing a pathological condition or a susceptibility to a pathological
condition based on the presence or absence of said mutation.

19. A method of diagnosing a pathological condition or a susceptibility to a
pathological condition in a subject comprising:

35

(a) determining the presence or amount of expression of the polypeptide of
claim 11 in a biological sample; and

(b) diagnosing a pathological condition or a susceptibility to a pathological
condition based on the presence or amount of expression of the polypeptide.

20. A method for identifying a binding partner to the polypeptide of claim 11 comprising:

- 5 (a) contacting the polypeptide of claim 11 with a binding partner; and
(b) determining whether the binding partner effects an activity of the polypeptide.

21. The gene corresponding to the cDNA sequence of SEQ ID NO:Y.

10 22. A method of identifying an activity in a biological assay, wherein the method comprises:

- (a) expressing SEQ ID NO:X in a cell;
(b) isolating the supernatant;
(c) detecting an activity in a biological assay; and
15 (d) identifying the protein in the supernatant having the activity.

23. The product produced by the method of claim 22.